

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:07 ; Search time 142 Seconds
(without alignments)
18.565 Million cell updates/sec

Title: US-10-660-118a-2

Sequence: 1 XCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	4	AA011508	Aar11508 Thioresox
2	31	100.0	4	AA009052	Aar09052 Thioresox
3	31	100.0	4	AA013337	Aar13337 Human Trx
4	31	100.0	4	AA049348	Aay49348 Active-si
5	31	100.0	4	ABP56403	Abp56403 Thioresox
6	31	100.0	4	AA022593	Aao22593 Redox act
7	31	100.0	4	ABG32509	Abg32509 M. tuberc
8	31	100.0	4	AAU97916	Aau97916 Tetrapept
9	31	100.0	4	AB005573	Ab005573 Dithiol p
10	31	100.0	4	AAE37340	Aae37340 E. coli t
11	31	100.0	4	ADJ47607	Adj47607 Trx catal
12	31	100.0	4	ADM32927	Adm32927 Amino aci
13	31	100.0	4	ADR46076	Adr46076 Antioxida
14	31	100.0	4	ADV11816	Adv11816 Thioresox
15	31	100.0	4	ADW97624	Adw97624 Human thi
16	31	100.0	4	ADY81685	Ady81685 Thioresox
17	31	100.0	5	AA078911	Aay78911 Thioresox
18	31	100.0	5	AA05156	Aao5156 Human thi
19	31	100.0	5	AA021523	Aao21523 Wild type
20	31	100.0	5	ABP71301	Abp71301 Thioresox
21	31	100.0	6	ABP71087	Abp71087 Sequence
22	31	100.0	6	ABP54936	Abp54936 Active si
23	31	100.0	6	ADA08451	Ada08451 Mammalian
24	31	100.0	6	ADH05024	Adh05024 Target pe

25	31	100.0	6	ADM32929	Adm32929 Amino aci
26	31	100.0	6	ADM32928	Adm32928 Amino aci
27	31	100.0	6	ADP87509	Adp87509 Thioresox
28	31	100.0	6	ADP67423	Adp67423 Thioresox
29	31	100.0	6	ADP97008	Adp97008 Thioresox
30	31	100.0	8	ADP50203	Adp50203 Sequence
31	31	100.0	8	ADC81369	Adc81369 Bovin THR
32	31	100.0	8	AAW05002	Aaw05002 Thymic hu
33	31	100.0	8	AA041664	Aa041664 Immunomod
34	31	100.0	8	ADH05029	Adh05029 Target pe
35	31	100.0	8	ADV60194	Adv60194 VEGF pept
36	31	100.0	8	ADZ28911	Adz28911 Calmoduli
37	31	100.0	9	ADV60195	Adv60195 VEGF pept
38	31	100.0	10	AA050846	Aa050846 Cyclic pe
39	31	100.0	10	AA050868	Aa050868 Cyclic pe
40	31	100.0	10	AA050834	Aa050834 Cyclic pe
41	31	100.0	10	AA050895	Aa050895 Cyclic pe
42	31	100.0	10	AA050830	Aa050830 Cyclic pe
43	31	100.0	10	AA094724	Aag94724 Human com
44	31	100.0	10	AA094776	Aag94776 Human com
45	31	100.0	10	AA086916	Aag86916 Saccharom
46	31	100.0	10	AA086918	Aag86918 Saccharom
47	31	100.0	10	ADV60196	Adv60196 VEGF pept
48	31	100.0	12	AAW45003	Aaw45003 Immunomod
49	31	100.0	12	AA094929	Aay94929 Immunoad
50	31	100.0	12	ADV60191	Adv60191 VEGF pept
51	31	100.0	13	ADV60192	Adv60192 VEGF pept
52	31	100.0	14	ADV60193	Adv60193 VEGF pept
53	31	100.0	14	ADM28625	Adm28625 VEGF165 e
54	31	100.0	17	ADV54876	Adv54876 G protein
55	31	100.0	17	ADV54992	Adv54992 G protein
56	31	100.0	17	ADV55097	Adv55097 G protein
57	31	100.0	19	AA023038	Aae23038 Human thi
58	31	100.0	20	ADV60188	Adv60188 VEGF pept
59	31	100.0	21	ADV60189	Adv60189 VEGF pept
60	31	100.0	23	AA038160	Aab38160 Human sec
61	31	100.0	24	ADV55042	Adv55042 G protein
62	31	100.0	24	ADV56216	Adv56216 G protein
63	31	100.0	24	ADV53880	Adv53880 G protein
64	31	100.0	24	ADV54929	Adv54929 G protein
65	31	100.0	24	ADV55148	Adv55148 G protein
66	31	100.0	25	AA038027	Aab38027 Fragment
67	31	100.0	25	ADV55146	Adv55146 G protein
68	31	100.0	25	ADV55040	Adv55040 G protein
69	31	100.0	25	ADV54928	Adv54928 G protein
70	31	100.0	28	ADC89744	Adc89744 Cyclic VE
71	31	100.0	29	AAU75045	Aau75045 Retrovira
72	31	100.0	29	ADV60190	Adv60190 VEGF pept
73	31	100.0	30	AAU75030	Aau75030 4070A amp
74	31	100.0	32	AA020162	Aam20162 Peptide #
75	31	100.0	32	AB040402	Ab040402 Peptide #
76	31	100.0	32	AA041108	Aam41108 Peptide #
77	31	100.0	32	AB024771	Abb24771 Protein #
78	31	100.0	32	AA073929	Aam73929 Human bon
79	31	100.0	32	AA061210	Aam61210 Human bira
80	31	100.0	32	AB055681	Ab055681 Human liv
81	31	100.0	32	AB043817	Ab043817 Human pep
82	31	100.0	35	AA060793	Aab60793 Androcton
83	31	100.0	35	AD112462	Adi12462 Moroccan
84	31	100.0	35	ADH089473	Adh089473 Moroccan
85	31	100.0	37	AAU08671	Aau08671 Thioresox
86	31	100.0	37	AB007837	Abb07837 Amino aci
87	31	100.0	37	AD112460	Adi12460 Moroccan
88	31	100.0	37	ADH089471	Adh089471 Moroccan
89	31	100.0	42	AB021076	Abb21076 Novel hum
90	31	100.0	42	AA015659	Aam15659 Peptide #
91	31	100.0	43	AB034663	Abb34663 Peptide #
92	31	100.0	43	AA028160	Aam28160 Peptide #
93	31	100.0	43	AB029484	Abb29484 Peptide #
94	31	100.0	43	AB020069	Abb20069 Protein #
95	31	100.0	43	AA067841	Aam67841 Human bon
96	31	100.0	43	AA055452	Aam55452 Human bira
97	31	100.0	43	AB049482	Abb49482 Human liv

390	31	100.0	111	5	ABP77457	Fungi str	463	31	100.0	122	7	AAE39920	AAE39920	Barley th
391	31	100.0	111	8	ADM80195	Human NOV	464	31	100.0	122	7	AAE39923	AAE39923	Barley H-
392	31	100.0	111	7	ADM60336	Staphyloc	465	31	100.0	122	7	ADF04112	ADF04112	Bacterial
393	31	100.0	111	8	ADR49062	Thiodendox	466	31	100.0	122	7	ADOS9274	ADOS9274	Rice thio
394	31	100.0	111	9	ABE39008	L. pneumo	467	31	100.0	122	7	ADOS9272	ADOS9272	Barley th
395	31	100.0	112	4	AAW25652	Human pro	468	31	100.0	123	3	AAE70482	AAE70482	Glycine m
396	31	100.0	112	4	AAU32348	Novel hum	469	31	100.0	123	3	AAE26780	AAE26780	Zea mays
397	31	100.0	112	5	ABP60738	Chlamydom	470	31	100.0	123	4	AAU64379	AAU64379	Propionib
398	31	100.0	112	5	ABP60780	Mycobacte	471	31	100.0	123	4	AAE37102	AAE37102	Wheat Tar
399	31	100.0	112	5	ABG60236	Human Th1	472	31	100.0	123	5	ABP65992	ABP65992	BLITCobac
400	31	100.0	112	5	AAU91276	Human NOV	473	31	100.0	123	6	ABM60798	ABM60798	Propionib
401	31	100.0	112	5	AAU78664	Human NOV	474	31	100.0	124	4	AAE78905	AAE78905	C. glutam
402	31	100.0	112	7	ADC97112	E. faeciu	475	31	100.0	124	4	AAE93165	AAE93165	C. glutam
403	31	100.0	112	8	ADT04590	Luteinisi	476	31	100.0	124	7	ADD13226	ADD13226	C. glutam
404	31	100.0	112	8	ADM07462	Human lut	477	31	100.0	124	7	ABO61500	ABO61500	Klebsatell
405	31	100.0	113	5	ABP52004	NOVGON ho	478	31	100.0	125	3	AAE17574	AAE17574	Arabidops
406	31	100.0	113	6	ABP56107	Human IGF	479	31	100.0	125	5	ABP60741	ABP60741	Picea mar
407	31	100.0	113	7	ADB65045	Human pro	480	31	100.0	125	7	ADOS9273	ADOS9273	Wheat th
408	31	100.0	113	7	ADM04461	Human pro	481	31	100.0	125	7	ABM55633	ABM55633	Human pro
409	31	100.0	113	8	ADM82093	Equine gr1	482	31	100.0	125	8	ADP07816	ADP07816	Human sec
410	31	100.0	114	3	AAE08114	Arabidops	483	31	100.0	125	9	ABM95048	ABM95048	M. xanthu
411	31	100.0	114	3	AAE54021	Arabidops	484	31	100.0	126	5	ABP60743	ABP60743	Triticum
412	31	100.0	114	4	AAU04622	Human lut	485	31	100.0	126	5	ABP60730	ABP60730	Nicotiana
413	31	100.0	114	4	AAE04494	Human lut	486	31	100.0	126	7	ADOS9275	ADOS9275	Tobacco t
414	31	100.0	114	5	ABP60696	Arabidops	487	31	100.0	126	8	ADQ39499	ADQ39499	Human myo
415	31	100.0	114	5	ABP60680	Phaseolin	488	31	100.0	126	8	AAE93016	AAE93016	Soft whea
416	31	100.0	114	5	ABP60727	Arabidops	489	31	100.0	127	2	AAW44907	AAW44907	Polyprol
417	31	100.0	114	5	ABG32916	Arabidops	490	31	100.0	127	3	AAE29248	AAE29248	Wheat th
418	31	100.0	114	5	ADOS9276	Arabidops	491	31	100.0	127	3	AAE26604	AAE26604	Arabidops
419	31	100.0	114	8	ADQ82092	Human gly	492	31	100.0	127	4	ABE18304	ABE18304	Novel hum
420	31	100.0	114	8	ADR94295	Novel S.	493	31	100.0	127	5	ABP60782	ABP60782	Neurospor
421	31	100.0	114	9	AEA58165	Streptoco	494	31	100.0	127	8	ADY04680	ADY04680	Plant ful
422	31	100.0	115	3	AAE12953	Arabidops	495	31	100.0	128	4	ABE23738	ABE23738	Novel hum
423	31	100.0	115	3	AAE45020	Zea mays	496	31	100.0	128	6	ABP78912	ABP78912	N. gonorr
424	31	100.0	115	5	ABP60781	Mycobacte	497	31	100.0	129	7	ADB63991	ADB63991	Human pro
425	31	100.0	115	5	ABP60799	Caenorhab	498	31	100.0	129	7	ADBE6961	ADBE6961	C. neofo
426	31	100.0	116	5	ABP60739	Pagopyrum	499	31	100.0	130	2	AAE93017	AAE93017	Hard whea
427	31	100.0	116	7	ABM55632	Mouise pro	500	31	100.0	130	2	AAE70535	AAE70535	Human th
428	31	100.0	117	5	ABP60749	Boirelia	501	31	100.0	130	3	AAE29249	AAE29249	Wheat th
429	31	100.0	118	3	AAE70480	Catalpa s	502	31	100.0	130	5	ABP60787	ABP60787	Rickettsi
430	31	100.0	118	3	AAE70483	Vernonia	503	31	100.0	131	2	AAW47027	AAW47027	ecg hormo
431	31	100.0	118	5	ABP27942	Streptoco	504	31	100.0	131	4	AAE83360	AAE83360	P patiens
432	31	100.0	118	5	ABP27941	Streptoco	505	31	100.0	131	4	AAU51778	AAU51778	Propionib
433	31	100.0	118	5	ABP60733	Nicotiana	506	31	100.0	131	4	AAE80910	AAE80910	Co-factor
434	31	100.0	118	5	ABP60742	Ricinus c	507	31	100.0	131	5	ABP60844	ABP60844	Phalaris
435	31	100.0	119	4	ABG01907	Novel hum	508	31	100.0	131	5	ABP60821	ABP60821	Hordeum b
436	31	100.0	119	5	ABP60826	Secale ce	509	31	100.0	131	5	ABP60822	ABP60822	Lolium pe
437	31	100.0	120	3	AAE70481	Glycine m	510	31	100.0	131	5	ABP60823	ABP60823	Oryza sat
438	31	100.0	120	4	AAE41837	Human pol	511	31	100.0	131	5	ABP60825	ABP60825	Secale ce
439	31	100.0	120	7	ADP70794	Minicell	512	31	100.0	131	6	ABM48297	ABM48297	Propionib
440	31	100.0	120	7	ADP70792	Minicell	513	31	100.0	131	7	ABM74315	ABM74315	DNA clone
441	31	100.0	120	7	ADP70791	Minicell	514	31	100.0	132	4	ABG13926	ABG13926	Novel hum
442	31	100.0	120	7	ADP70793	Minicell	515	31	100.0	132	5	ADK36696	ADK36696	Novel hum
443	31	100.0	120	8	ADNA9430	Seven-pas	516	31	100.0	132	7	ADC33012	ADC33012	Human nov
444	31	100.0	121	2	AAE96043	Human vas	517	31	100.0	133	3	AAE10853	AAE10853	Arabidops
445	31	100.0	121	2	AAE96043	Human vas	518	31	100.0	133	3	ABP60731	ABP60731	Arabidops
446	31	100.0	121	2	AAE93977	Vascular	519	31	100.0	133	5	AAU72822	AAU72822	Human NKG
447	31	100.0	121	2	AAW09091	Human VEG	520	31	100.0	133	7	ADP70773	ADP70773	Minicell
448	31	100.0	121	2	AAW40597	VEGF/Vprr	521	31	100.0	133	8	ADY06180	ADY06180	Plant ful
449	31	100.0	121	3	AAE99848	Human vas	522	31	100.0	134	2	AAW47025	AAW47025	ecg hormo
450	31	100.0	121	3	AAE92001	Human lut	523	31	100.0	134	3	AAE04653	AAE04653	Arabidops
451	31	100.0	121	7	ADM24204	Human VEG	524	31	100.0	134	3	ADCE1418	ADCE1418	Human th1
452	31	100.0	121	7	ADM24204	Hyperther	525	31	100.0	134	8	ADM32939	ADM32939	Amino ac1
453	31	100.0	121	8	ADL92176	Lutropin	526	31	100.0	135	4	AAE15055	AAE15055	Peptide #
454	31	100.0	122	2	AAE15123	hCG/HLH	527	31	100.0	135	4	AAE34043	AAE34043	Peptide #
455	31	100.0	122	2	AAE65908	Protein f	528	31	100.0	135	4	AAE27498	AAE27498	Peptide #
456	31	100.0	122	2	AAE29594	Human lut	529	31	100.0	135	4	ABE28866	ABE28866	Peptide #
457	31	100.0	122	3	AAE19159	Amino act	530	31	100.0	135	4	ABE19484	ABE19484	Protein #
458	31	100.0	122	3	AAE29247	Barley th	531	31	100.0	135	4	AAE67204	AAE67204	Human bon
459	31	100.0	122	3	AAE70479	Memordica	532	31	100.0	135	4	AAE54823	AAE54823	Human bra
460	31	100.0	122	3	AAE03775	Human sec	533	31	100.0	135	4	ABE48868	ABE48868	Human liv
461	31	100.0	122	3	AAE35810	Rice thio	534	31	100.0	135	4	AAE02790	AAE02790	Peptide #
462	31	100.0	122	5	ABP60740	Oryza sat	535	31	100.0	135	5	ABE36860	ABE36860	Human pep

536	31	100.0	136	2	AAV12478	Hay12478 Human 5'	609	31	100.0	144	3	AAAG54790	Agag54790 Arabidops
537	31	100.0	136	8	ADG16382	Adg16382 TRIAP-aldp	610	31	100.0	144	8	ADX79859	Adx79859 Plant ful
538	31	100.0	136	8	ADY06635	Ady06635 plant ful	611	31	100.0	145	2	AAAR15122	Aar15122 hcg/hlh c
539	31	100.0	137	2	AAW55082	Aaw55082 Streptoco	612	31	100.0	145	2	AAAR15106	Aar15106 hcg/BLH c
540	31	100.0	137	2	AAW47026	Aaw47026 eCG hormo	613	31	100.0	145	2	AAAR15124	Aar15124 hcg/BLH c
541	31	100.0	137	2	ABP54576	Abp54576 S. pneumo	614	31	100.0	145	2	AAAR15125	Aar15125 hcg/BLH c
542	31	100.0	137	7	ADCA45121	Adca45121 S. pneumo	615	31	100.0	145	2	AAAR15102	Aar15102 hcg/BLH c
543	31	100.0	137	8	ADP07819	Adp07819 Human sec	616	31	100.0	145	2	AAAR15118	Aar15118 hcg/BLH c
544	31	100.0	137	8	ADX90438	Adx90438 plant ful	617	31	100.0	145	2	AAAR15116	Aar15116 hcg/BLH c
545	31	100.0	137	8	ADY09660	Ady09660 plant ful	618	31	100.0	145	5	ABP60759	Abp60759 Corynebac
546	31	100.0	137	8	ADY08622	Ady08622 plant ful	619	31	100.0	145	6	ADA34073	Ada34073 Acinetoba
547	31	100.0	137	8	ADY78867	Ady78867 plant ful	620	31	100.0	146	7	ADL17747	Adl17747 Human TRP
548	31	100.0	137	8	ADY04779	Ady04779 Plant ful	621	31	100.0	146	7	ADY56820	Ady56820 Human TRP
549	31	100.0	138	4	AAU47482	Aau47482 Propionib	622	31	100.0	147	3	AAAB09393	Aab09393 Hepaticis
550	31	100.0	138	4	AAAB71791	Aab71791 Dog lntro	623	31	100.0	147	3	AAAC30361	Aac30361 Arabidops
551	31	100.0	138	5	AAUB3040	Aaub3040 Dog lntro	624	31	100.0	147	4	AAU55797	Aau55797 Propionib
552	31	100.0	138	6	ABM44001	Abm44001 Propionib	625	31	100.0	147	6	ABM52316	Abm52316 Propionib
553	31	100.0	138	6	ADG16354	Adg16354 TRIAP-aldp	626	31	100.0	147	8	ABM52316	Abm52316 Plant ful
554	31	100.0	139	1	AAPE6061	Aape6061 Sequence	627	31	100.0	148	4	ABG29964	Abg29964 Novel hum
555	31	100.0	139	1	AAW47024	Aaw47024 eCG hormo	628	31	100.0	148	9	ADX85123	Adx85123 Vascular
556	31	100.0	139	4	AAAG41167	Aag41167 Zea mays	629	31	100.0	148	9	ADZ79967	Adz79967 Human vas
557	31	100.0	139	4	ABBB68209	Abbb68209 Drosophil	630	31	100.0	149	2	AAAR31001	Aar31001 Equine ch
558	31	100.0	139	4	AAU30551	Aau30551 Novel hum	631	31	100.0	149	4	AAAG93039	Aag93039 C glutami
559	31	100.0	139	5	ABPE60770	Abpe60770 Escherich	632	31	100.0	150	8	ADY09570	Ady09570 Plant ful
560	31	100.0	139	8	ADY10883	Ady10883 plant ful	633	31	100.0	151	3	AAAG44847	Aag44847 Zea mays
561	31	100.0	140	3	AAAG09942	Aag09942 Arabidops	634	31	100.0	151	3	AAAG44847	Aag44847 Zea mays
562	31	100.0	140	3	AAAG37258	Aag37258 Arabidops	635	31	100.0	151	5	ABBP60819	Abp60819 Arabidops
563	31	100.0	140	3	AAAG37257	Aag37257 Arabidops	636	31	100.0	151	8	ADP90872	Adp90872 Brevibaci
564	31	100.0	140	3	AAAG38662	Aag38662 Arabidops	637	31	100.0	152	3	AAAG41898	Aag41898 Arabidops
565	31	100.0	140	3	AAAG10594	Aag10594 Arabidops	638	31	100.0	152	3	AAAG26778	Aag26778 Zea mays
566	31	100.0	140	5	ABPE60814	Abpe60814 Arabidops	639	31	100.0	152	7	ABMB9602	Abmb9602 Rice abio
567	31	100.0	140	5	ABPE60715	Abpe60715 Chlamydom	640	31	100.0	152	8	ADY06632	Ady06632 Plant ful
568	31	100.0	140	8	ADP24746	Adp24746 PRO polyp	641	31	100.0	153	8	ADX87889	Adx87889 Plant ful
569	31	100.0	140	8	ADY04782	Ady04782 plant ful	642	31	100.0	154	6	ABR62385	Abrr62385 Secreted
570	31	100.0	141	1	AAPE6062	Aape6062 Sequence	643	31	100.0	154	7	ADP70797	Adp70797 PMPX-91 M
571	31	100.0	141	2	AAW99519	Aaw99519 Glycoprot	644	31	100.0	154	7	ADP70798	Adp70798 PMPX-96 M
572	31	100.0	141	2	AAW99548	Aaw99548 hLH-Delta	645	31	100.0	154	7	ADP70795	Adp70795 PMPX-80 M
573	31	100.0	141	2	AAW99516	Aaw99516 Glycoprot	646	31	100.0	154	7	ADP70796	Adp70796 PMPX-81 M
574	31	100.0	141	2	AAW99523	Aaw99523 Glycoprot	647	31	100.0	155	5	ABBB97761	Abbb97761 Human sec
575	31	100.0	141	2	AAW99518	Aaw99518 Glycoprot	648	31	100.0	157	4	ABG22533	Abg22533 Novel hum
576	31	100.0	141	2	AAW99520	Aaw99520 Glycoprot	649	31	100.0	157	4	ABG22533	Abg22533 Novel hum
577	31	100.0	141	2	AAW99547	Aaw99547 hLH-Delta	650	31	100.0	157	8	ABO58969	Abos8969 Human gen
578	31	100.0	141	2	AAW99522	Aaw99522 Glycoprot	651	31	100.0	159	3	AAAG36125	Aag36125 Arabidops
579	31	100.0	141	2	AAW99525	Aaw99525 Glycoprot	652	31	100.0	159	5	ABBB97952	Abbb97952 Thioredox
580	31	100.0	141	2	AAW99517	Aaw99517 Glycoprot	653	31	100.0	160	5	ABBP60832	Abp60832 Neisseria
581	31	100.0	141	2	AAW99524	Aaw99524 Glycoprot	654	31	100.0	160	7	ABO65111	Abos65111 Klebsiell
582	31	100.0	141	2	AAW99521	Aaw99521 Glycoprot	655	31	100.0	161	5	ABP59105	Abp59105 Protein k
583	31	100.0	141	4	ABBB76824	Abbb76824 Single ch	656	31	100.0	161	9	ADZ66921	Adz66921 Trx-DP-TM
584	31	100.0	141	4	ABBB71792	Abbb71792 Bovine lu	657	31	100.0	161	9	ADZ66921	Adz66921 Trx-DP-TM
585	31	100.0	141	4	ABBB71790	Abbb71790 Pig lntro	658	31	100.0	161	9	ADZ66918	Adz66918 Trx-DP-TM
586	31	100.0	141	4	ABBB71789	Abbb71789 Sheep lnt	659	31	100.0	162	3	AAAG30360	Aag30360 Arabidops
587	31	100.0	141	4	ABBB71788	Abbb71788 Sheep lnt	660	31	100.0	162	5	AAU72820	Aau72820 Human NKG
588	31	100.0	141	4	ABBB71795	Abbb71795 Human lnt	661	31	100.0	162	5	ADSI10583	Adsi10583 Human tne
589	31	100.0	141	4	AAAB71793	Aaab71793 Rat lntel	662	31	100.0	163	8	ADQ66065	Adq66065 Novel hum
590	31	100.0	141	5	AAUB3039	Aaub3039 Pig lntro	663	31	100.0	163	8	ADRO8958	Adro8958 Human pro
591	31	100.0	141	5	AAUB3038	Aaub3038 Sheep lnt	664	31	100.0	163	8	ADRO8958	Adro8958 Human pro
592	31	100.0	141	5	AAUB3042	Aaub3042 Rat lnten	665	31	100.0	163	8	ADY72134	Ady72134 plant ful
593	31	100.0	141	5	AAUB3041	Aaub3041 Bovine lu	666	31	100.0	164	2	AAAR10911	Aar10911 Bovine va
594	31	100.0	141	5	AAUB3044	Aaub3044 Beta-chai	667	31	100.0	164	2	AAAR38920	Aar38920 Bovine VE
595	31	100.0	141	5	ABP52007	Abp52007 NOVCON ho	668	31	100.0	164	5	ABBP41742	Abp41742 Human ova
596	31	100.0	141	5	ABP52008	Abp52008 NOVCON ho	669	31	100.0	165	2	AAAR10917	Aar10917 Human vas
597	31	100.0	141	7	AAEA90318	Aaea90318 Human NOV	670	31	100.0	165	2	AAAR38921	Aar38921 Human VEG
598	31	100.0	141	8	ADZ820914	Adz820914 Bovine lu	671	31	100.0	165	2	AAW31085	Aaw31085 Vascular
599	31	100.0	141	8	ADZ78767	Adz78767 Plant ful	672	31	100.0	165	2	AAW31088	Aaw31088 Vascular
600	31	100.0	141	8	ADY06170	Ady06170 Plant ful	673	31	100.0	165	2	AAW31091	Aaw31091 Vascular
601	31	100.0	141	8	ADY04783	Ady04783 Plant ful	674	31	100.0	165	2	AAW31095	Aaw31095 Vascular
602	31	100.0	141	8	ADX78677	Adx78677 Plant ful	675	31	100.0	165	2	AAW31096	Aaw31096 Vascular
603	31	100.0	143	4	AAAB71794	Aaab71794 Cat lntel	676	31	100.0	165	2	AAW31087	Aaw31087 Vascular
604	31	100.0	143	4	AAAB71794	Aaab71794 Cat lntel	677	31	100.0	165	2	AAW31089	Aaw31089 Vascular
605	31	100.0	143	5	AAU83043	Aau83043 Cat lnten	678	31	100.0	165	2	AAW31093	Aaw31093 Vascular
606	31	100.0	143	5	AAU72821	Aau72821 Human NKG	679	31	100.0	165	2	AAW31092	Aaw31092 Vascular
607	31	100.0	143	8	ADP19385	Adp19385 Human sec	680	31	100.0	165	2	AAW31090	Aaw31090 Vascular
608	31	100.0	144	3	AAAG20218	Aag20218 Arabidops	681	31	100.0	165	2	AAW31094	Aaw31094 Vascular

682	31	100.0	165	2	AAW1086	AAW1086	Vascular	755	31	100.0	171	5	ABP06779	ABP06779	Human ORF
683	31	100.0	165	2	AAV08280	AAV08280	Human gpro	756	31	100.0	171	8	ADY07711	ADY07711	Plant full
684	31	100.0	165	6	ABP56770	ABP56770	Human vas	757	31	100.0	171	8	ADX97324	ADX97324	Plant full
685	31	100.0	165	6	ABR82055	ABR82055	Human VEG	758	31	100.0	172	1	AAp94809	AAp94809	Human int
686	31	100.0	165	7	ADd42006	ADd42006	Human VEG	759	31	100.0	172	1	AAc15597	AAc15597	Arabidops
687	31	100.0	165	8	ADd119317	ADd119317	CocciIdioI	760	31	100.0	172	5	ABP60718	ABP60718	Pisum sat
688	31	100.0	165	8	ADJ47601	ADJ47601	W11d-type	761	31	100.0	172	5	ABP60717	ABP60717	Oryza sat
689	31	100.0	165	8	ADM24881	ADM24881	Human mat	762	31	100.0	172	7	ABM87854	ABM87854	Rice abio
690	31	100.0	165	8	ADP40207	ADP40207	Human VEG	763	31	100.0	172	8	ADM32941	ADM32941	Amino aci
691	31	100.0	165	8	ADU17883	ADU17883	Human vas	764	31	100.0	173	3	AAg45018	AAg45018	Zea mays
692	31	100.0	165	8	ADU07202	ADU07202	Amtno aci	765	31	100.0	173	5	ABP60712	ABP60712	Arabidops
693	31	100.0	165	8	ADT78147	ADT78147	Human VEG	766	31	100.0	173	4	ABM86658	ABM86658	Rice, abio
694	31	100.0	165	8	ADT99246	ADT99246	Partial v	767	31	100.0	174	4	AAU17068	AAU17068	Novel, b1g
695	31	100.0	165	8	ADT36536	ADT36536	Partial v	768	31	100.0	174	4	AAAB82531	AAAB82531	Vascular
696	31	100.0	165	8	ADT98421	ADT98421	Human VEG	769	31	100.0	174	7	ADBR4512	ADBR4512	Mycobacte
697	31	100.0	165	8	ADU17609	ADU17609	Human VEG	770	31	100.0	174	7	ADB93776	ADB93776	Human nov
698	31	100.0	165	8	ADU17466	ADU17466	Human vas	771	31	100.0	174	9	ADV60207	ADV60207	VEGF, l80f
699	31	100.0	165	8	ADU00628	ADU00628	Human vas	772	31	100.0	175	5	ABP60720	ABP60720	Triticum
700	31	100.0	165	8	ADT55064	ADT55064	Human vas	773	31	100.0	175	5	ABP60817	ABP60817	Arabidops
701	31	100.0	165	8	ADX55423	ADX55423	Human Vas	774	31	100.0	175	8	ADX88193	ADX88193	Plant full
702	31	100.0	165	8	ADX55424	ADX55424	Human Vas	775	31	100.0	177	3	ADCI4129	ADCI4129	Chimeric
703	31	100.0	165	8	ADX85122	ADX85122	Vascular	776	31	100.0	177	5	ABP60714	ABP60714	Brassic
704	31	100.0	165	9	ADZ79964	ADZ79964	Human vas	777	31	100.0	177	8	ADP90870	ADP90870	Brevibact
705	31	100.0	166	2	AAW59885	AAW59885	Amtno aci	778	31	100.0	177	8	ADX71846	ADX71846	Plant full
706	31	100.0	166	2	AAW59886	AAW59886	Amtno aci	779	31	100.0	178	3	AAg19366	AAg19366	Arabidops
707	31	100.0	166	4	AAW49006	AAW49006	Human thi	780	31	100.0	178	4	AAW95211	AAW95211	Human rep
708	31	100.0	166	4	AAU58218	AAU58218	Propionib	781	31	100.0	178	5	ABP60703	ABP60703	Arabidops
709	31	100.0	166	5	ABP41978	ABP41978	Human ova	782	31	100.0	178	8	ADN74765	ADN74765	Thale cre
710	31	100.0	166	5	ABP60804	ABP60804	Homo sapl	783	31	100.0	179	3	AAg30359	AAg30359	Arabidops
711	31	100.0	166	5	ABP60798	ABP60798	Bos tauru	784	31	100.0	179	5	ABP60710	ABP60710	Arabidops
712	31	100.0	166	5	ABP60807	ABP60807	Mus muscu	785	31	100.0	179	7	ADG46659	ADG46659	Arabidops
713	31	100.0	166	5	ABP60811	ABP60811	Rattus no	786	31	100.0	179	8	ADY06451	ADY06451	Plant full
714	31	100.0	166	6	ABM54737	ABM54737	Propionib	787	31	100.0	179	8	ADY10996	ADY10996	Plant full
715	31	100.0	166	7	ADC27624	ADC27624	Human col	788	31	100.0	180	8	ADY78704	ADY78704	Plant full
716	31	100.0	166	7	ADZ62952	ADZ62952	Rat, Prote	789	31	100.0	180	8	ADX99807	ADX99807	Plant full
717	31	100.0	167	2	AAW44910	AAW44910	"polyprol	790	31	100.0	180	8	ADY10998	ADY10998	Plant full
718	31	100.0	167	4	AAAB85253	AAAB85253	Thioredox	791	31	100.0	181	3	AAAG09380	AAAG09380	Arabidops
719	31	100.0	167	4	AAAB85254	AAAB85254	Thioredox	792	31	100.0	181	5	ABP60719	ABP60719	Spinacia
720	31	100.0	167	4	AAU17909	AAU17909	Novel hum	793	31	100.0	182	3	AAAG52357	AAAG52357	Arabidops
721	31	100.0	167	5	ABP60716	ABP60716	Zea mays	794	31	100.0	182	3	AAAG77356	AAAG77356	Arabidops
722	31	100.0	167	7	ADG41289	ADG41289	Human res	795	31	100.0	182	5	ABP60707	ABP60707	Pisum sat
723	31	100.0	167	7	AD197063	AD197063	Human tes	796	31	100.0	182	5	ABP60705	ABP60705	Brassic
724	31	100.0	167	8	AAAG32940	AAAG32940	Amtno aci	797	31	100.0	182	8	ADN74793	ADN74793	Thale cre
725	31	100.0	168	3	AAAG20217	AAAG20217	Arabidops	798	31	100.0	182	8	ADY11299	ADY11299	Plant full
726	31	100.0	169	2	AAW33773	AAW33773	Equine ch	799	31	100.0	183	3	AAAG11492	AAAG11492	Arabidops
727	31	100.0	169	2	AAW33775	AAW33775	Equine ch	800	31	100.0	183	4	AAU20503	AAU20503	Human sec
728	31	100.0	169	2	AAW33777	AAW33777	Equine ch	801	31	100.0	183	5	ABP99365	ABP99365	Arabidops
729	31	100.0	169	4	AAAG63110	AAAG63110	Equine ch	802	31	100.0	183	8	ADY72703	ADY72703	Trix-Conot
730	31	100.0	169	4	AAAG63110	AAAG63110	P patens	803	31	100.0	183	9	ADX85121	ADX85121	Vascular
731	31	100.0	169	4	AAAB71788	AAAB71788	Co-factor	804	31	100.0	183	9	ABM95783	ABM95783	M. xanthu
732	31	100.0	169	4	AAAG80909	AAAG80909	Horse cho	805	31	100.0	183	9	ADZ79966	ADZ79966	Human vas
733	31	100.0	169	5	AAU83037	AAU83037	Horse cho	806	31	100.0	184	3	AAAG38651	AAAG38651	Arabidops
734	31	100.0	169	5	ABP60682	ABP60682	Phaseolin	807	31	100.0	184	4	AAAG41965	AAAG41965	Human pol
735	31	100.0	169	7	ABM73604	ABM73604	DNA clone	808	31	100.0	185	4	AAAG80918	AAAG80918	Thioredox
736	31	100.0	169	8	ADP18553	ADP18553	Horse pla	809	31	100.0	185	5	ABP60704	ABP60704	Arabidops
737	31	100.0	169	9	ABM91297	ABM91297	M. xanthu	810	31	100.0	185	6	ABU01415	ABU01415	S. pneumo
738	31	100.0	170	2	AAW63623	AAW63623	Human tum	811	31	100.0	185	8	ADK48707	ADK48707	Streptoco
739	31	100.0	170	2	AAW90358	AAW90358	Human tum	812	31	100.0	185	8	ADT56788	ADT56788	Plant pol
740	31	100.0	170	3	AAAG09381	AAAG09381	Arabidops	813	31	100.0	185	8	ADT56140	ADT56140	Plant pol
741	31	100.0	170	3	AAAB75114	AAAB75114	Thioredox	814	31	100.0	186	3	AAAG41897	AAAG41897	Arabidops
742	31	100.0	170	4	ABG04973	ABG04973	Novel hum	815	31	100.0	186	5	ABP60711	ABP60711	Arabidops
743	31	100.0	170	5	AAE20849	AAE20849	Human tum	816	31	100.0	187	7	ABM90060	ABM90060	Rice abio
744	31	100.0	170	8	ADJ96153	ADJ96153	Human tum	817	31	100.0	187	7	ABM90026	ABM90026	Rice abio
745	31	100.0	170	8	AD033544	AD033544	Thioredox	818	31	100.0	187	8	AD065445	AD065445	Novel hum
746	31	100.0	170	8	AD033539	AD033539	Thioredox	819	31	100.0	188	3	AAAG15556	AAAG15556	Arabidops
747	31	100.0	170	9	ADZ66909	ADZ66909	Trix-DP-TM	820	31	100.0	188	5	AAU83082	AAU83082	Novel sec
748	31	100.0	170	9	ADZ66912	ADZ66912	Trix-DP-TM	821	31	100.0	188	7	ABO84188	ABO84188	Pseudom
749	31	100.0	170	9	ADZ66915	ADZ66915	Trix-DP-TM	822	31	100.0	189	2	AAAY08281	AAAY08281	Human gpro
750	31	100.0	170	9	ADZ66906	ADZ66906	Trix-DP-TM	823	31	100.0	189	3	AAAY92005	AAAY92005	Human vas
751	31	100.0	171	3	AAAB40484	AAAB40484	Human ORF	824	31	100.0	189	4	ADAS6457	ADAS6457	Human VEG
752	31	100.0	171	3	AAAG27357	AAAG27357	Arabidops	825	31	100.0	189	6	ADAS5208	ADAS5208	Human pro
753	31	100.0	171	3	AAAG52358	AAAG52358	Arabidops	826	31	100.0	189	8	ADN05035	ADN05035	Ant-1p9071
754	31	100.0	171	4	AAAM24391	AAAM24391	Human EST	827	31	100.0	189	9	ADX85120	ADX85120	Vascular

828	31	100.0	189	9	ADZ79963	Adz79963	Human vas	901	31	100.0	196	7	ADBR08098	AdBr08098	Novel pro
829	31	100.0	190	2	AAR08001	Aar08001	Bovine va	902	31	100.0	196	7	ADBR08261	AdBr08261	Novel pro
830	31	100.0	190	2	AAV33440	Aav33440	Parapox v	903	31	100.0	196	8	ADBR93354	AdBr93354	Coliae eu
831	31	100.0	190	5	ABP60708	Abp60708	Spinacia	904	31	100.0	197	8	ADBr67695	AdBr67695	Novel hum
832	31	100.0	191	2	AAR08002	Aar08002	Human vas	905	31	100.0	199	8	ADBr42114	AdBr42114	Human ORF
833	31	100.0	191	2	AAR91076	Aar91076	Human vas	906	31	100.0	201	8	ADBr72965	AdBr72965	Plant ful
834	31	100.0	191	2	AAW00724	Aaw00724	Vascular	907	31	100.0	203	3	AAg39661	Aag39661	Arabi-dops
835	31	100.0	191	2	AAAR94002	Aaar94002	VEGF165	908	31	100.0	204	8	ADBr77747	AdBr77747	Plant ful
836	31	100.0	191	2	AAW38242	Aaw38242	Vascular	909	31	100.0	205	8	ADBr67129	AdBr67129	Hybrid pr
837	31	100.0	191	2	AAW62525	Aaw62525	Amino aci	910	31	100.0	205	8	ADBr10015	AdBr10015	Human pro
838	31	100.0	191	2	AAW69331	Aaw69331	Human VEG	911	31	100.0	206	8	ADBr9864	AdBr9864	Fusion pr
839	31	100.0	191	2	AAW57398	Aaw57398	Variant v	912	31	100.0	206	8	ADBr40208	AdBr40208	Human VEG
840	31	100.0	191	2	AAW57399	Aaw57399	Variant v	913	31	100.0	206	9	ADBr90273	AdBr90273	Protease-
841	31	100.0	191	2	AAV33439	Aav33439	Parapox v	914	31	100.0	206	9	ADBr85119	AdBr85119	Vascular
842	31	100.0	191	2	AAV07725	Aav07725	Human VEG	915	31	100.0	206	9	ADBr79962	AdBr79962	Human vas
843	31	100.0	191	3	AAV59414	Aav59414	Amino aci	916	31	100.0	207	3	AAg22069	Aag22069	Arabi-dops
844	31	100.0	191	3	AAV18305	Aav18305	Human vas	917	31	100.0	207	3	AAg38804	Aag38804	Arabi-dops
845	31	100.0	191	3	AAV90403	Aav90403	VEGF enco	918	31	100.0	208	2	AAV43483	Aav43483	Amino aci
846	31	100.0	191	3	AAAB28235	Aaab28235	Mutant hu	919	31	100.0	209	2	AAAR31931	Aaar31931	Human TC-
847	31	100.0	191	3	AAAB28232	Aaab28232	Wild-type	920	31	100.0	209	2	AAW04250	Aaw04250	10A1 muti
848	31	100.0	191	3	AAAB28233	Aaab28233	Mutant hu	921	31	100.0	209	2	AAW04249	Aaw04249	4070A ret
849	31	100.0	191	3	AAAB28236	Aaab28236	Mutant hu	922	31	100.0	209	5	AAAB79754	Aaab79754	Thioredox
850	31	100.0	191	3	AAAB28234	Aaab28234	Mutant hu	923	31	100.0	209	6	AAAB80982	Aaab80982	N. gonorr
851	31	100.0	191	4	AAAB84603	Aaab84603	Amino aci	924	31	100.0	209	9	ADBr60205	AdBr60205	VEGF iso
852	31	100.0	191	4	AAAB2856	Aaab2856	Human vas	925	31	100.0	210	4	AAAB05136	Aaab05136	Human T c
853	31	100.0	191	4	AAAB50433	Aaab50433	Human VEG	926	31	100.0	211	3	AAAB28560	Aaab28560	Human sol
854	31	100.0	191	4	AAV97568	Aav97568	Human VEG	927	31	100.0	211	4	AAAB59678	Aaab59678	Drosophi1
855	31	100.0	191	4	AAAB31562	Aaab31562	Amino aci	928	31	100.0	214	5	AAAB09175	Aaab09175	Leptin-VE
856	31	100.0	191	4	AAU08401	Aau08401	Human VEG	929	31	100.0	214	6	ABU10041	Abu10041	Leptin-VE
857	31	100.0	191	5	AAAB19434	Aaab19434	Human vas	930	31	100.0	214	8	ADBr00679	AdBr00679	Leptin-VE
858	31	100.0	191	5	ABP60706	Abp60706	Mesembrya	931	31	100.0	215	2	AAAR05102	Aaar05102	Human vas
859	31	100.0	191	5	ABP65133	Abp65133	Hypoxia-r	932	31	100.0	215	2	AAAR91077	Aaar91077	Human vas
860	31	100.0	191	5	ABAB76301	Abab76301	Human vas	933	31	100.0	215	2	AAAR94003	Aaar94003	VEGF189
861	31	100.0	191	6	ABU79137	Abu79137	Vascular	934	31	100.0	215	2	AAAB62526	Aaab62526	Amino aci
862	31	100.0	191	6	ABP81583	Abp81583	Streptoco	935	31	100.0	215	2	AAAY07726	Aaay07726	Human VEG
863	31	100.0	191	6	ABBB80135	Abbb80135	VEGF-165	936	31	100.0	215	3	AAAB94415	Aaab94415	Amino aci
864	31	100.0	191	6	ABP97880	Abp97880	Amino aci	937	31	100.0	215	3	AAAB10645	Aaab10645	Human VEG
865	31	100.0	191	7	ABU62245	Abu62245	Human vas	938	31	100.0	215	3	AAAY90404	Aaay90404	VEGF enco
866	31	100.0	191	7	ADBr4696	Adbr4696	Human vas	939	31	100.0	215	3	AAAY94803	Aaay94803	Human VEG
867	31	100.0	191	7	ADBr08944	Adbr08944	Human VEG	940	31	100.0	215	3	AAAY57035	Aaay57035	Human A21
868	31	100.0	191	7	ADBr25450	Adbr25450	Binding d	941	31	100.0	215	4	AAAB37512	Aaab37512	Human VEG
869	31	100.0	191	7	ADBr25492	Adbr25492	Binding d	942	31	100.0	215	4	ABG10788	Abg10788	Novel hum
870	31	100.0	191	7	ADBr43402	Adbr43402	VEGF poly	943	31	100.0	215	6	ADBr25611	Adbr25611	Human VEG
871	31	100.0	191	7	ADBr92127	Adbr92127	Human vas	944	31	100.0	215	7	ADBr62246	Adbr62246	Human vas
872	31	100.0	191	8	ADBr17128	Adbr17128	Human vas	945	31	100.0	215	7	ADBr34697	Adbr34697	Human vas
873	31	100.0	191	8	ADBr62205	Adbr62205	Human vas	946	31	100.0	215	7	ADBr92128	Adbr92128	Human vas
874	31	100.0	191	8	ADBr147222	Adbr147222	Human nat	947	31	100.0	215	8	ADBr62207	Adbr62207	Human vas
875	31	100.0	191	8	ADBr05122	Adbr05122	Protein #	948	31	100.0	215	8	ADBr147224	Adbr147224	Human nat
876	31	100.0	191	8	ADBr071599	Adbr071599	Amino aci	949	31	100.0	215	8	ADBr573979	Adbr573979	Vascular
877	31	100.0	191	8	ADBr026337	Adbr026337	Human vas	950	31	100.0	215	9	ADBr60204	Adbr60204	VEGF iso
878	31	100.0	191	8	ADBr46385	Adbr46385	Human vas	951	31	100.0	215	9	ADBr28638	Adbr28638	VEGF, SER
879	31	100.0	191	8	ADBr31430	Adbr31430	Human vas	952	31	100.0	215	9	ADBr81008	Adbr81008	Human vas
880	31	100.0	191	8	ADBr54918	Adbr54918	Human PRO	953	31	100.0	215	9	ADBr69290	Adbr69290	Human VEG
881	31	100.0	191	8	ADBr18045	Adbr18045	Human can	954	31	100.0	215	9	ADBr16584	Adbr16584	PRO polyP
882	31	100.0	191	8	ADBr06703	Adbr06703	Novel brio	955	31	100.0	215	9	ADBr59379	Adbr59379	Human VEG
883	31	100.0	191	8	ADBr06206	Adbr06206	VEGF iso	956	31	100.0	215	9	ADBr49900	Adbr49900	Human VEG
884	31	100.0	191	9	ADBr28644	Adbr28644	VEGF165 i	957	31	100.0	215	9	ADBr81220	Adbr81220	Human vas
885	31	100.0	191	9	ADBr81007	Adbr81007	Mature hu	958	31	100.0	216	2	ADBr28120	Adbr28120	Human vas
886	31	100.0	191	9	ADBr69287	Adbr69287	Human VEG	959	31	100.0	216	7	ADBr06452	Adbr06452	Human MTC
887	31	100.0	191	9	ADBr16437	Adbr16437	PRO polyP	960	31	100.0	216	8	ADBr93627	Adbr93627	Human C-t
888	31	100.0	191	9	ADBr200436	Adbr200436	VEGF-A. 6	961	31	100.0	216	8	ADBr82971	Adbr82971	Human PRO
889	31	100.0	191	9	ADBr03073	Adbr03073	IGF-1 rec	962	31	100.0	216	8	ADBr17796	Adbr17796	Human sof
890	31	100.0	192	2	ADBr40040	Adbr40040	VEGF165 C	963	31	100.0	216	8	ADBr56126	Adbr56126	Human PRO
891	31	100.0	192	2	ADBr94039	Adbr94039	VEGF165 C	964	31	100.0	216	8	ADBr10550	Adbr10550	Plant ful
892	31	100.0	193	3	ADBr11491	Adbr11491	Arabi-dops	965	31	100.0	216	8	ADBr19952	Adbr19952	Plant ful
893	31	100.0	193	3	ADBr37884	Adbr37884	Arabi-dops	966	31	100.0	216	9	ADBr15632	Adbr15632	PRO polyP
894	31	100.0	193	5	ADBr60713	Adbr60713	Arabi-dops	967	31	100.0	217	3	ADBr37883	Adbr37883	Arabi-dops
895	31	100.0	194	3	ADBr40095	Adbr40095	Arabi-dops	968	31	100.0	217	8	ADBr07461	Adbr07461	Plant ful
896	31	100.0	194	3	ADBr32511	Adbr32511	Arabi-dops	969	31	100.0	218	6	ADBr27423	Adbr27423	Protein e
897	31	100.0	194	3	ADBr67218	Adbr67218	Arabi-dops	970	31	100.0	219	4	ADBr19517	Adbr19517	Human dia
898	31	100.0	194	8	ADBr96469	Adbr96469	Novel S.	971	31	100.0	219	7	ADBr74148	Adbr74148	DNA clone
899	31	100.0	194	9	ADBr60339	Adbr60339	Streptoco	972	31	100.0	221	3	ADBr61101	Adbr61101	Arabi-dops
900	31	100.0	195	9	ADBr96249	Adbr96249	M. xanthu	973	31	100.0	221	3	ADBr15609	Adbr15609	Arabi-dops

974	31	100.0	221	8	ADN0244	Adn02744	Human rec
975	31	100.0	222	3	AAg38803	AAg38803	Arabidops
976	31	100.0	222	3	AAg15608	AAg15608	Arabidops
977	31	100.0	222	3	AAg61100	AAg61100	Arabidops
978	31	100.0	222	3	AAg622068	AAg622068	Arabidops
979	31	100.0	222	8	ADX90428	Adx90428	Plant full
980	31	100.0	223	8	AAH13572	Abh13572	Sterptomy
981	31	100.0	223	4	ABH1846	Abh1846	Human int
982	31	100.0	223	7	ADD46716	Adde4716	Rat prote
983	31	100.0	223	7	ADD46720	Adde4720	Rat prote
984	31	100.0	223	7	ADDE55402	Ades55402	Rat prote
985	31	100.0	223	7	ADDE55406	Ades5406	Rat prote
986	31	100.0	223	7	ADD46724	Adde4724	Rat prote
987	31	100.0	223	7	ADD46712	Adde4712	Rat prote
988	31	100.0	223	7	ADDE9087	Adde9087	Novel pro
989	31	100.0	223	9	ADU40604	Adu40604	Novel hum
990	31	100.0	224	6	ADA21146	Ada21146	Human sec
991	31	100.0	224	7	ABG65189	Abg65189	Human pro
992	31	100.0	226	4	ABG09456	Abg09456	Novel hum
993	31	100.0	227	3	AAg34398	AAg34398	Arabidops
994	31	100.0	227	4	AABy5374	Abby5374	Human pro
995	31	100.0	227	8	AD124503	Adi24503	Human mod
996	31	100.0	227	8	ADK60183	Adk60183	Angiogene
997	31	100.0	227	8	ADK60484	Adk60484	Angiogene
998	31	100.0	227	8	ADP73107	Adp73107	Angiogene
999	31	100.0	227	9	AEA21064	Nea21064	Novel hum
1000	31	100.0	228	4	AAU55184	Neu55184	Propionib

ALIGNMENTS

```

RESULT 1
AAR11508
ID AAR11508 standard; peptide; 4 AA.
XX
XX AAR11508;
XX AC
XX 09-JAN-2003 (revised)
DT 12-JUN-1991 (first entry)
XX
XX Thioxedoxin active site.
DE
XX Thioxedoxin; colon cancer; B-lymphocytic leukaemia; MP6/Trx.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO9104320-A.
XX
XX 04-APR-1991.
XX
XX 12-SEP-1989; 89SE-00003003.
XX
XX 12-SEP-1989; 89SE-00003003.
XX
XX (ASTR ) ASTRA AB.
XX
XX Rosen A;
XX PI
XX WPI; 1991-117511/16.
XX
XX Use of thioxedoxin alone or with co-factor(s) e.g. interferon(s) etc. -
PT for treatment of malignant cells e.g. B lymphocytic leukaemia, colon
PT cancer etc.
XX
XX Claim 1; Page 27; 41pp; English.
XX
XX Thioxedoxin analogues containing this motif are used to treat malignantly
CC transformed cells. The analogue may be used with a co-factor such as
CC interleukin-1, -2, -3 or -4, interferons, TNF-alpha, etc. The preferred
CC thioxedoxin analogue is derived from the MP6 human CD4+ T cell hybridoma
CC and is designated MP6/Trx. (Updated on 09-JAN-2003 to add missing OS

```

```
CC      field.)
XX
SQ      Sequence 4 AA;
```

```

every Match      100.0%; Score 31; DB 2; Length 4;
1st Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	2	CGPC 5
Db	1	CGPC 4

RESULT 2
AAW09052
ID AAW09052 standard; peptide; 4 AA.

AC	AAW09052;
XX	
DT	20-AUG-1997 (first entry)

Thioredoxin motif of enzymes used in branched protein synthesis method.

Thioredoxin; protein folding; branched; disulphide bond;
 KM prokaryotic recombinant production; biologically active;
 KM protein disulphide oxidoreductase; glutaredoxin; redox buffer
 KM

OS Synthetic.

PN SE9501285-A.

PD 07-OCT-1996.

PF 06-APR-1995; 95SE-00001285.

PR 06-APR-1995; 95SE-00001285.

PA (LJUN/) LJUNG J.

PA (ASLU/) ASLUND F.

PI Ljung J, Holmgren A, Aslund F,

DR WPI; 1997-032920/03.

PT Preparing correctly branched proteins contg. di: sulphide linkages -

PT oxido:reductase enzyme in glutaredoxin and redox buffer.

PS Claim 2; Page 16; 22pp; Swedish.

CC AA09052-W09054 are motifs that are present in thioredoxin or enzymes

CC These enzymes are used in a method for producing biologically active,

CC reacting the corresponding non-branched, reduced protein with a protein-

CC in the presence of glutaredoxin and redox buffer (glutathione disulphide

CC biological activity. The method is used for producing human proteins in

CC such as (pro)insulin, IGF-I, IGF-II, t-PA, growth hormone, Factor VIII,

CC lysozymes, pancreatic mammalian trypsin inhibitors, interferons, rennin,

CC cells in a biologically active form

SQ Sequence 4 AA;

Query Match	100.0%;	Score 31;	DB 2;	Length 4;
-------------	---------	-----------	-------	-----------

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 3

AAAB13337
 ID AAB13337 standard; protein; 4 AA.

AC AAB13337;

DT 06-NOV-2000 (first entry)

XX Human Trx-homology domain conserved motif.

DE Human; thioredoxin; Trx; PICOT; PKC-interacting cousin of thioredoxin;
 KW Protein kinase C theta; PKCtheta; c-Jun N-terminal kinase; JNK; AP-1;
 KW NF-kappaB; interleukin-2; IL-2; TCR/CD28 signaling cascade;
 KW PICOT-homology domain; PIH domain; protein activity modulation; stress;
 inflammation.

XX Homo sapiens.

XX WO200036083-A2.

PD 22-JUN-2000.

PF 17-DEC-1999; 99WO-US030285.

PR 17-DEC-1998; 98US-00112649.

XX (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.

XX Altman A, Witte S;

XX WPI; 2000-442379/38.

DR A PKC-interacting cousin of Trx (PICOT) polypeptide and the nucleic
 PT acids that encode it, useful e.g. for modulating Jun N-terminal kinase,
 AP-1 and/or nuclear factor-kappa-B expression and activity.

PS Example 4; Page 43; 68pp; English.

XX The present polypeptide is a conserved motif found in the Trx-homology
 CC domain of the thioredoxin (Trx) family of proteins. The motif is
 CC important for catalytic activity. The N-terminal region of PKC-
 CC interacting cousin of thioredoxin (PICOT) shows homology to the Trx-
 CC homology domain but it lacks the conserved motif and contains instead an
 CC Ala-Pro-Gln-Cys motif. PICOT modulates the function of PKCtheta and
 CC inhibits activation of c-Jun N-terminal kinase (JNK) and the
 CC transcription factors AP-1 and NF-kappaB. These polypeptides are involved
 CC in the TCR/CD28 signaling cascade which leads to IL-2 production. PICOT
 CC also modulates activity of the Trx system. PICOT may be useful for
 CC ameliorating physiological conditions, e.g. an inflammation or stress
 CC response, associated with these polypeptides. The cDNA encoding PICOT was
 CC isolated using yeast two-hybrid screening. PKCtheta polypeptides were
 CC screened for binding to polypeptides encoded by a Jurkat T lymphoma cDNA
 CC library. The two longest cDNAs from the PKCtheta-interacting positive
 CC clones were sequenced and the putative 37.5 kDa polypeptide encoded by
 CC the open reading frame was named PICOT

XX Sequence 4 AA;

XX Query Match

Best Local Similarity 100.0%; Score 31; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 4

AAAY9348
 ID AAY9348 standard; peptide; 4 AA.

XX AAY9348;

DT 14-MAR-2000 (first entry)

XX Active-site loop of E. coli thioredoxin.

DE Saccharomyces; mammalian; fusion protein; interactor peptide;
 KW conformation-constraining protein; DNA binding moiety; thioredoxin;
 KW gene activating moiety; protein interaction; gene purification.

XX Escherichia coli.

XX US6004746-A.

PD 21-DEC-1999.

PF 20-JUL-1995; 95US-00504538.

PR 20-JUL-1994; 94US-00278082.

XX (GEHO) GEN HOSPITAL CORP.

XX (GEMV) GENETICS INST INC.

PI McCoy JM, Jessen TH, Brent R;

XX WPI; 2000-072059/06.

DR Population of Saccharomyces and/or mammalian cells comprising recombinant
 PT DNA encoding fusion proteins, useful for detecting protein interactions.
 PS Disclosure; Col 15; 24pp; English.

XX The invention relates to a population of Saccharomyces and/or mammalian
 CC cells comprising recombinant DNA molecules encoding fusion proteins, each
 CC consisting of a candidate interactor peptide, a conformation-constraining
 CC protein and a DNA binding moiety and/or gene activating moiety. The cells
 CC are useful for detecting protein interactions. The cells may also be used
 CC in a method for identifying and purifying genes encoding a wide range of
 CC useful proteins based on their physical interaction with a second
 CC polypeptide

XX Sequence 4 AA;

XX Query Match

Best Local Similarity 100.0%; Score 31; DB 3; Length 4;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 5

ABP56403
 ID ABP56403 standard; peptide; 4 AA.

XX ABP56403;

XX 12-MAR-2003 (first entry)

DT Thioredoxin related peptide #2.

DE Thioredoxin; TrxA; fusion protein; allogenic protein.

XX Synthetic.

XX CN1189539-A.

PD 05-AUG-1998.

XX

PF 31-JAN-1997; 97CN-00100362.
 XX
 PR 31-JAN-1997; 97CN-00100362.
 XX
 PA (BIOI-) BIOLOGICAL ENG INST ACAD MILITARY MEDICI.
 XX
 PI Cui L, Ma Q;
 XX
 DR WPI; 2002-733391/80.
 XX
 PT Soluble expression carrier and its fusion protein of novel thioredoxin.
 XX
 PS Disclosure; Page 2 (Disclosure); 14pp; Chinese.
 XX
 CC The present invention describes a DNA molecule of a fusion protein which
 CC is composed of the DNA sequence similar to encoded thioredoxin in
 CC structure and the DNA sequence of an encoded allogenic protein. The
 CC soluble expression of the fusion protein is efficient. The expressed
 CC fusion protein can be easily purified as several amino acid sequences are
 CC inserted at active sites of the thioredoxin gene sequence, and hydrolysed
 CC by a specific protease as the junction between the two encoded DNA
 CC sequences can be cut by the specific protease, obtaining a recombinant
 CC allergenic protein the same as the natural protein in one-class structure.
 CC The present sequence represents a peptide which is given in the
 CC exemplification of the present invention
 CC
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 6
 AAO22593
 ID AAO22593 standard; peptide; 4 AA.
 XX
 AC AAO22593;
 XX
 DT 30-OCT-2002 (first entry)
 XX
 DE Redox active peptide sequence CGPC.

XX Antiinflammatory; immunosuppressive; antiaesthetic; antibacterial;
 KM nephrotropic; antiarteriosclerotic; antirheumatic; antiarthritic;
 KM Helicobacter pylori protein; inhibitor; activator; NF-kappaB; rheumatoid;
 KM inflammation; inflammatory bowel disease; autoimmune arthritis;
 KM chronic disease; autoimmune disease; asthma; septic shock; lung fibrosis;
 KM glomerulonephritis; atherosclerosis; autoimmune encephalomyelitis;
 KM soft tissue injury; reduction catalyst; chronic inflammatory disease;
 KM systemic inflammatory response; NF-kappaB-mediated inflammatory disease;
 KM inducible surface expression; CD44; intercellular adhesion molecule;
 KM ICAM-1; NF-kappaB activation; redox active peptide.

XX Unidentified.
 OS
 XX
 PN WO200260933-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 30-JAN-2002; 2002WO-IE000011.
 XX
 PR 30-JAN-2001; 2001IE-00000069.

PA (QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
 XX
 PI Windle HJ, Dermot K, Dermot O, Abdel-Latif MM,
 XX
 DR WPI; 2002-627466/67.

XX Novel Helicobacter pylori protein useful for treating inflammation,
 PT autoimmune diseases, septic shock and glomerulonephritis, has redox
 PT active peptide sequence inhibiting activation of NF-kappaB.
 XX
 PS Claim 4; Page 22; 34pp; English.

XX The invention relates to a Helicobacter pylori protein, its derivatives,
 CC fragments, mutants and variants capable of inhibiting the activation of
 CC NF-kappaB and having a sequence of 106 amino acids defined in the
 CC specification. The protein is useful for preventing and/or treating
 CC inflammation, inflammatory bowel disease, rheumatoid/autoimmune
 CC arthritis, chronic disease where NF-kappaB is transcriptionally
 CC activated, autoimmune diseases, asthma, septic shock, lung fibrosis,
 CC glomerulonephritis, atherosclerosis or autoimmune encephalomyelitis, and
 CC soft tissue injury. The Helicobacter pylori protein is also used for
 CC treating chronic diseases where NF-kappaB is transcriptionally activated.
 CC The Helicobacter pylori protein catalyses the reduction of proteins. The
 CC H. pylori protein is also useful for treating chronic inflammatory
 CC diseases, particularly systemic inflammatory response syndrome or other
 CC NF-kappaB-mediated inflammatory disease states, down regulates the
 CC resting and inducible surface expression of CD44 and intercellular
 CC adhesion molecule (ICAM)-1, prevents NF-kappaB activation both prior to
 CC stimulation with inducers of NF-kappaB and secondary to induction of NF-
 CC kappaB, and prevents or inhibits constitutive NF-kappaB activity. This
 CC sequence represents the redox active peptide sequence CGPC relating to
 CC the invention
 CC
 XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 1 CGPC 4

RESULT 7
 ABG32509
 ID ABG32509 standard; peptide; 4 AA.
 XX
 AC ABG32509;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE M. tuberculosis thioredoxin active site peptide.

XX Thioredoxin; TRX; tuberculosis; antibacterial; active site;
 KM tuberculostatic; vaccine; superoxide dismutase; SOD; bacterial infection;
 KM attenuated intracellular bacterium.

XX Mycobacterium tuberculosis.
 OS
 XX
 PN WO200262298-A2.
 XX
 PD 15-AUG-2002.
 XX
 PF 07-FEB-2002; 2002WO-US003451.
 XX
 PR 07-FEB-2001; 2001US-0267328P.
 XX
 PR 18-SEP-2001; 2001US-0322989P.

PA (UYVA-) UNIV VANDERBILT.
 XX
 PI (USGO) US DEPT VETERANS AFFAIRS.
 XX
 PI Kernodle DS, Bochan MR;
 XX
 DR WPI; 2002-643367/69.

PT Modifying a bacterium to enhance immunogenicity, as vaccines for
 PT preventing bacterial infections, e.g. tuberculosis comprises reducing the

PT activity of an anti-apoptotic enzyme, e.g. superoxide dismutase produced
PT by the bacterium.
XX
PS Example 13; Page 94; 164pp; English.
XX
CC The invention relates to modifying a bacterium to enhance immunogenicity
CC of the bacterium comprising reducing the activity of an anti-apoptotic
CC enzyme produced by the bacterium e.g. superoxide dismutase (SOD) where
CC the bacterium has enhanced immunogenicity in a subject. Also included are
CC the modified bacterium, an immunogenic composition comprising the
CC modified bacterium, an attenuated intracellular bacterium (further
CC modified to reduce the activity of an anti-apoptotic enzyme of the
CC bacterium), modifying a bacterium so it retains or increases
CC immunogenicity but loses or reduces pathogenicity in a subject.
CC comprising reducing but not eliminating an activity of an enzyme produced
CC by the bacterium, where reducing the activity of the enzyme attenuates
CC the bacterium. The methods are useful for preventing bacterial
CC infections, e.g. tuberculosis. The attenuated intracellular bacterium is
CC useful as a vaccine for preventing bacterial infections. The present
CC sequence is the active site of M. tuberculosis thioredoxin (Trx) which
CC was eliminated by mutagenesis to create an attenuated bacterium of the
CC invention
CC
XX
SQ Sequence 4 AA;
XX
Query Match 100.0%; Score 31; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
XX
RESULT 8
AAU97916 standard; peptide; 4 AA.
ID AAU97916;
AC AAU97916;
XX
DT 14-AUG-2002 (first entry)
XX
DE Tetrapeptide antioxidant peptide composition CB.
XX
DE Antioxidant; oxidative stress; central nervous system; cancer; ageing;
XX neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX Creutzfeldt Jakob's disease; cerebral ischaemia; multiple sclerosis;
XX motor neuron disease; scrapie; spongiform encephalopathy;
XX acute respiratory distress syndrome; amyotrophic lateral sclerosis;
XX atherosclerosis; acquired immunodeficiency syndrome; AIDS.
XX
OS Synthetic.
XX
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N terminal acetylation"
FT Modified-site 4 /note= "C terminal amide"
FT
XX
PN GB2368339-A.
XX
PN 01-MAY-2002.
XX
PD 26-OCT-2000; 2000GB-00026254.
XX
PF 26-OCT-2000; 2000GB-00026254.
XX
PR 26-OCT-2000; 2000GB-00026254.
XX
XX (YISS) YISSUM RES & DEV CO.
PA
XX
PI Atlas D;
XX
DR WPI; 2002-419127/45.
XX

PT Antioxidant compound used for treating e.g. Alzheimer's disease and
PT multiple sclerosis comprises peptide including cysteine residues having
PT sulphydryl groups and hydrophobic or non charged groups attached to amino
PT and carboxy terminal.
XX
XX
PS Example 1; Page 32; 62pp; English.
XX
CC This invention relates to an antioxidant compound comprising a peptide
CC including at least 3 amino acid residues of which at least 2 are cysteine
CC residues each having a readily oxidisable sulphydryl group for effecting
CC autooxidation, and a first hydrophobic or non charged group attached to
CC an amino terminal of the peptide and a second hydrophobic or non charged
CC group attached to a carboxy terminal. the antioxidant peptide compound
CC may be used for preventing or reducing oxidative stress and for treating
CC central nervous system neurodegenerative disorders, particularly
CC Parkinson's disease, Alzheimer's disease, Creutzfeldt Jakob's disease,
CC cerebral ischaemia, multiple sclerosis, basal ganglia degenerative
CC disease, motor neuron diseases, scrapie, spongiform encephalopathy and
CC loss or impaired memory, peripheral tissue disorders, particularly acute
CC respiratory distress syndrome, amyotrophic lateral sclerosis,
CC atherosclerotic cardiovascular disease, multiple lateral organ
CC dysfunction, complication resulting from inflammatory processes, acquired
CC immunodeficiency syndrome, AIDS, cancer and ageing. The antioxidant
CC compound of the invention has the advantage that it may cross a blood
CC barrier. The present sequence represents an antioxidant peptide of the
CC invention
CC
XX
SQ Sequence 4 AA;
XX
Query Match 100.0%; Score 31; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
XX
RESULT 9
ABB05573
ID ABB05573 standard; peptide; 4 AA.
AC ABB05573;
XX
DT 22-APR-2002 (first entry)
XX
DE Dithiol peptide #1.
XX
XX Dithiol; disulfide bond; chemical reagent; sulphydryl group; SH group;
XX trans-(Pt(ethylenediamine)2Cl2)2+.
XX
OS Synthetic.
XX
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 4 /note= "amidated"
FT
XX
PN W0200192466-A2.
XX
PN 06-DEC-2001.
XX
PD 16-MAY-2001; 2001WO-US015923.
XX
PF 16-MAY-2001; 2001WO-US015923.
XX
PR 26-MAY-2000; 2000US-00579883.
XX
XX (REGC) UNIV CALIFORNIA.
PA
XX
PI Rabenstein DA, Shi T;
XX
XX
DR WPI; 2002-114335/15.
XX

PT Forming an intramolecular disulfide bond in a peptide, comprises
 PT contacting a peptide comprising at least two sulfhydryl groups with an
 PT oxidizing agent that forms disulfide linkages in peptides.
 XX
 XX Example 1; Page 14; 40pp; English.
 PS
 CC The present invention describes a method of forming an intramolecular
 CC disulfide bond in a peptide, comprising contacting a peptide comprising
 CC at least two sulfhydryl (SH) groups with a compound (trans-
 CC (Pt(ethylenediamine)2Cl2)2+) (I). Also describes are: (1) a solution (II)
 CC comprising a peptide which comprises at least two sulfur groups, and (1);
 CC (2) a peptide synthesizer (III) for the synthesis of a peptide having an
 CC intramolecular disulfide linkage, comprises a number of vials containing
 CC amino acids derivatised for chemical peptide synthesis, where at least
 CC one of the vials comprises an amino acid that, when fully deprotected,
 CC bears a SH group, and a vial comprising (1); (3) chemically synthesising
 CC a peptide comprising a disulfide linkage, involving chemically coupling a
 CC number of amino acids to form a peptide comprising at least two SH
 CC groups, and contacting the peptide with (1); and (4) a kit for forming an
 CC intramolecular disulfide bond in a peptide, comprises a container
 CC containing (II). The method can be used for forming an intramolecular
 CC disulfide bond in a peptide. (II) is useful as a positive control when
 CC evaluating the efficacy of particular reagent species, and as a sample
 CC solution when optimising a purification protocol to clean up or to
 CC isolate the desired reaction product (e.g., when optimising a high
 CC pressure liquid chromatography (HPLC) protocol or evaluating a particular
 CC chromatography column). The present sequence represents a dithiol peptide
 CC which is used in an example from the present invention
 CC
 SQ Sequence 4 AA;
 XX
 XX
 Query Match 100.0%; Score 31; DB 5; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 XX
 RESULT 10
 AAE37340
 ID AAE37340 standard; peptide; 4 AA.
 XX
 AC AAE37340;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE E. coli thioredoxin active site peptide.
 XX
 KM Disulphide bond formation protein; Dsb protein; gene therapy; vaccine;
 KM HME; human monocytotropic ehrlichiosis; canine monocytic ehrlichiosis;
 KM CME; antibacterial; immunostimulant; thioredoxin.
 XX
 OS Escherichia coli.
 OS
 PN MO2003038061-A2.
 XX
 PD 08-MAY-2003.
 XX
 PF 01-NOV-2002; 2002WO-US035226.
 XX
 PR 01-NOV-2001; 2001US-0335611P.
 XX
 PA (RERE-) RES DEV FOUND.
 XX
 PI McBride JW, Walker DH;
 XX
 DR WPI; 2003-441356/41.
 XX
 PT New isolated DNA encoding a disulfide bond formation (Dsb) protein from
 PT bacteria of the genus Ehrlichia, useful for preventing human
 PT monocytotropic ehrlichiosis, or canine monocytic ehrlichiosis.

XX
 XX Example 10; Page 71; 73pp; English.
 PS
 CC The present invention relates to disulphide bond formation (Dsb) proteins
 CC and polynucleotides encoding such proteins from bacteria of the genus
 CC Ehrlichia. Sequences of the invention are useful for preventing human
 CC monocytotropic ehrlichiosis (HME) or canine monocytic ehrlichiosis (CME).
 CC The kits are useful for determining whether an animal or individual has
 CC been infected with a species of the bacteria of the Ehrlichia genus. Dsb
 CC sequences are also used in gene therapy and as vaccines. The present
 CC sequence is Escherichia coli thioredoxin protein active site peptide
 CC (conserved cysteine motif) used in the exemplification of the invention
 CC
 SQ Sequence 4 AA;
 XX
 XX
 Query Match 100.0%; Score 31; DB 6; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 XX
 RESULT 11
 ADJ47607
 ID ADJ47607 standard; peptide; 4 AA.
 XX
 AC ADJ47607;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Trx catalytic site consensus sequence, SEQ ID 15.
 XX
 KM Antidiabetic; Antiartherosclerotic; Neuroprotective; Nootropic;
 KM Antiparkinsonian; Anticonvulsant; Cardiac; Cardiovascular;
 KM Antirheumatic; Antiarthritic; Cytostatic; Antiproliferative; Gene Therapy;
 KM thioredoxin; Trx; atherosclerosis; diabetes; apoptotic disease;
 KM mitochondrial disease; cardiac dysfunction;
 KM angiogenesis dependent disease; neurodegenerative disease;
 KM rheumatoid arthritis; cancer; psoriasis; catalytic site.
 XX
 OS Unidentified.
 OS
 PN MO2004013283-A2.
 XX
 PD 12-FEB-2004.
 XX
 PF 22-JUL-2003; 2003WO-US022847.
 XX
 PR 02-AUG-2002; 2002US-0401073P.
 XX
 PA (UYRP) UNIV ROCHESTER.
 XX
 PI Min W, Yingmei L;
 XX
 DR WPI; 2004-157111/15.
 XX
 PT New mutant thioredoxin molecule which is resistant to oxidizing effects
 PT of cytokines or reactive oxygen species, useful for treating or
 PT diagnosing atherosclerosis, diabetes, Alzheimer's disease, myocardial
 PT infarction or cancer.
 XX
 PS Disclosure; SEQ ID NO 15; 145pp; English.
 XX
 CC The present invention relates to mutant thioredoxin (Trx) proteins and
 CC their coding sequences, where the thioredoxin molecule is resistant to
 CC the oxidizing effects of cytokines or reactive oxygen species or
 CC resistant to S-nitrosylation of a SH-group by nitrous oxide. The mutant
 CC Trx proteins are useful for treating or diagnosing atherosclerosis,
 CC diabetes, apoptotic disease, mitochondrial dysfunction disease or cardiac
 CC dysfunction. Mitochondrial dysfunction diseases include Kearns-Sayre
 CC syndrome or encephalomyopathy lactic acidosis and stroke-like episodes.

CC Apoptotic diseases include neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, multiple sclerosis or peripheral neuropathy. Cardiac
 CC dysfunction includes myocardial infarction, cardiomyopathy, arterial
 CC hypertension or heart failure. The mutant Trx proteins are also useful
 CC for treating or diagnosing angiogenesis dependent diseases, e.g.
 CC rheumatoid arthritis, cancer or psoriasis. The present sequence is the
 CC consensus sequence for the catalytic site of the Trx protein (residues 32
 CC to 35).

XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 1 CGPC 4

RESULT 12

ADM32927
 ID ADM32927 standard; peptide; 4 AA.

XX
 AC ADM32927;

XX
 DT 17-JUN-2004 (first entry)

XX
 DE Amino acid sequence of the thioredoxin active site.

XX
 KM mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 XX lung disease; cystic fibrosis.

OS Synthetic.

XX
 PN WO2004024868-A2.

XX
 PD 25-MAR-2004.

XX
 PF 10-SEP-2003; 2003WO-US028526.

XX
 PR 10-SEP-2002; 2002US-0409960P.

XX
 PR 11-APR-2003; 2003US-0462082P.

XX
 PA (NAJR-) NAT JEWISH MEDICAL & RES CENT.

XX
 PI White CW;

XX
 DR WPI; 2004-270016/25.

XX
 PT Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.

XX
 PS Disclosure; Page 15; 69pp; English.

XX The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the

CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.

XX
 SQ Sequence 4 AA;

Query Match 100.0%; Score 31; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 1 CGPC 4

RESULT 13

ADR46076
 ID ADR46076 standard; peptide; 4 AA.

XX
 AC ADR46076;

XX
 DT 04-NOV-2004 (first entry)

XX
 DE Antioxidant CB4.

XX
 KM Antioxidant; CB4; L-DOPA amide; levodopa amide; antiparkinsonian;
 XX neuroleptic; cytostatic.

OS Synthetic.

XX
 FH Key Location/Qualifiers

XX
 FT Modified-site 1 /note= "N-terminal acetyl"

XX
 FT Modified-site 4 /note= "C-terminal amide"

XX
 PN WO2004069146-A2.

XX
 PD 19-AUG-2004.

XX
 PF 03-FEB-2004; 2004WO-11000103.

XX
 PR 07-FEB-2003; 2003US-0445439P.

XX
 PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.

XX
 PI Atlas D;

XX
 DR WPI; 2004-625378/60.

XX
 PT New L-dihydroxy phenyl alanine derivatives useful for the treatment of
 PT e.g. Parkinson's disease, Tourette's syndrome, attention deficit
 PT hyperactive disorder and schizophrenia.

XX
 PS Disclosure; Page 18; 44pp; English.

XX The present sequence is that of the antioxidant peptide, CB4. This
 CC peptide is used in a claimed pharmaceutical composition of the invention
 CC also comprising an L-DOPA amide derivative. The pharmaceutical
 CC composition is useful for treatment of a condition associated with
 CC impaired dopaminergic signalling, such as Parkinson's disease, Tourette's
 CC syndrome, attention deficit hyperactive disorder, generation of pituitary
 CC tumours and schizophrenia. The inclusion of an antioxidant in the
 CC pharmaceutical composition provides for improved stability particularly
 CC in vivo, and also provides neuroprotection against oxidative stress,
 CC which is typically associated with L-DOPA treatment, and with the
 CC biosynthesis and degradation of dopamine and other catecholamines.

SEQ Sequence 4 AA;
Query Match 100.0%; Score 31; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 CGPC 5
1 CGPC 4
Db 1 CGPC 4
RESULT 14
ADV11816
ADV11816 standard; peptide; 4 AA.
XX
AC ADV11816;
XX
DT 24-MAR-2005 (revised)
DT 24-FEB-2005 (first entry)
XX
DE Thioresoxin conserved active site motif, SEQ ID NO:149.
XX
XX Antisense therapy; thioresoxin inhibitor; cancer; neoplasm; carcinoma;
XX melanoma; basal cell carcinoma; ovary tumor; breast tumor;
XX non-small-cell lung cancer; renal cell carcinoma; bladder tumor;
XX stomach tumor; prostatic cancer; pancreas tumor; lung tumor;
XX uterine cervix tumor; cervical dysplasia; colon tumor; colorectal tumor;
XX sarcoma; osteosarcoma; Kaposi's sarcoma; anti-HIV; glioma; cytostatic;
XX endocrine disease; gynecology and obstetrics; genitourinary disease;
XX respiratory disease; musculoskeletal disease; dermatological disease;
XX proliferative disease; atherosclerosis; antiarteriosclerotic;
XX cardiovascular disease; metabolic disorder; psoriasis; antipsoriatic;
XX immune disorder; diabetic retinopathy; antidiabetic; ophthalmological;
XX cardiovascular disease; ocular disease; rheumatoid arthritis;
XX antirheumatic; antirheumatic; inflammation; asthma; antiasthmatic;
XX skin allergy; anti-allergic; anti-inflammatory; dermatological;
XX verruca vulgaris; virucide; metabolism; cell proliferation;
XX apoptosis modulation; cell cycle; thioresoxin; cyclic.
XX
XX cellular organisms.
OS
FH Key Location/Qualifiers
FT Disulfide-bond 1..4
FT /note = Formation of this disulfide bond is reversible
XX
PN US2004241717-A1.
XX
PD 02-DEC-2004.
XX
PF 10-FEB-2004; 2004US-0076933.
XX
PR 10-FEB-2003; 2003US-0446374P.
XX
PA (SANT-) SANTARIS PHARMA AS.
XX
PI Hansen B, Thue CA, Westergaard M, Petersen KD, Wissenbach M;
XX WPI; 2005-056301/06.
XX
PT Novel compound useful for modulating expression of gene involved in
PT cancer disease, or for modulating red blood cell proliferation, cellular
PT proliferation, ion metabolism or glucose and energy metabolism.
XX
XX Disclosure; SEQ ID NO 149; 92pp; English.
PS
XX The invention relates to antisense oligonucleotides consisting of 8-50
XX nucleotides and/or nucleotide analogs which inhibit expression of the
XX putative human oncogene thioresoxin (TRX). The antisense oligonucleotides
XX comprise a subsequence of 8 or more nucleotides or nucleotide analogs,
XX wherein the subsequence is located within a sequence selected from
XX ADV11669-ADV11724. The oligonucleotides preferably contain at least
XX nucleotide analog, especially a locked nucleic acid (LNA) or a modified
XX nucleobase selected from 5-methylcytosine, isocytosine,

CC pseudoisocytosine, 5-bromouracil, 5-propynyluracil, 6-aminopurine, 2-
CC aminopurine, inosine, diaminopurine and 2-chloro-6-aminopurine. The
CC invention also relates to a conjugate comprising a TRX antisense
CC oligonucleotide of the invention and one or more non-nucleotide or non-
CC polynucleotide moieties covalently attached to the oligonucleotide; and a
CC pharmaceutical composition comprising a TRX antisense oligonucleotide or
CC conjugate of the invention, optionally further comprising a
CC chemotherapeutic agent, an anti-inflammatory compound or an antiviral
CC compound. The TRX antisense oligonucleotides, and conjugates and
CC compositions containing them, are useful in the treatment of cancers such
CC as carcinomas (e.g., malignant melanoma, basal cell carcinoma, ovarian
CC carcinoma, breast carcinoma, non-small cell lung cancer, renal cell
CC carcinoma, bladder carcinoma, recurrent superficial bladder cancer,
CC stomach carcinoma, prostatic carcinoma, pancreatic carcinoma, lung
CC carcinoma, cervical carcinoma, cervical dysplasia, laryngeal
CC papillomatosis, colon carcinoma, colorectal carcinoma and carcinoma
CC tumors); sarcomas (e.g., osteosarcoma, Ewing's sarcoma, chondrosarcoma,
CC malignant fibrous histiocytoma, fibrosarcoma, and Kaposi's sarcoma); or
CC gliomas. The TRX antisense oligonucleotides are also useful in the
CC treatment of conditions such as atherosclerosis, psoriasis, diabetic
CC retinopathy, rheumatoid arthritis, asthma, warts, and allergic
CC dermatitis. They may additionally be used for inhibiting cellular
CC proliferation and for modulating red blood cell proliferation, ion
CC metabolism, glucose and energy metabolism, pH regulation, matrix
CC metabolism, apoptosis, cytokinesis or the cell cycle. The TRX antisense
CC oligonucleotides of the invention have increased specificity and affinity
CC for TRX mRNA, and are resistant to degradation. The present sequence
CC represents the reversibly disulfide-bonded conserved active site motif of
CC thioresoxin which is referred to in the invention.
CC
CC Revised record issued on 24-MAR-2005 : Correction to comments field
XX
SQ Sequence 4 AA;
Query Match 100.0%; Score 31; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 2e+06; 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2 CGPC 5
1 CGPC 4
Db 1 CGPC 4
RESULT 15
ADM97624
ADM97624 standard; peptide; 4 AA.
XX
AC ADM97624;
XX
DT 19-MAY-2005 (first entry)
XX
DE Human thioresoxin protein-related active center peptide #1.
XX
XX chronic obstructive pulmonary disease; thioresoxin; respiratory-Gen.;
XX anti-inflammatory; cytokine antagonist; histamine antagonist;
XX interleukin 2 antagonist; interleukin 4 antagonist;
XX interleukin 6 antagonist; TNF alpha antagonist; emphysema;
XX chronic bronchitis.
XX
OS Homo sapiens.
XX
XX JP2005060408-A.
XX
PN 10-MAR-2005.
PD
XX 30-NOV-2004; 2004JP-00346572.
XX
PF 13-FEB-2004; 2004JP-00071691.
XX
PR (JPCF-) JPC KK.
XX
PA WPI; 2005-200153/21.
XX
XX

PT Agent e.g. tablet or capsules, for preventing and treating chronic
 PT obstructive pulmonary disease, contains polypeptide of thioredoxin super
 PT family as active ingredient.
 XX
 PS Disclosure; SEQ ID NO 3; 10pp; Japanese.
 XX
 CC This invention relates to a novel prophylactic or therapeutic agent of
 CC chronic obstructive pulmonary disease which contains a polypeptide of the
 CC thioredoxin super family as active ingredient, preferably human
 CC thioredoxin. The invention may be used for the production of compounds
 CC with a respiratory-Gen. or antiinflammatory activity acting as cytokine-
 CC antagonists, histamine-antagonists, interleukin-2-antagonists,
 CC interleukin-4-antagonists, interleukin-6-antagonists or TNF-alpha
 CC antagonists. The invention may be used for preventing and treating
 CC chronic obstructive pulmonary disease (COPD), preferably pulmonary
 CC emphysema or chronic bronchitis, caused by contaminants such as smoking
 CC gas, waste gas, dust and soot, and COPD accompanied with inflammation of
 CC cell or tissue, fibrosis and necrosis. The agent effectively prevents and
 CC treats chronic obstructive pulmonary disease, with negligible side
 CC effects. The present sequence is that of a peptide which represents the
 CC active center of thioredoxin and which is related to the
 CC prophylactic/therapeutic agent of the invention.
 CC
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 31; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 XX
 RESULT 16
 ADY81685
 ID ADY81685 standard; peptide; 4 AA.
 XX
 AC ADY81685;
 XX
 DT 02-JUN-2005 (first entry)
 XX
 DE Thioredoxin TrxA wild type redox active disulfide motif SEQ ID NO:2.
 XX
 KM genetic engineering; protein production; antimicrobial; antifungal;
 KM antiparasitic; antiviral; immunostimulant; thioredoxin.
 XX
 OS Synthetic.
 OS
 PN US6872563-B1.
 PN
 PD 29-MAR-2005.
 PD
 XX 05-OCT-2000; 2000US-00679705.
 PF
 XX 05-OCT-1999; 99US-0157770P.
 PR 08-NOV-1999; 99US-0163939P.
 PR 17-NOV-1999; 99US-0166044P.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA
 PI Beckwith J, Aslund F, Bessette PH, Georgiou G, Ritz D, Lim JB;
 XX WPI; 2005-239572/25.
 DR
 XX New prokaryotic cell that is genetically modified to shift the redox
 PT status of the cytoplasm to a more oxidative state, useful for producing
 PT disulfide bond containing proteins.
 PT
 XX Example 6; SEQ ID NO 2; 44pp; English.
 PS
 XX The invention relates to a prokaryotic cell that is genetically modified

CC to shift the redox status of the cytoplasm to a more oxidative state that
 CC favors disulfide bond formation, relative to a prokaryotic cell that is
 CC not genetically modified. The cell further comprises a mutated Ahpc gene
 CC comprising an insertion of three nucleotides in the TGT triplet rich
 CC region located at codons 36-39 of an Ahpc gene. The insertion increases
 CC the cell's ability to proliferate relative to a cell that is not further
 CC genetically modified. Also described is a method for producing a protein
 CC having at least one disulfide bond. The prokaryotic cell and method are
 CC useful for producing disulfide bond containing proteins. The proteins,
 CC polypeptides, and compositions are used for diagnostic, therapeutic, or
 CC prophylactic purposes. They are useful for inhibiting the growth of
 CC bacteria, viruses, fungi, or other parasites and for stimulating an
 CC immune response. They may be used as food supplements, as well as
 CC components of wash powders and creams. The present sequence represents a
 CC thioredoxin TrxA redox active disulfide motif.
 CC
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 31; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 1 CGPC 4
 XX
 RESULT 17
 AAY78911
 ID AAY78911 standard; peptide; 5 AA.
 XX
 AC AAY78911;
 XX
 DT 05-JUN-2000 (first entry)
 DT
 XX Thioredoxin conserved active site amino acid sequence.
 XX
 DE Thioredoxin reductase; redox inhibitor; cellular proliferation; cancer;
 XX apoptosis; reperfusion injury; hepatitis; amyotrophic lateral sclerosis;
 KM Alzheimer's disease; autoimmune disease; Sjogren's syndrome; lupus;
 KM rheumatoid arthritis; HIV; Heremansky-Pudlak syndrome; retinopathy;
 KM wound healing; Crohn's disease; ulcerative colitis; angiogenesis;
 KM adult respiratory distress syndrome; ARDS; infection;
 KM inflammatory conditions; psoriasis; inflammatory bowel disease;
 KM hyperproliferative disease; mycosis fungoides.
 XX
 OS Synthetic.
 OS
 PN WO200006088-A2.
 PN
 PD 10-FEB-2000.
 PD
 XX 02-AUG-1999; 99WO-US017496.
 PF
 XX 31-JUL-1998; 98US-00127219.
 PR
 XX (KIRK/) KIRKPATRICK D L.
 PA (PORT/) POWIS G.
 PA
 PI Kirpatrick DL, Powis G;
 PI
 DR WPI; 2000-195158/17.
 DR
 XX New composition for preventing inhibition of apoptosis and for treating
 PT e.g. cancer or reperfusion injuries comprises inhibitor of cellular redox
 PT signaling.
 PT
 XX Disclosure; Page 12; 55pp; English.
 PS
 XX This sequence represents a conserved active site found in thioredoxins.
 CC The thioredoxins are a class of low molecular weight redox proteins.
 CC Thioredoxin exerts specific redox control over a number of transcription
 CC factors to modulate their DNA binding and therefore regulates gene

transcription. Thioredoxin reductase catalyses the reduction of thioredoxin. The thioredoxin redox system plays an important role in a number of diseased states. The invention relates to a composition comprising an inhibitor of cellular redox signalling and a carrier. The composition can be used for inhibiting cellular proliferation or preventing inhibition of apoptosis and is therefore useful for treating cancer, reperfusion injury following ischaemia, hepatitis, amyotrophic lateral sclerosis, neurodegenerative diseases, Alzheimer's disease, autoimmune diseases, Sjogren's syndrome, lupus, rheumatoid arthritis, HIV, Herpesvirus, Kaposi's sarcoma, retinal oxidative damage, retinopathy, skin hyperplasia, aging, ultraviolet damage, wound healing, Crohn's disease, ulcerative colitis, angiodysplasia, uterine disorders, adult respiratory distress syndrome (ARDS), lung disorders, viral infections such as herpes virus, pox virus and adenovirus infections, inflammatory conditions, autoimmune diseases (such as systemic lupus erythematosus, rheumatoid arthritis, psoriasis, inflammatory bowel disease and autoimmune diabetes), immune mediated glomerular nephritis and hyperproliferative diseases (such as fibrosis) and mycosis fungoides

Sequence 5 AA;

Query Match 100.0%; Score 31; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 1 CGPC 4

RESULT 18

AAE05156
ID AAE05156 standard; peptide; 5 AA.

XX AAE05156;

DT 12-SEP-2001 (first entry)

XX Human thioredoxin (ADF) active site.

XX T cell-derived colony stimulating factor; TC-CSF; immunostimulant;

KM acquired immune deficiency syndrome; AIDS; cancer; gene therapy;

KM haematopoietic growth factor; human; thioredoxin; ADF; active site.

OS Homo sapiens.

PN US6254861-B1.

PD 03-JUL-2001.

PF 24-JAN-1994; 94US-00180371.

PR 23-MAY-1989; 89US-00356006.

PR 12-JUL-1991; 91US-00729135.

PR 19-AUG-1991; 91US-00747784.

PR 01-NOV-1991; 91US-00788115.

PR 01-JUL-1992; 92US-00906866.

XX (CHOU/) CHOUHURY C.

XX Choudhury C;

XX WPI; 2001-432041/46.

XX New T cell-derived colony stimulating factor for treating immune-

PT compromised patients, including acquired immunodeficiency syndrome

PT patients and certain types of cancer patients.

XX Example 33; Col 36; 38pp; English.

XX The invention relates to T-cell derived colony stimulating factors (TC-

CSF) and nucleic acid molecules encoding them. TC-CSF which is a novel haematopoietic growth factor is useful for treating immune-compromised

patients, including acquired immune deficiency syndrome (AIDS) patients and certain types of cancer patients. TC-CSF DNA is used in gene therapy. The present sequence is human thioredoxin active site which is used in the exemplification of the invention

Sequence 5 AA;

Query Match 100.0%; Score 31; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 2 CGPC 5

RESULT 19

AAO21523
ID AAO21523 standard; peptide; 5 AA.

XX AAO21523;

DT 02-SEP-2002 (first entry)

XX Wild type thioredoxin active site peptide sequence.

XX Cytostatic; thioredoxin; cell growth stimulator; modulating; apoptosis;

KM tumour; wild type.

XX Unidentified.

PN US2002055131-A1.

PD 09-MAY-2002.

PF 06-JUN-2001; 2001US-00875578.

PR 03-JUN-1999; 99US-00319292.

XX (POWI/) POWIS G.

XX Powis G;

DR WPI; 2002-470971/50.

XX Modulating thioredoxin-associated inhibition of apoptosis for the

PT treatment of tumors.

PS Disclosure; Page 1; 59pp; English.

XX The invention relates to the use of thioredoxin as a cell growth

CC stimulator, for modulating thioredoxin cell growth stimulator-associated

CC inhibition of apoptosis, comprising controlling the expression and/or

CC activity of the thioredoxin. The invention is useful for treating tumours

CC associated with aberrant thioredoxin expression and activity. This

CC sequence represents a wild type thioredoxin active site peptide sequence

XX relating to the invention

XX Sequence 5 AA;

Query Match 100.0%; Score 31; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 1 CGPC 4

RESULT 20

ABG71301
ID ABG71301 standard; peptide; 5 AA.

XX

AC ABG71301;
 XX
 DT 16-DEC-2002 (first entry)
 XX
 DE Thioresdoxin protein active site disulphide/dithiol conserved sequence.
 XX
 KM Thioresdoxin, TRXP-2; cancer; actinic keratosis;
 KM cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
 KM cirrhosis; hepatitis; mixed connective tissue disease; AIDS; trauma;
 KM polyarthritis; primary thrombocytopaenia; psoriasis; anaemia;
 KM inflammatory disorder; acquired immunodeficiency syndrome; infection;
 KM adult respiratory distress syndrome; Addison's disease; allergy; asthma;
 KM atherosclerosis; gout; myocardial inflammation; scleroderma;
 KM pericardial inflammation; osteoporosis; rheumatoid arthritis;
 KM systemic lupus erythematosus; ulcerative colitis; Reiter's syndrome;
 KM haemodialysis; Crohn's disease; atopic dermatitis; viral disorder;
 KM autoimmune thyroiditis; diabetes mellitus; Graves' disease;
 KM glomerulonephritis; active site disulphide/dithiol conserved sequence.
 XX
 OS Unidentified.
 XX
 PN US2002102654-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 17-SEP-2001; 2001US-00954846.
 XX
 PR 30-JUN-1998; 98US-00107248.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Corley NC, Guegler KJ, Patterson C, Baughn MR;
 DR WPI; 2002-690612/74.
 XX
 PT Novel human thioresdoxin protein and polynucleotide for diagnosing,
 PT preventing and treating cell proliferative, inflammatory and viral
 PT disorders.
 XX
 PS Disclosure; Page 1; 41pp; English.
 XX
 CC The invention relates to isolated human thioresdoxin polypeptide TRXP-2, a
 CC naturally occurring polypeptide comprising an amino acid sequence 90%
 CC identical to TRXP-2, a biologically active or immunogenic fragment of
 CC TRXP-2 and its encoding polynucleotide (TRXP-2 NA). Also included are a
 CC recombinant polynucleotide comprising a promoter sequence operably linked
 CC to TRXP-2 NA, a cell transformed with the recombinant sequence, a TRXP-2
 CC transgenic organism, an anti-TRXP-2 antibody and a composition comprising
 CC TRXP-2, an agonist or antagonist compound identified using TRXP-2, or the
 CC above antibody. TRXP-2 is useful for screening a compound for
 CC effectiveness as an agonist or antagonist of TRXP-2. TRXP-2, the
 CC identified agonist and antagonist are useful for treating a disease or
 CC condition associated with decreased or overexpression of functional TRXP
 CC in a patient. TRXP-2 is useful for screening for a compound that
 CC modulates the activity of the polypeptide or that binds to the
 CC polypeptide. TRXP-2 is also useful as an immunogen for preparing
 CC polyclonal or monoclonal antibodies by hybridoma technology. TRXP-2 NA is
 CC useful for screening a compound for effectiveness in altering expression
 CC of a target polynucleotide comprising the sequence of TRXP-2 NA. The
 CC antibody is useful for detecting the presence of TRXP-2 and purifying
 CC TRXP-2 from a sample. The antibody, optionally labeled, is useful for
 CC diagnosing a condition or disease associated with expression of TRXP in a
 CC subject or in a biological sample. TRXP-2 and TRXP-2 NA and modulators of
 CC TRXP-2 are useful for diagnosis, treatment and prevention of cell
 CC proliferative (e.g. cancer, actinic keratosis, arteriosclerosis,
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue
 CC disease, polycythaemia vera, primary thrombocytopaenia and psoriasis),
 CC inflammatory (e.g. adult respiratory distress syndrome, Addison's
 CC disease, allergies, anaemia, asthma, atherosclerosis, gout, myocardial or
 CC pericardial inflammation, osteoporosis, rheumatoid arthritis,
 CC scleroderma, systemic lupus erythematosus, ulcerative colitis, Reiter's
 CC syndrome, haemodialysis, Crohn's disease, atopic dermatitis, autoimmune
 CC thyroiditis, diabetes mellitus, Graves' disease and glomerulonephritis),

CC infection (e.g. viral, bacterial, fungal, parasitic, protozoal and
 CC helminthic), viral disorders (e.g. acquired immunodeficiency syndrome
 CC (AIDS) and trauma. The present sequence represents a thioresdoxin active
 CC site disulphide/dithiol conserved sequence as found in TRXP-2
 XX
 SQ Sequence 5 AA;
 XX
 Query Match 100.0%; Score 31; DB 5; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 2 CGPC 5
 DB 2 CGPC 5
 XX
 RESULT 21
 AAP71087
 ID AAP71087 standard; peptide; 6 AA.
 XX
 AC AAP71087;
 XX
 DT 25-MAR-2003 (revised)
 DT 31-OCT-2002 (revised)
 DT 06-JUN-1991 (first entry)
 XX
 DB Sequence of thioresdoxin analogue.
 XX
 KM Redox active peptide; antioxidant; stress; ischaemia; lipid peroxidation;
 KM food industry; cosmetics; antibiotic.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note="Optional, and may optionally be joined to a
 FT FT terminal blocking gp."
 FT Misc-difference 6 /note="see above"
 FT
 XX
 PN BP237189-A.
 XX
 PD 16-SEP-1987.
 XX
 PF 10-FEB-1987; 87EP-00301150.
 XX
 PR 10-FEB-1986; 86US-00828112.
 PR 14-MAR-1986; 86US-00839857.
 PR 20-OCT-1986; 86US-00921287.
 XX
 PA (REPK) REPLIGEN CORP.
 XX
 PI Piglet VP, Millis CD;
 PT
 PT New and known thioresdoxin derivs. and analogues - useful for preventing
 PT metal catalysed oxidative damage in biological reactions and disease
 PT states.
 XX
 DR WPI; 1987-258442/37.
 XX
 PT Claim 7; Page 7; 7pp; English.
 XX
 CC It is a redox active peptide which can be used in cpds. to treat stress
 CC and ischaemia, for inhibiting lipid peroxidn. due to drugs or toxic
 CC effects, as anti-inflammatory agents, to prevent DNA damage, and to
 CC maintain the biological activity of antibiotics or proteins. Thioresdoxin
 CC can be used as a general antioxidant in the food and cosmetic industry.
 CC It may be used in prodn. processes for antibiotics, proteins or
 CC polypeptides. Therapeutic dose is 1 microgram/kg - 10mg/kg. (Updated on
 CC 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PA field.)
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 22

ABP54936 standard; peptide; 6 AA.

ABP54936;

08-JAN-2003 (first entry)

Active site peptide of thioredoxin.

Thioredoxin; organoarsenical; arsenoxide; antiarthritic; antigout;

osteopathic; antineumatic; arthritis; therapy.

Homo sapiens.

WO200274305-A1.

26-SEP-2002.

19-MAR-2002; 2002WO-AU000310.

19-MAR-2001; 2001AU-00003798.

(UNIX) UNISEARCH LTD.

Hogg PJ, Donoghue N;

WPI; 2002-750519/81.

Use of an impermeable cell membrane compound for the treatment of
arthritis in vertebrates.

Example 2 (b) ; Page 42; 91pp; English.

The present sequence is that of a hexapeptide comprising the active site
sequence of thioredoxin. The hexapeptide was used in an example from the
invention that examined the binding of 4-(N-(S-
glutathionylacetyl)amino)phenylarsenoxide (GSNO) to peptide and protein
dithiols. The results indicated that GSNO selectively binds proteins
containing closely spaced thiols. The invention provides a method for the
treatment and/or prophylaxis of arthritis using a compound of formula A-
(L-Y)P, where A is a cell-membrane impermeable pendant group, L is a
linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and P
is an integer from 1 to 10. The compound, e.g. GSNO, is useful for the
treatment of arthritic conditions such as calcific periarthritis,
enteropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid,
septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,
CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).
The compound blocks angiogenesis in the synovial tissue and leucocyte
ingress that triggers inflammation, with no signs or symptoms of toxicity

Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 23

ADA08451
ADA08451 standard; peptide; 6 AA.

ADA08451;

06-NOV-2003 (first entry)

Mammalian peptide found in thioredoxin and protein disulphide isomerase.

Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
plasmin reductase; reduced plasmin protein; anti-angiogenesis activity;
uokinase-type plasminogen activator; A61; annexin II heterotetramer;
annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
protein disulphide isomerase; modulating angiogenesis; mammalian;
cleavage peptide.

Mammalia.

US2003083234-A1.

01-MAY-2003.

26-NOV-2002; 2002US-00304287.

28-NOV-2001; 2001US-0333866P.

(WAIS/) WAISMAN D.
(KMON/) KMON M.

Waisman D, Kwon M;

WPI; 2003-596985/56.

Producing an anti-angiogenesis plasmin fragment, useful for modulating,
e.g. promoting or inhibiting angiogenesis, comprises contacting a
plasminogen polypeptide with a plasminogen activator and a plasmin
reductase.

Example 2; Page 6; 29pp; English.

The present invention relates to a method for producing an anti-
angiogenesis plasmin fragment. The method comprises contacting a
plasminogen polypeptide with a plasminogen activator and a plasmin
reductase, where a reduced plasmin protein is produced and the anti-
angiogenesis plasmin fragment having anti-angiogenesis activity, is
released from the reduced plasmin protein. The plasminogen activator is
preferably a uokinase-type plasminogen activator. The angiogenesis
plasmin fragment is A61. The plasmin reductase is selected from annexin
II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
disulphide isomerase. The annexin II heterotetramer is associated with a
cell membrane. The method of the invention is useful for modulating (e.g.
promoting or inhibiting) angiogenesis. The present sequence represents a
mammalian cleavage peptide found in thioredoxin and protein disulphide
isomerase.

Sequence 6 AA;

Query Match 100.0%; Score 31; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 24

ADH05024
ADH05024 standard; peptide; 6 AA.

ADH05024;

11-MAR-2004 (first entry)

XX Target peptide #5 of the invention.
 DE pendant phenylarsine moieties; labeling; target peptide.
 XX
 XX Synthetic.
 XX WO2003107010-A1.
 XX
 PD 24-DEC-2003.
 XX
 XX 13-JUN-2003; 2003WO-US018792.
 XX
 XX 14-JUN-2002; 2002US-0386699P.
 XX
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Ebright RH, Ebright YW;
 XX
 DR WPI; 2004-156348/15.
 XX
 XX New bis-phenylarsine derivatives useful for labeling protein in living
 PT cells and for screening a library of peptides and identifying a cysteine
 PT containing peptides.
 XX
 PS Claim 23; SEQ ID NO 5; 82pp; English.
 XX
 CC The present invention relates to a molecule with two pendant phenylarsine
 CC moieties. The invention is useful for imparting detectable properties to
 CC target material, for detecting target material, for monitoring binding
 CC process, for isolating and immobilizing at least one target material, for
 CC screening a library of peptides and identifying a cysteine containing
 CC peptides and for labeling protein in living cells. The present sequence
 CC represents a target peptide of the invention.
 XX
 SQ Sequence 6 AA;
 QY
 Db 2 CGPC 5
 ||||
 2 CGPC 5
 Best Local Similarity 100.0%; Score 31; DB 8; Length 6;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 25
 ADM32929
 ID ADM32929 standard; peptide; 6 AA.
 XX
 AC ADM32929;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of the thioredoxin active site.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1..6 /note="active site of thioredoxin"
 FT Modified-site 2 /note="this residue is in a reduced state"
 FT Modified-site 5 /note="this residue is in a reduced state"
 FT
 XX WO2004024868-A2.
 PN
 XX 25-MAR-2004.
 PD
 XX

PF 10-SEP-2003; 2003WO-US028526.
 XX
 XX 10-SEP-2002; 2002US-0409960P.
 PR 11-APR-2003; 2003US-0462082P.
 XX
 XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
 XX
 XX White CW;
 XX
 DR WPI; 2004-270016/25.
 XX
 XX Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Claim 13; Page 51; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or a
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.
 XX
 SQ Sequence 6 AA;
 QY
 Db 2 CGPC 5
 ||||
 2 CGPC 5
 Best Local Similarity 100.0%; Score 31; DB 8; Length 6;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 26
 ADM32928
 ID ADM32928 standard; peptide; 6 AA.
 XX
 AC ADM32928;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of the thioredoxin active site.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Active-site 1..6 /note="active site of thioredoxin"
 FT Misc-difference 1 /note="any amino acid"
 FT

FT Modified-site 2 /note= "this residue is in a reduced state"
 FT Misc-difference 3 /note= "any amino acid"
 FT Misc-difference 4 /note= "any amino acid"
 FT Modified-site 5 /note= "this residue is in a reduced state"
 FT Misc-difference 6 /note= "any amino acid"
 PN WO2004024868-A2.
 XX 25-MAR-2004.
 XX 10-SEP-2003; 2003MO-US028526.
 XX 10-SEP-2002; 2002US-0409960P.
 PR 11-APR-2003; 2003US-0462082P.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI White CW;
 XX
 DR WPI; 2004-270016/25.
 XX
 PT Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Claim 12; Page 51; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
 CC cause of the disease. The present sequence represents an active site of a
 CC thioredoxin which is used in the method of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Thioredoxin family conserved catalytic site peptide.
 XX
 KW 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone;
 KW cytoskeletal; thioredoxin reductase inhibitor; proliferative condition;
 KW colon cancer; renal cancer; thioredoxin; thioredoxin reductase;
 KW cell cycle progression; cell proliferation; apoptosis;
 KW catalytic site peptide.
 XX
 OS Synthetic.
 OS
 PN WO2004056361-A1.
 XX
 PD 08-JUL-2004.
 XX
 PF 20-DEC-2002; 2002MO-GB005842.
 XX
 PR 20-DEC-2002; 2002MO-GB005842.
 XX
 PR (CANC-) CANCER RES TECHNOLOGY LTD.
 XX
 PA Stevens MFG, Westwell AD, Poole TD, Wells G, Berry JM;
 XX
 PI WPI; 2004-517586/49.
 XX
 DR
 XX
 PT New 4-(1(sulfonyl)-1H-indol-2-yl)-4(hydroxy)-cyclohexa-2,5-dienone
 PT derivatives are thioredoxin reductase inhibitors useful for treating e.g.
 PT colon or renal cancer.
 XX
 PS Disclosure; Page 82; 141pp; English.
 XX
 CC The present invention described 4-(1(Sulfonyl)-1H-indol-2-yl)-4(hydroxy)-
 CC cyclohexa-2,5-dienone derivatives (I) and their salts, esters, amides,
 CC solvates, hydrates or protected forms. (I) have cytostatic activities,
 CC and can be used as thioredoxin reductase inhibitors. (I) can be used for
 CC treating a proliferative condition (especially colon or renal cancer) or
 CC a condition mediated by thioredoxin/thioredoxin reductase in the human or
 CC animal body. (I) are also useful for inhibiting thioredoxin/thioredoxin
 CC reductase and cell cycle progression, to regulate/inhibit cell
 CC proliferation and/or to promote apoptosis in a cell in vitro or in vivo.
 CC The present sequence represents a thioredoxin family conserved catalytic
 CC site peptide, which is given in the exemplification of the present
 CC invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 27
 ID ADP87509
 XX ADP87509 standard; peptide; 6 AA.
 AC ADP87509;

RESULT 28
 ID ADP67423
 XX ADP67423 standard; peptide; 6 AA.
 AC ADP67423;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Thioredoxin and protein disulfide isomerase common sequence SEQ ID NO:4.
 XX
 KW p11; p11 activity modulator; plasminogen activation; cytoskeletal;
 KW antisense therapy; cancer; tumour; tumour growth inhibition; thioredoxin;
 KW protein disulfide isomerase.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX	PN		WO2004054517-A2.
XX	PD	01-JUL-2004.	
XX	PF	12-DEC-2003; 2003WO-US040029.	
XX	PR	13-DEC-2002; 2002US-0433140P.	
XX	PA	(MEDI-) MEDIONICS LLC.	
XX	PA	(WALS/) WALSMAN D.	
XX	P1	Walsman D;	
XX	DR	WPI, 2004-487995/46.	
XX	PT	Composition useful for inhibiting growth of tumor in patient, modulates	
XX	PT	activity of p11 protein and effects change in level of plasminogen	
XX	PS	activation by a cell.	
XX	PS	Example 2; SEQ ID NO 4; 140pp; English.	
XX	CC	The present invention describes a composition (I) which modulates the	
XX	CC	activity of a p11 protein and effects a change in the level of	
XX	CC	plasminogen activation by a cell. Also described: (1) making (M1) a	
XX	CC	clonal cell line, which involves isolating a cell, then characterizing	
XX	CC	the activity of a protein produced by the cell or clonal progeny of the	
XX	CC	cell, where the protein is involved in plasminogen activation; and (2) a	
XX	CC	clonal cell line (II) useful in the identification of composition that	
XX	CC	modulate p11 activity, where the clonal cell line is obtained by (M1).	
XX	CC	(1) has cytostatic activity, and can be used in antisense therapy. (1) is	
XX	CC	useful for modulating the activity of p11 which involves administering	
XX	CC	(1) to a cell. The cell can be a human cancer cell, chosen from a HT1080	
XX	CC	fibrosarcoma cell, a IMCAP prostate cancer cell and a CCR-22 colorectal	
XX	CC	adenocarcinoma cell. (1) is also useful for reducing the development of	
XX	CC	cancer in a patient e.g., mouse which involves administering (1) to a	
XX	CC	cancer cell in the patient. (1) is useful for inhibiting the growth of	
XX	CC	tumours or inhibiting tumour cell invasion in a patient, which involves	
XX	CC	administering (1) to a cancer cell in the patient. (II) is useful for	
XX	CC	identifying a composition that modulates p11 activity which involves	
XX	CC	administering the composition to (II) obtained by (M1), determining the	
XX	CC	change in p11 activity of a cell of the clonal cell line relative to a	
XX	CC	cell of a clonal cell line that had not received the composition, and	
XX	CC	identifying the composition that produces a change in p11 activity. The	
XX	CC	change in p11 activity is a change in the level of plasminogen activation	
XX	CC	activity. The present sequence represents a thiorodoxin and protein	
XX	CC	dissulfide isomerase common sequence, which is used in the exemplification	
XX	CC	of the present invention.	
XX	SQ	Sequence 6 AA;	
		Query Match 100.0%; Score 31; DB 8; Length 6;	
		Best Local Similarity 100.0%; Pred. No. 2e+06;	
		Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY		2 CGPC 5	
DB		2 CGPC 5	
RESULT 29			
ID	AD097008		
	AD097008 standard; peptide; 6 AA.		
AC	AD097008;		
DT	07-OCT-2004 (first entry)		
DE	Thiorodoxin and protein disulphide isomerase common sequence.		
KM	p11 protein; plasminogen activation; tumour growth; metastasis; treating.		
OS	Synthetic.		

[illegible]

PT Prepn. of anti-HCG and anti-LH vaccines - by use of oligo-peptide(s)
 PT specific to beta-sub-unit of LH and HCG.
 PS Claim 1, Page 17, 22pp; English.
 XX
 CC Oligopeptides AAP50198-P50205, specific to the beta-subunit of LH and of
 CC HCG, located near cysteine groups, are used in a claimed process for the
 CC preparation of anti-HCG and anti-LH vaccines. The vaccines are
 CC characterised in that these oligopeptides are complexed upon themselves
 CC and between themselves by disulphur bridges, upon their own beta-subunit
 CC of HCG and LH or upon oligopeptides containing cysteine whose AA chain is
 CC common to LH and HCG, namely the peptides in AAP50208-P50212. Throug
 CC sulphur bridges the specific oligopeptides are administered by injection
 CC in vaccines to cause prohn. of antibodies so that a contraceptive effect
 CC is achieved; and the antibodies are also useful in assays for HCG and LH
 CC in body fluids
 CC
 CC Sequence 8 AA;
 SQ
 QY Query Match 100.0%; Score 31; DB 1; Length 8;
 DB Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 CGPC 5
 4 CGPC 7
 DB
 RESULT 31
 ADP81369
 ID ADC81369 standard; peptide; 8 AA.
 XX
 AC ADC81369;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Bovin THF-gamma2 analogue C3-C6-cyclicTHF gamma2.
 XX
 KW Cow; thymic humoral factor gamma2; THF-gamma2; concanavalin A;
 KW Con A-induced interleukin-2 production; mouse spleen cells;
 KW granulocyte-monocyte colony forming cell; GM-CFC; mouse bone marrow;
 KW immunomodulatory agent; congenital immune defect;
 KW primary T cell deficiency; thymic dysplasia; Down's syndrome;
 KW viral infection; herpes; adenovirus infection; HIV infection;
 KW subacute sclerosing pan-encephalitis; immune suppression; leukopenia;
 KW cancer; chemotherapy; radiotherapy; autoimmune inflammatory disorder;
 KW rheumatoid arthritis; systemic lupus erythematosus; psoriasis;
 KW bone marrow transplantation; atopic condition; asthma; atopic dermatitis;
 KW mutant; muten; cyclic.
 XX
 OS Synthetic.
 XX
 OS Bos taurus.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..6
 FT /note= "This bond cyclilises the molecule"
 FT Misc-difference 3
 FT /note= "Wild-type Asp substituted by Cys"
 FT Misc-difference 6
 FT /note= "Wild-type Lys substituted by Cys"
 XX
 PN WO9501182-A1.
 XX
 PD 12-JAN-1995.
 XX
 PF 28-JUN-1994; 94WO-US007304.
 XX
 PR 01-JUL-1993; 93IL-00106214.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA
 XX Rycus A, Burstein Y, Trainin N;
 XX

DR WPI; 1995-060814/08.
 XX
 XX New thymic humoral factor gamma 2 analogues - used as immunomodulatory
 PT agents for treating e.g. immune defects, viral infections or auto-immune
 PT disease.
 PS Example 2; Page 17; 10pp; English.
 XX
 CC A peptide is claimed which is a thymic humoral factor (THF)-gamma2
 CC analogue of at least 4 amino acid (AA) residues or a functional
 CC derivative or salt, capable of enhancing concanavalin A (con A)-induced
 CC interleukin-2 (IL-2) production in mouse spleen cells and/or the number
 CC of granulocyte-monocyte colony forming cells (GM-CFC) of mouse bone
 CC marrow. The peptide comprises one or more sequences corresponding to the
 CC sequence of the wild-type THF-gamma2 but differing by (i) deletion of one
 CC or more AA residues, (ii) addition of one or more AA residues at the N-
 CC and/or C-terminus, (iii) substitution of one or more AA residues by a
 CC protein natural or non-natural AA residue, (iv) cyclisation through a
 CC free carboxyl group and a free amino group or through disulphide bonds of
 CC cysteine residues or (v) linkage of two or more sequences or modified
 CC sequences corresponding to (i)-(iv), either directly or through a peptide
 CC or non-peptide chain. The peptides are used as immunomodulatory agents.
 CC They can be used for treating e.g. congenital immune defects involving
 CC primary T cell deficiencies such as thymic dysplasia and Down's syndrome,
 CC HIV), as well as subacute infections such as subacute sclerosing pan-
 CC encephalitis, immune suppression and leukopenia following cancer
 CC treatment by chemotherapy and/or radiotherapy, autoimmune inflammatory
 CC disorders, e.g. rheumatoid arthritis, systemic lupus erythematosus and
 CC psoriasis, in bone marrow transplantation to prevent viral infections and
 CC in atopic conditions such as asthma and atopic dermatitis. The present
 CC sequence is a bovine THF-gamma2 analogue peptide of the invention.
 CC
 CC Sequence 8 AA;
 SQ
 QY Query Match 100.0%; Score 31; DB 2; Length 8;
 DB Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 CGPC 5
 3 CGPC 6
 DB
 RESULT 32
 AAW05002
 ID AAW05002 standard; peptide; 8 AA.
 XX
 AC AAW05002;
 XX
 DT 03-DEC-1996 (first entry)
 XX
 DE Thymic humoral factor gamma-2 cyclic analogue.
 XX
 KW Immunomodulation; immunomodulator; immune system; deficiency;
 KW aberrant response; chronic bronchitis; atopic disease; AIDS;
 KW acquired immune deficiency syndrome; herpes virus infection; cyclic.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 3..6
 FT
 FT Disulfide-bond 3..6
 XX
 PN WO9611943-A1.
 XX
 PD 25-APR-1996.
 XX
 PF 06-OCT-1995; 95WO-SB001151.
 XX
 PR 14-OCT-1994; 94SE-00003526.
 XX
 XX (ASTR) ASTRA AB.
 PA
 XX

PI Bergstrand H, Eriksson T, Karabelas K, Lindvall M, Saernstrand B;
 XX WPI; 1996-221938/22.
 XX
 PT Peptide(s) with immunomodulatory activity - useful for treating e.g.
 XX chronic bronchitis, malignancies, herpes, AIDS or atopic disease, as
 XX adjuvants in vaccines, or for inhibiting graft rejection.
 PS Claim 1; Page 50; 63pp; English.
 CC The present peptide is a known immunomodulatory agent. It is described as
 CC a cyclic analogue of thymic humoral factor gamma-2 and was disclosed in
 CC WO9501182. The peptide is one of 6 known peptides which concord with a
 CC highly genetic sequence covering immunomodulatory peptides of 4-15 amino
 CC acids being claimed in the present patent application; all 6 peptides are
 CC specifically excluded from the claim
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 31; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 XX
 RESULT 33
 AAM41664
 ID AAM41664 standard; peptide; 8 AA.
 XX
 AC AAM41664;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Immunomodulatory peptide.
 XX
 KW Immunomodulator; immunosuppressant; immunostimulator; treatment;
 KW transplant rejection; autoimmune disease; cancer; infection.
 XX
 OS Synthetic.
 XX
 PN WO9739023-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 04-APR-1997; 97WO-SE000574.
 XX
 PR 12-APR-1996; 96SE-00001422.
 PR 23-SEP-1996; 96SE-00003463.
 XX
 PA (ASTR) ASTRA AB.
 XX
 PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX WPI; 1997-526397/48.
 DR
 XX
 PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immunostimulatory or immunosuppressive activity - can be used
 PT to treat, e.g. cancers, infection, autoimmune disease or transplant
 PT rejection.
 XX
 PS Disclosure; Page 19; 183pp; English.
 CC A novel immunosuppressing or immunostimulatory peptide conforms to the
 CC motifs represented by the formulae of the invention, with the proviso
 CC that the peptides described in AAM36999, AAM37000 and AAM41647 to
 CC AAM41682 are excluded. An immunosuppressant can be used to treat
 CC transplant rejection or autoimmune disease, e.g. rheumatoid arthritis,
 CC systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed
 CC connective tissue disease, dermatomyositis, polymyositis, Reiter's
 CC syndrome, Behcet's disease, type I diabetes, Hashimoto's thyroiditis,

CC Graves' disease, multiple sclerosis, myasthenia gravis,
 CC encephalomyelitis, phemphigus vulgaris, vegetans or foliaceus, Seneac-
 CC Usher syndrome or Brazilian phemphigus. An immunostimulator can be used
 CC to treat conditions such as cancer or infection
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 31; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 XX
 RESULT 34
 ADH05029
 ID ADH05029 standard; peptide; 8 AA.
 XX
 AC ADH05029;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Target peptide #10 of the invention.
 XX
 KW pendant phenylarsine moieties; labeling; target peptide.
 XX
 OS Synthetic.
 XX
 PN WO2003107010-A1.
 XX
 PD 24-DEC-2003.
 XX
 PF 13-JUN-2003; 2003WO-US018792.
 XX
 PR 14-JUN-2002; 2002US-0388699P.
 XX
 PA (RUPF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Ebright RH, Ebright YW;
 XX
 DR WPI; 2004-156348/15.
 XX
 PT New bis-phenylarsine derivatives useful for labeling protein in living
 PT cells and for screening a library of peptides and identifying a cysteine
 PT containing peptides.
 XX
 PS Claim 25; SEQ ID NO 10; 82pp; English.
 XX
 CC The present invention relates to a molecule with two pendant phenylarsine
 CC moieties. The invention is useful for imparting detectable properties to
 CC target material, for detecting target material, for monitoring binding
 CC process, for isolating and immobilizing at least one target material, for
 CC screening a library of peptides and identifying a cysteine containing
 CC peptides and for labeling protein in living cells. The present sequence
 CC represents a target peptide of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 31; DB 8; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 1 CGPC 4
 XX
 RESULT 35
 ADV60194
 ID ADV60194 standard; peptide; 8 AA.
 XX

```

AC ADV60194;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7699.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food, feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004MO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX 17-JUN-2003; 2003US-0479061P.
XX
PA (VIRB-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
PS Example; SEQ ID NO 7699; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a VEGF peptide combo.
XX
SQ Sequence 8 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 CGPC 5
Db 2 CGPC 5
XX
RESULT 36
ADZ28911
ID ADZ28911 standard; protein; 8 AA.
AC ADZ28911;
XX

```

```

DT 30-JUN-2005 (first entry)
XX
DE Calmodulin Ortho C-terminus.
XX
KM cell culture; DNA detection; RNA detection; protein purification;
XX calmodulin ortho; Cam.
XX
OS Unidentified.
XX
PN WO2005033266-A2.
XX
PD 14-APR-2005.
XX
PF 01-OCT-2004; 2004MO-US032337.
XX
PR 01-OCT-2003; 2003US-0508142P.
XX
PA (INVI-) INWITROGEN CORP.
XX
PI Hanson G, Kudlicki WA, Kepertipola S;
XX
DR WPI; 2005-296136/30.
XX
PT New cellular extract from an organism comprises a SlyD gene,
XX substantially free of a SlyD polypeptide that binds to a bi-
XX arsenical reagent. Also described are: (i) a kit for the in vitro
XX production of protein, the kit comprising a cellular extract above; (ii)
XX a polypeptide comprising an amino acid sequence that binds specifically
XX to EDR 2 [4,5'-bis(1,3,2-dithioarsolan-2-yl)fluorescein-(1,2-
XX ethanedithio)2; and (iii) a fusion protein comprising an amino acid
XX sequence that binds specifically to EDR 2 [5'-bis(1,3,2-dithioarsolan-2-
XX yl)fluorescein-(1,2-ethanedithio)2. Preferably, the cellular extract is
XX an Escherichia coli extract or from an E. coli comprising a SlyD mutant
XX gene. The SlyD mutant gene encodes a SlyD that is mutated in an amino
XX acid sequence that binds a bi-arsenical molecule. The SlyD mutant gene
XX also encodes a truncated SlyD protein. The cellular extract further
XX comprises a nuclease inhibitor, which is a Gam protein. The extract has
XX reduced activity of at least one enzyme that catalyzes hydrolysis of high
XX -energy phosphate bonds or hydrolysis or formation of phosphodiester
XX bonds. It further comprises at least one inhibitor of at least one enzyme
XX that catalyzes hydrolysis of high-energy phosphate bonds or hydrolysis or
XX formation of phosphodiester bonds. The cellular extract further comprises
XX at least two energy sources providing chemical energy for synthesis. It
XX also comprises a nucleic acid encoding a fusion protein encoding an
XX exogenous protein fused to a tag, where the tag binds a bi-arsenical
XX reagent. The cellular extract is useful for synthesizing, purifying, and
XX detecting biomolecules, e.g. nucleic acids and polypeptides. It is
XX preferably useful for purifying and detecting recombinant polypeptides
XX having polyhistidine or polycysteine tags. The present sequence
XX represents calmodulin ortho C-terminus used as a control in measurement
XX of real-time in vitro protein synthesis.
XX
SQ Sequence 8 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 CGPC 5
Db 1 CGPC 4
XX
RESULT 37
ADV60195
ID ADV60195 standard; peptide; 9 AA.

```

```

XX AC ADV60195;
XX XX 10-MAR-2005 (first entry)
XX DE VEGF peptide SEQ ID NO 7700.
XX KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX KM food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX OS Unidentified.
XX PN WO200411636-A2.
XX XX
XX PD 23-DEC-2004.
XX PF 17-JUN-2004; 2004WO-EP051158.
XX PR 17-JUN-2003; 2003EP-00101775.
XX PR 17-JUN-2003; 2003US-0479061P.
XX PA (VIBV-) VIB VZM.
XX PA (UYGE-) UNIV GENT.
XX PI Kas K, Vandekerckhove J, Krols L;
XX DR MPI; 2005-057893/06.
XX PT Identifying a peptide combo which corresponds with a family of proteins,
XX PT useful for diagnosing a variety of diseases, drug development or in
XX PT agriculture, comprises generating peptides by applying a digest on the
XX PT family of protein.
XX PS Example; SEQ ID NO 7700; 265pp; English.
XX
XX CC The invention relates to a method of identifying a peptide combo which
XX CC corresponds with a family of proteins where each of the members of the
XX CC peptide combo is derived from a unique protein from the family. The
XX CC peptide combo is useful for quantifying specific known splice variants of
XX CC one or more particular proteins in a sample, for diagnosing complex
XX CC genetic diseases such as cancer, obesity, diabetes, asthma and
XX CC inflammation, neuropsychiatric disorders such as depression, for
XX CC quantifying one to several hundreds of protein disease markers
XX CC simultaneously leading to a more accurate diagnostic sub-classification,
XX CC for determining the extent of protein modification in a particular sample
XX CC of proteins, for tissue-typing analysis, for prenatal testing to detect
XX CC the presence of a congenital disease or for quantitating protein levels
XX CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX CC or neurological diseases, as biomarkers preclinical drug development,
XX CC development of improved animal models, biomarkers related with
XX CC toxicology, clinical drug development, guidance marketed drugs,
XX CC prognostic or diagnostic disease markers, drug target validation and
XX CC selection, monitoring protein splicing, drug lead profiling, pathway
XX CC analysis, answering basic disease biology questions, and in the fields of
XX CC food and feed, cosmetics, agriculture and animal breeding. The present
XX CC sequence represents a peptide from a VEGF peptide combo.
XX SQ Sequence 9 AA;
XX
XX Query Match 100.0%; Score 31; DB 9; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 CGPC 5
XX DB 2 CGPC 5
XX
XX RESULT 38
XX ID AAR50846 standard; peptide; 10 AA.
XX AC AAR50846;

```

```

XX XX
XX DT 25-MAR-2003 (revised)
XX DT 27-SEP-1994 (first entry)
XX DE Cyclic peptide inhibitor of selectins and integrins.
XX KM Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
XX KM inflammation; coagulation; ischaemia; reperfusion injury;
XX KM bacterial sepsis; tumour metastasis;
XX KM disseminated intravascular coagulation; rheumatoid arthritis;
XX KM adult respiratory distress syndrome; atherosclerosis; treatment;
XX KM prevention; detection; tumour; leucocyte; imaging.
XX OS Synthetic.
XX XX
XX PH Key Location/Qualifiers
XX FT Misc-difference 1 /note= "D-form residue."
XX FT Misc-difference 2 /note= "D-form residue."
XX FT Disulfide-bond 3 . 6
XX FT Misc-difference 3 /note= "D-form residue."
XX FT Modified-site 5 /label= Other.
XX FT FT /note= "3,4-dehydro-D-Pro."
XX FT Misc-difference 6 /note= "D-form residue."
XX FT Misc-difference 7 /note= "D-form residue."
XX FT Misc-difference 8 /note= "D-form residue."
XX FT Misc-difference 9 /note= "D-form residue."
XX FT FT /note= "D-form residue."
XX FT Misc-difference 10 /note= "D-form residue."
XX PN WO9405310-A1.
XX PD 17-MAR-1994.
XX PF 08-SEP-1993; 93WO-US008504.
XX PR 08-SEP-1992; 92US-00941653.
XX PA (CENZ ) CENTOCOR INC.
XX PI Heavner GA;
XX DR MPI; 1994-100848/12.
XX PT New cyclic peptide(s) inhibiting selections and integrins - prevent
XX PT cellular adhesion in treatment of inflammation, perfusion, injury,
XX PT metastasis, etc. also for diagnosis.
XX PS Claim 2; Page 25; 175pp; English.
XX
XX CC The peptide modifies the binding of P-, E- and L-selectin and of
XX CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
XX CC inhibits cellular adhesion. It can be used to treat or prevent
XX CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
XX CC sepsis, disseminated intravascular coagulation, adult respiratory
XX CC distress syndrome, tumour metastasis, rheumatoid arthritis and
XX CC atherosclerosis. When labelled it can be used to detect defective
XX CC selectin (or integrin) binding ligands or high (localised) concentrations
XX CC of selectin (or integrin) binding cells, especially leucocytes or tumour
XX CC cells. It can also be used for in vivo imaging. This is a specific
XX CC example of a degenerate sequence given in the specification. (Updated on
XX CC 25-MAR-2003 to correct PN field.)
XX SQ Sequence 10 AA;
XX
XX Query Match 100.0%; Score 31; DB 2; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
| | | |
Db 3 CGPC 6

RESULT 39

AAR50868
ID AAR50868 standard; peptide; 10 AA.

AC AAR50868;

XX 25-MAR-2003 (revised)

DT 27-SRP-1994 (first entry)

XX Cyclic peptide inhibitor of selectins and integrins.

XX Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;

KM inflammation; coagulation; ischaemia; reperfusion injury;

KM bacterial sepsis; tumour metastasis;

KM disseminated intravascular coagulation; rheumatoid arthritis;

KW adult respiratory distress syndrome; atherosclerosis; treatment;

KW prevention; detection; tumour; leucocyte; imaging.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue."

FT Misc-difference 2 /note= "D-form residue."

FT Disulfide-bond 3 .6

FT Misc-difference 3 /note= "D-form residue."

FT Modified-site 5 /label= Other.

FT /note= "D-thio-proline."

FT Misc-difference 6 /note= "D-form residue."

FT Misc-difference 7 /note= "D-form residue."

FT Misc-difference 8 /note= "D-form residue."

FT Misc-difference 9 /note= "D-form residue."

FT Misc-difference 10 /note= "D-form residue."

FT /note= "D-form residue."

XX WO9405310-A1.

XX 17-MAR-1994.

XX 08-SEP-1993; 93WO-US008504.

XX 08-SEP-1992; 92US-00941653.

XX (CENZ) CENTOCOR INC.

XX Heavner GA;

XX WPI; 1994-100848/12.

XX New cyclic peptide(s) inhibiting selections and integrins - prevent

PT cellular adhesion in treatment of inflammation, pertusion, injury,

XX metacastis, etc. also for diagnosis.

XX Claim 2; Page 26; 175pp; English.

XX The peptide modifies the binding of P-, E- and L-selectin and of

CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It

CC inhibits cellular adhesion. It can be used to treat or prevent

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
CC sepsis, disseminated intravascular coagulation, adult respiratory
CC distress syndrome, tumour metastasis, rheumatoid arthritis and
CC atherosclerosis. When labelled it can be used to detect defective
CC selectin (or integrin) binding ligands or high (localised) concentrations
CC of selectin (or integrin) binding cells, especially leucocytes or tumour
CC cells. It can also be used for in vivo imaging. This is a specific
CC example of a degenerate sequence given in the specification. (Updated on
CC 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
| | | |
Db 3 CGPC 6

RESULT 40

AAR50834
ID AAR50834 standard; peptide; 10 AA.

AC AAR50834;

XX 25-MAR-2003 (revised)

DT 27-SRP-1994 (first entry)

XX Cyclic peptide inhibitor of selectins and integrins.

XX Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;

KM inflammation; coagulation; ischaemia; reperfusion injury;

KM bacterial sepsis; tumour metastasis;

KM disseminated intravascular coagulation; rheumatoid arthritis;

KW adult respiratory distress syndrome; atherosclerosis; treatment;

KW prevention; detection; tumour; leucocyte; imaging.

XX Synthetic.

OS Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue."

FT Misc-difference 2 /note= "D-form residue."

FT Disulfide-bond 3 .6

FT Misc-difference 3 /note= "D-form residue."

FT Misc-difference 3 /note= "D-form residue."

FT Misc-difference 6 /note= "D-form residue."

FT Misc-difference 7 /note= "D-form residue."

FT Misc-difference 8 /note= "D-form residue."

FT Misc-difference 9 /note= "D-form residue."

FT Misc-difference 10 /note= "D-form residue."

FT /note= "D-form residue."

XX WO9405310-A1.

XX 17-MAR-1994.

XX 08-SEP-1993; 93WO-US008504.

XX 08-SEP-1992; 92US-00941653.

XX (CENZ) CENTOCOR INC.

XX Heavner GA;

XX WPI; 1994-100848/12.

XX New cyclic peptide(s) inhibiting selections and integrins - prevent

PT cellular adhesion in treatment of inflammation, pertusion, injury,

XX metacastis, etc. also for diagnosis.

XX Claim 2; Page 26; 175pp; English.

XX The peptide modifies the binding of P-, E- and L-selectin and of

CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It

CC inhibits cellular adhesion. It can be used to treat or prevent

XX

XX

XX

XX

XX

XX New cyclic peptide(s) inhibiting selections and integrins - prevent
 PT cellular adhesion in treatment of inflammation, perfusion, injury,
 PT metastasis, etc. also for diagnosis.
 XX
 PS Claim 2; Page 24; 175pp; English.
 XX
 CC The peptide modifies the binding of P-, E- and L-selectin and of
 CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
 CC inhibits cellular adhesion. It can be used to treat or prevent
 CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravascular coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis. When labelled it can be used to detect defective
 CC selectin (or integrin) binding ligands or high (localised) concentrations
 CC of selectin (or integrin) binding cells, especially leucocytes or tumour
 CC cells. It can also be used for in vivo imaging. This is a specific
 CC example of a degenerate sequence given in the specification. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 31; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 RESULT 41
 AAR50895
 ID AAR50895 standard; peptide; 10 AA.
 AC AAR50895;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1994 (first entry)
 XX
 DE Cyclic peptide inhibitor of selectins and integrins.
 XX
 KW Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
 KW inflammation; coagulation; ischaemia; reperfusion injury;
 KW bacterial sepsis; tumour metastasis;
 KW disseminated intravascular coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; atherosclerosis; treatment;
 KW prevention; detection; tumour; leucocyte; imaging.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue."
 FT Misc-difference 2 /note= "D-form residue."
 FT Disulfide-bond 3 .6
 FT Misc-difference 3 /note= "D-form residue."
 FT Misc-difference 6 /note= "D-form residue."
 FT Misc-difference 7 /note= "D-form residue."
 FT Misc-difference 8 /note= "D-form residue."
 FT Misc-difference 9 /note= "D-form residue."
 FT Misc-difference 10 /note= "D-form residue."
 FT Misc-difference 10 /note= "D-form residue."
 XX
 PN WO9405310-A1.
 XX
 PD 17-MAR-1994.

XX
 PF 08-SEP-1993; 93WO-US008504.
 XX
 PR 08-SEP-1992; 92US-00941653.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA;
 XX
 DR WPI, 1994-100848/12.
 XX
 PT New cyclic peptide(s) inhibiting selections and integrins - prevent
 PT cellular adhesion in treatment of inflammation, perfusion, injury,
 PT metastasis, etc. also for diagnosis.
 XX
 PS Claim 2; Page 28; 175pp; English.
 XX
 CC The peptide modifies the binding of P-, E- and L-selectin and of
 CC integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
 CC inhibits cellular adhesion. It can be used to treat or prevent
 CC inflammation, coagulation, ischaemia, reperfusion injury, bacterial
 CC sepsis, disseminated intravascular coagulation, adult respiratory
 CC distress syndrome, tumour metastasis, rheumatoid arthritis and
 CC atherosclerosis. When labelled it can be used to detect defective
 CC selectin (or integrin) binding ligands or high (localised) concentrations
 CC of selectin (or integrin) binding cells, especially leucocytes or tumour
 CC cells. It can also be used for in vivo imaging. This is a specific
 CC example of a degenerate sequence given in the specification. (Updated on
 CC 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 31; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 3 CGPC 6
 RESULT 42
 AAR50830
 ID AAR50830 standard; peptide; 10 AA.
 AC AAR50830;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-SEP-1994 (first entry)
 XX
 DE Cyclic peptide inhibitor of selectins and integrins.
 XX
 KW Selectin; integrin; intercellular adhesion molecule; ICAM-1; inhibition;
 KW inflammation; coagulation; ischaemia; reperfusion injury;
 KW bacterial sepsis; tumour metastasis;
 KW disseminated intravascular coagulation; rheumatoid arthritis;
 KW adult respiratory distress syndrome; atherosclerosis; treatment;
 KW prevention; detection; tumour; leucocyte; imaging.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "D-form residue."
 FT Misc-difference 2 /note= "D-form residue."
 FT Disulfide-bond 3 .6
 FT Misc-difference 3 /note= "D-form residue."
 FT Misc-difference 5 /note= "D-form residue."
 FT Misc-difference 6 /note= "D-form residue."
 FT Misc-difference 6 /note= "D-form residue."

```

PT Misc-difference 7 /note= "D-form residue."
PT Misc-difference 8 /note= "D-form residue."
PT Misc-difference 9 /note= "D-form residue."
PT Misc-difference 9 /note= "D-form residue."
PT Misc-difference 10 /note= "D-form residue."
PT Misc-difference 10 /note= "D-form residue."
XX WO9405310-A1.
XX 17-MAR-1994.
XX
XX PF 08-SEP-1993; 93WO-US008504.
XX
XX PR 08-SEP-1992; 92US-00941653.
XX (CENZ ) CENTOCOR INC.
XX
XX PI Heavner GA;
XX
XX DR WPI; 1994-100848/12.
XX
XX PT New cyclic peptide(s) inhibiting selections and integrins - prevent
XX cellular adhesion in treatment of inflammation, perfusion, injury,
XX metastasis, etc. also for diagnosis.
XX
XX PS Claim 2; Page 24; 175pp; English.
XX
XX CC The peptide modifies the binding of P-, E- and L-selectin and of
XX integrins, especially intercellular adhesion molecule-1 (ICAM-1). It
XX inhibits cellular adhesion. It can be used to treat or prevent
XX inflammation, coagulation, ischaemia, reperfusion injury, bacterial
XX sepsis, disseminated intravascular coagulation, adult respiratory
XX distress syndrome, tumour metastasis, rheumatoid arthritis and
XX atherosclerosis. When labeled it can be used to detect defective
XX selectin (or integrin) binding ligands or high (localised) concentrations
XX of selectin (or integrin) binding cells, especially leucocytes or tumour
XX cells. It can also be used for in vivo imaging. This is a specific
XX example of a degenerate sequence given in the specification. (Updated on
XX 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 43
AAG94724
ID AAG94724 standard; peptide; 10 AA.
XX
XX AAAG94724;
XX
XX DT 18-SEP-2001 (first entry)
XX
XX DB Human complementary peptide, SEQ ID NO: 918.
XX
XX KM Human; complementary peptide; ligand; drug discovery; drug design.
XX
XX OS Homo sapiens.
XX
XX PN WO200142277-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 13-DEC-2000; 2000WO-GB004776.
XX

```

```

PR 13-DEC-1999; 99GB-00029464.
XX
XX (PROT-) PROTEOM LTD.
XX
XX PI Roberts GW, Heal JR;
XX
XX DR WPI; 2001-408419/43.
XX
XX PT A set of peptide ligands consisting of specific complementary peptides to
XX proteins encoded by genes of the human genome, useful in an assay for
XX screening and identifying of one or more novel peptides which are drug
XX candidates or pro-drugs.
XX
XX PS Example 4; Page 171; 646pp; English.
XX
XX CC The invention relates to a set of complementary peptide ligands generated
XX from the human genome. The complementary peptides interact with their
XX relevant target proteins encoded in the human genome. They can be used as
XX reagents in drug discovery and as lead ligands to facilitate drug design
XX and development. The present sequence is a complementary peptide provided
XX in the specification
XX
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 6 CGPC 9

RESULT 44
AAG94776
ID AAG94776 standard; peptide; 10 AA.
XX
XX AAAG94776;
XX
XX DT 18-SEP-2001 (first entry)
XX
XX DE Human complementary peptide, SEQ ID NO: 970.
XX
XX KM Human; complementary peptide; ligand; drug discovery; drug design.
XX
XX OS Homo sapiens.
XX
XX PN WO200142277-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 13-DEC-2000; 2000WO-GB004776.
XX
XX PR 13-DEC-1999; 99GB-00029464.
XX
XX (PROT-) PROTEOM LTD.
XX
XX PI Roberts GW, Heal JR;
XX
XX DR WPI; 2001-408419/43.
XX
XX PT A set of peptide ligands consisting of specific complementary peptides to
XX proteins encoded by genes of the human genome, useful in an assay for
XX screening and identifying of one or more novel peptides which are drug
XX candidates or pro-drugs.
XX
XX PS Example 4; Page 178; 646pp; English.
XX
XX CC The invention relates to a set of complementary peptide ligands generated
XX from the human genome. The complementary peptides interact with their
XX relevant target proteins encoded in the human genome. They can be used as
XX reagents in drug discovery and as lead ligands to facilitate drug design
XX and development. The present sequence is a complementary peptide provided
XX

```


CC in the specification
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 6 CGPC 9

RESULT 45
AAG86916
ID AAG86916 standard; peptide; 10 AA.

AC AAG86916;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1865.

KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KM drug discovery; drug design.

XX Saccharomyces cerevisiae.

OS WO200142276-A1.

PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB004773.

PF 13-DEC-1999; 99GB-00029471.

PR (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and nucleotide
sequence databases, useful in drug design.

PS Example 3; Page 287; 488pp; English.

XX The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae

XX Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 3 CGPC 6

RESULT 46
AAG86918
ID AAG86918 standard; peptide; 10 AA.
XX AAG86918;
XX

DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1867.

KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KM drug discovery; drug design.

XX Saccharomyces cerevisiae.

OS WO200142276-A1.

PN 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB004773.

PF 13-DEC-1999; 99GB-00029471.

PR (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and nucleotide
sequence databases, useful in drug design.

PS Example 3; Page 287; 488pp; English.

XX The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae

XX Sequence 10 AA;

Query Match 100.0%; Score 31; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 47
ADV60196
ID ADV60196 standard; peptide; 10 AA.

XX ADV60196;

DT 10-MAR-2005 (first entry)

DE VEGF peptide SEQ ID NO 7701.

KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KM food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

XX Unidentified.

OS WO2004111636-A2.

PN 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

PF 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZM.
XX

PA (UYGE-) UNIV GENT.
 XX
 PI Kas K, Vandekerckhove J, Krols L;
 XX
 DR WPI; 2005-057893/06.
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 PS
 PS Example; SEQ ID NO 7701; 265pp; English.
 XX
 XX The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a VEGF peptide combo.
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 100.0%; Score 31; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 4 CGPC 7
 XX
 RESULT 48
 AAW45003
 ID AAW45003 standard; peptide; 12 AA.
 XX
 AC AAW45003;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Immunomodulatory peptide D7233.
 XX
 XX Immunomodulator; immunosuppressant; immunostimulatory; treatment;
 KW transplant rejection; autoimmune disease; cancer; infection.
 XX
 OS Synthetic.
 OS
 PN WO9739023-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 04-APR-1997; 97WO-SE000574.
 XX
 PR 12-APR-1996; 96SE-00001422.
 PR 23-SEP-1996; 96SE-00003469.
 XX
 PA (ASTR) ASTRA AB.
 PA
 PI Bertrand H, Eriksson T, Lindvall M, Saernstrand B;

XX
 DR WPI; 1997-526397/48.
 XX
 PT Nucleic acids encoding cysteine- or methionine-containing peptide(s)
 PT which have immuno:stimulatory or immunosuppressive activity - can be used
 PT to treat, e.g. cancers, infection, auto:immune disease or transplant
 PT rejection.
 XX
 PS Claim 12; Page 155; 183pp; English.
 XX
 XX The present peptide is an immunosuppressant or immunostimulator. An
 CC immunosuppressant can be used to treat transplant rejection or autoimmune
 CC disease, e.g. rheumatoid arthritis, systemic lupus erythematosus,
 CC Sjogren's syndrome, scleroderma, mixed connective tissue disease,
 CC dermatomyositis, polymyositis, Reiter's syndrome, Behcet's disease,
 CC I diabetes, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis,
 CC myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans or
 CC folliculitis, Senechal-Usher syndrome or Brazilian pemphigus. An
 CC immunostimulator can be used to treat conditions such as cancer or
 CC infection.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 100.0%; Score 31; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 2 CGPC 5
 XX
 RESULT 49
 AAY09429
 ID AAY09429 standard; peptide; 12 AA.
 XX
 AC AAY09429;
 XX
 DT 14-JUL-1999 (first entry)
 XX
 DE Immunoactive peptide SEQ ID NO:54.
 XX
 XX Immunoactive; immunomodulation; immunosuppression; immunostimulation;
 KW immune response; immunoreactive; autoimmune disease.
 KW
 OS Synthetic.
 OS
 PN WO9919347-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 06-OCT-1998; 98WO-SE001801.
 XX
 PR 10-OCT-1997; 97US-00949024.
 XX
 PA (ASTR) ASTRA AB.
 PA
 PI Bertrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX
 DR WPI; 1999-287953/24.
 XX
 PT Synthetic genes encoding immunoreactive peptides containing cysteine or
 PT methionine.
 PT
 PS Claim 32; Page 52; 104pp; English.
 XX
 XX The present invention describes nucleic acid molecules comprising a
 CC coding sequence encoding an immunoreactive peptide and further encoding a
 CC protein targeting sequence. The nucleic acid is administered to a patient
 CC so that its expression product, an immunoreactive peptide, modulates an
 CC immune response in a patient. The nucleic acid can also be used to treat
 CC cancer, either after surgery to remove a portion of the cancer or after
 CC ionizing radiation. A cytokine is also administered in conjunction with

CC the nucleic acid. Cells containing the nucleic acid molecule can also be
CC used for treatment. The immunoreactive peptide is immunosuppressive and can
CC be used in patients with autoimmune disease. The present sequence
CC represents a specifically claimed immunoreactive peptide from the present
CC invention
XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 31; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 2 CGPC 5

RESULT 50
ADV60191
ID ADV60191 standard; peptide; 12 AA.

XX ADV60191;

XX 10-MAR-2005 (first entry)

XX VEGF peptide SEQ ID NO 7696.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004MO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX Example; SEQ ID NO 7696; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital abnormality, for quantitating immune levels
XX diagnostic of a chromosomal abnormality, for quantitating immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway

CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.

XX SQ Sequence 12 AA;

Query Match 100.0%; Score 31; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 6 CGPC 9

RESULT 51
ADV60192
ID ADV60192 standard; peptide; 13 AA.

XX ADV60192;

XX 10-MAR-2005 (first entry)

XX VEGF peptide SEQ ID NO 7697.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004MO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

XX (UYGE-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krols L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX Example; SEQ ID NO 7697; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital abnormality, for quantitating immune levels
XX diagnostic of a chromosomal abnormality, for quantitating immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present

CC sequence represents a peptide from a VEGF peptide combo.
 XX
 SQ Sequence 13 AA;
 Query Match 100.0%; Score 31; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGPC 5
 Db 6 CGPC 9

RESULT 52
 ADV60193
 ID ADV60193 standard; peptide; 14 AA.
 AC ADV60193;
 XX
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE VEGF peptide SEQ ID NO 7698.
 XX
 KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
 XX
 OS Unidentified.
 XX
 PN WO2004111636-A2.
 XX
 PD 23-DEC-2004.
 XX
 PF 17-JUN-2004; 2004WO-EP051158.
 XX
 PR 17-JUN-2003; 2003EP-00101775.
 PR 17-JUN-2003; 2003US-0479061P.
 PA (VIBV-) VIB VZW.
 PA (UYGB-) UNIV GENT.
 XX
 PI Kas K, Vandekerckhove J, Krols L;
 XX
 DR WPI; 2005-057893/06.
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 7698; 265pp; English.

The invention relates to a method of identifying a peptide combo which corresponds with a family of proteins where each of the members of the peptide combo is derived from a unique protein from the family. The peptide combo is useful for quantifying specific known splice variants of one or more particular proteins in a sample, for diagnosing complex genetic diseases such as cancer, obesity, diabetes, asthma and inflammation, neuropsychiatric disorders such as depression, for quantifying one to several hundreds of protein disease markers simultaneously leading to a more accurate diagnostic sub-classification, for determining the extent of protein modification in a particular sample, of proteins, for tissue-typing analysis, for prenatal testing to detect the presence of a congenital disease or for quantitating protein levels diagnostic of a chromosomal abnormality, for diagnosing immune diseases or neurological diseases, as biomarkers preclinical drug development, development of improved animal models, biomarkers related with toxicology, clinical drug development, guidance marketed drugs, prognostic or diagnostic disease markers, drug target validation and selection, monitoring protein splicing, drug lead profiling, pathway analysis, answering basic disease biology questions, and in the fields of food and feed, cosmetics, agriculture and animal breeding. The present sequence represents a peptide from a VEGF peptide combo.

SQ Sequence 14 AA;
 Query Match 100.0%; Score 31; DB 9; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 CGPC 5
 Db 8 CGPC 11

RESULT 53
 ADW28625
 ID ADW28625 standard; peptide; 14 AA.
 XX
 AC ADW28625;
 XX
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE VEGF165 epitope, SEQ ID 2.
 XX
 KW Cytostatic; Antineumatic; Antidiabetic; Cardiant; Nootropic;
 KW Neuroprotective; antibody identification; antibody production;
 KW antibody therapy; cancer; vascular endothelial cell growth factor; VEGF.
 XX
 OS Homo sapiens.
 XX
 PN US2005009110-A1.
 XX
 PD 13-JAN-2005.
 XX
 PF 08-JUL-2003; 2003US-00615343.
 XX
 PR 08-JUL-2003; 2003US-00615343.
 XX
 PA (CHAN/) CHANG X.
 XX
 PI Chang X;
 XX
 DR WPI; 2005-099971/11.
 DR N-PSDB; ADW28624.
 XX
 PT Identifying antibody to protein, involves contacting solid surface coated
 PT with antibodies with fusion protein having portion of target protein and
 PT carrier protein and conducting assay to determine presence of carrier
 PT protein.
 XX
 PS Claim 32; SEQ ID NO 2; 55pp; English.

The present invention relates to a method for identifying antibodies for target proteins. The method comprises: (1) contacting an antibody-coated solid surface with a fusion protein, where the antibodies bind specifically to the fusion protein and the fusion protein comprises at least a portion of the target protein linked to a carrier protein, and (1) conducting an assay to determine the presence of the carrier protein, where the presence of a carrier protein indicates the presence of an antibody to the target protein. The target protein may be an isoform of a protein that is associated with disease, e.g. Vascular Endothelial Growth Factor (VEGF) isoforms VEGF165 (ADW28644) and VEGF121 (ADW28645), which are associated with cancer; Prostate Specific Antigen (PSA; ADW28642), which is associated with breast cancer, and Her2 (ADW28640), which is associated with breast cancer. Also claimed are methods for: generating (M2) monoclonal antibodies, where each monoclonal antibody binds to a target protein, specifically at least one monoclonal antibody that binds to an isoform of a protein that is associated with a disease; isolating (M3) an antibody binding specifically to a target protein from several antibodies that are associated with the nucleic acid(s) encoding the antibody; determining (M4) the presence of an antigen in a sample; and identifying (M5) an epitope on a target protein. The antibodies identified by (M1) are useful for treating or preventing diseases in which the presence of an antibody to a particular molecule is beneficial. The antibodies are useful for targeting agents such as toxins to particular cells e.g., cancer cell. (M1) is useful for identifying

CC epitopes on target protein which are used for preparing DNA vaccines
CC having nucleotide sequences encoding epitope of a disease associated
CC protein isoforms used for prevention or treatment of diseases such as
CC cancer, rheumatoid arthritis, diabetes, acute myeloid leukemia (AML),
CC chronic lymphocytic leukemia (CLL), ovarian cancer, prostate cancer,
CC cardiovascular disease, Alzheimer's disease, etc. The antibodies are
CC useful for detecting antigens e.g. in specific cells, tissue or bodily
CC fluids such as serum, or for affinity purification of antigen from
CC recombinant cell culture or natural sources. The present sequence is a
CC VEGF isoform epitope, which can be used to produce a VEGF isoform fusion
CC protein.
XX

SQ Sequence 14 AA;

Query Match 100.0%; Score 31; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||
Db 9 CGPC 12

RESULT 54

ADV54876
ID ADV54876 standard; peptide; 17 AA.

XX ADV54876;

XX 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2373.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krois L;

DR WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX

PS Example; SEQ ID NO 2373; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels

CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognosis or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||
Db 8 CGPC 11

RESULT 55

ADV54992
ID ADV54992 standard; peptide; 17 AA.

XX ADV54992;

XX 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2489.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX MO2004111636-A2.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004WO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZW.

PA (UYGE-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krois L;

DR WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX

PS Example; SEQ ID NO 2489; 265pp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases

CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 8 CGPC 11
XX
RESULT 56
ADV55097
ID ADV55097 standard; peptide; 17 AA.
XX
AC ADV55097;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 2594.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
PA (UYGE-) UNIV GENT.
PI Kas K, Vandekerckhove J, Krols L;
PI WPI; 2005-057893/06.
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 2594; 265PP; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,

CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 31; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 8 CGPC 11
XX
RESULT 57
AAE23038
ID AAE23038 standard; peptide; 19 AA.
XX
AC AAE23038;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human thiorodoxin, 47916 peptide.
XX
KM Human; thiorodoxin; 22108; 47916; haematopoietic disorder; leukaemia;
KW cancer; lung; breast; thyroid; head; neck; prostate; genitourinary tract;
KW cardiovascular disease; angina pectoris; arteriosclerosis; heart failure;
KW brain disorder; brain abscess; meningitis; Alzheimer's disease; sarcoma;
KW cytostatic; carcinoma; cardiac; neuroprotective; antiinflammatory;
KW gene therapy; nootropic.
XX
OS Homo sapiens.
XX
PN WO200226803-A2.
XX
PD 04-APR-2002.
XX
PF 25-SEP-2001; 2001WO-US023967.
PF 25-SEP-2001; 2001WO-US023967.
XX
PR 25-SEP-2000; 2000US-0235049P.
XX
PA (MILL-) MILLIENIUM PHARM INC.
PA (MILL-) MILLIENIUM PHARM INC.
PI Bandaru R, Kapeller-Libermann R;
PI WPI; 2002-416475/44.
XX
DR WPI; 2002-416475/44.
XX
PT New human thiorodoxin nucleic acid and polypeptide molecules, designated
PT 22108 and 47916, useful for diagnosing, preventing or treating cancer
PT (e.g. carcinoma), cardiovascular diseases (e.g. heart failure) or brain
PT disorders.
XX
PS Disclosure; Page 11; 124PP; English.
XX
CC The invention relates to human thiorodoxin nucleic acid and polypeptide
CC molecules, designated 22108 and 47916. The compound that modulates the
CC activity or expression of 22108 and 47916 nucleic acid is useful for
CC treating or preventing a disorder characterised by aberrant activity of
CC 22108 and 47916-expressing cell, specifically for reducing or inhibiting
CC the aberrant activity of the 22108 and 47916-expressing cancer cell. The
CC 22108 and 47916 nucleic acid and polypeptide are useful for diagnosing,
CC preventing or treating cancer in a subject (e.g. carcinoma, sarcoma,
CC metastatic or haematopoietic disorders (e.g. leukaemia), or cancers of the
CC lung, breast, thyroid, head neck, prostate or genito-urinary tract),
CC cardiovascular diseases (e.g. angina pectoris, arteriosclerosis or heart
CC failure) or brain disorders (e.g. brain abscess, meningitis, Alzheimer's
CC diseases). The thiorodoxin DNA is also useful in gene therapy. The

CC present sequence is human thioredoxin, 47916 peptide
XX
SQ Sequence 19 AA;
Query Match 100.0%; Score 31; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 9 CGPC 12
RESULT 58
ADV60188
ID ADV60188 standard; peptide; 20 AA.
XX
AC ADV60188;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7693.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krois L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 7693; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.
XX

SQ Sequence 20 AA;
Query Match 100.0%; Score 31; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 14 CGPC 17
RESULT 59
ADV60189
ID ADV60189 standard; peptide; 21 AA.
XX
AC ADV60189;
XX
DT 10-MAR-2005 (first entry)
XX
DE VEGF peptide SEQ ID NO 7694.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
KW food; feedstuff; cosmetics; agriculture; animal breeding; VEGF.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PT 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZM.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krois L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.
XX
PS Example; SEQ ID NO 7694; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a VEGF peptide combo.
XX
SQ Sequence 21 AA;
XX

Query Match 100.0%; Score 31; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 14 CGPC 17

RESULT 60
 AAB38160
 ID AAB38160 standard; protein; 23 AA.
 XX
 AC AAB38160;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 42 SEQ ID NO:99.
 XX
 XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 XX anti-rheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 XX cerebroprotective; nootropic; neuroprotective; antibacterial; vinicide;
 XX fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
 XX hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 XX cerebrovascular disorder; nervous system disorder; ocular disorder;
 XX wound healing; skin aging; food additive; preservative.
 XX
 OS Homo sapiens.
 XX
 PN WO200058468-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 22-MAR-2000; 2000MO-US007526.
 XX
 XX 26-MAR-1999; 99US-0126600P.
 PR 22-DEC-1999; 99US-0171550P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-611713/58.
 DR N-PSDB; AAC69440.
 XX
 PT Nucleic acids encoding human secreted proteins, used to prevent, treat,
 PT ameliorate, or diagnose conditions such as autoimmune disorders, skin
 PT disorders and cancer.
 XX
 PS Claim 11; Page 358; 374pp; English.

The polynucleotide sequences given in AAC69399 to AAC69445 encode the
 human secreted proteins given in AAB38119 to AAB38165. AAB38166 to
 AAB38201 represent human secreted polypeptide sequences and proteins
 homologous to them, which are given in the exemplification of the present
 invention. Human secreted proteins have activities based on the tissues
 and cells the genes are expressed in. Example of activities include:
 immunosuppressive; antiarthritic; anti-rheumatic; antiproliferative;
 cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
 neuroprotective; antibacterial; vinicide; fungicide; and
 ophthalmological. The polynucleotides and polypeptides can be used to
 prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 in diagnosing a pathological condition or susceptibility to a
 pathological condition. Disorders which are diagnosed or treated include
 autoimmune diseases, hyperproliferative disorders, cardiovascular
 disorders, cerebrovascular disorders, angiogenesis, nervous system
 disorders, infections caused by bacteria, viruses and fungi and ocular
 disorders. The polypeptides can also be used to aid wound healing and
 epithelial cell proliferation, to prevent skin aging due to sunburn, to
 maintain organs before transplantation, for supporting cell culture of
 primary tissues, to regenerate tissues and in chemotaxis. The
 polypeptides can also be used as a food additive or preservative to

CC increase or decrease storage capabilities. AAC69390 to AAC69398 and
 CC AAB38118 represent sequences used in the exemplification of the present
 CC invention
 XX

Sequence 23 AA;
 SQ

Query Match 100.0%; Score 31; DB 3; Length 23;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 17 CGPC 20

RESULT 61
 ADV55042
 ID ADV55042 standard; peptide; 24 AA.
 XX
 AC ADV55042;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE G protein coupled receptor peptide SEQ ID NO 2539.
 XX
 XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
 XX
 OS Unidentified.
 XX
 PN WO2004111636-A2.
 XX
 PD 23-DEC-2004.
 XX
 PF 17-JUN-2004; 2004MO-EP051158.
 XX
 XX 17-JUN-2003; 2003EP-00101775.
 PR 17-JUN-2003; 2003US-0479061P.
 XX
 XX (VIBV-) VIB VZW.
 PA (UYGR-) UNIV GENT.
 XX
 PI Kas K, Vandekerckhove J, Krols L;
 XX
 DR WPI; 2005-057893/06.
 DR
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 2539; 265pp; English.

The invention relates to a method of identifying a peptide combo which
 corresponds with a family of proteins where each of the members of the
 peptide combo is derived from a unique protein from the family. The
 peptide combo is useful for quantifying specific known splice variants of
 one or more particular proteins in a sample, for diagnosing complex
 genetic diseases such as cancer, obesity, diabetes, asthma and
 inflammation, neuropsychiatric disorders such as depression, for
 quantifying one to several hundreds of protein disease markers
 simultaneously leading to a more accurate diagnostic sub-classification,
 for determining the extent of protein modification in a particular sample
 of proteins, for tissue-typing analysis, for prenatal testing to detect
 the presence of a congenital disease or for quantitating protein levels
 diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 or neurological diseases, as biomarkers preclinical drug development,
 development of improved animal models, biomarkers related with
 toxicology, clinical drug development, guidance marketed drugs,
 prognostic or diagnostic disease markers, drug target validation and
 selection, monitoring protein splicing, drug lead profiling, pathway
 analysis, answering basic disease biology questions, and in the fields of
 food and feed, cosmetics, agriculture and animal breeding. The present

CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 15 CGPC 18
RESULT 62
ADV56216
ID ADV56216 standard; peptide; 24 AA.
XX
AC ADV56216;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 3718.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
PS Example; SEQ ID NO 3718; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide

CC combo.
XX
SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
DB 15 CGPC 18
RESULT 63
ADV53880
ID ADV53880 standard; peptide; 24 AA.
XX
AC ADV53880;
XX
DT 10-MAR-2005 (first entry)
XX
DE G protein coupled receptor peptide SEQ ID NO 1377.
XX
KM diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
OS Unidentified.
XX
PN WO2004111636-A2.
XX
PD 23-DEC-2004.
XX
PF 17-JUN-2004; 2004WO-EP051158.
XX
PR 17-JUN-2003; 2003EP-00101775.
XX
PR 17-JUN-2003; 2003US-0479061P.
XX
PA (VIBV-) VIB VZW.
XX (UYGE-) UNIV GENT.
XX
PI Kas K, Vandekerckhove J, Krols L;
XX
DR WPI; 2005-057893/06.
XX
PT Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
PS Example; SEQ ID NO 1377; 265pp; English.
XX
CC The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide

```
XX SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 64
ADV54929
ID ADV54929 standard; peptide; 24 AA.
XX
XX ADV54929;
AC
XX
XX 10-MAR-2005 (first entry)
DT
XX
DE G protein coupled receptor peptide SEQ ID NO 2426.
XX
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
XX Unidentified.
XX
XX MO2004111636-A2.
XX
XX 23-DEC-2004.
XX
XX 17-JUN-2004; 2004MO-EP051158.
XX
XX 17-JUN-2003; 2003EP-00101775.
XX
XX 17-JUN-2003; 2003US-0479061P.
XX
XX (VIBV-) VIB VZW.
XX
XX (UYGE-) UNIV GENT.
XX
XX Kas K, Vandekerckhove J, Krols L;
XX
XX WPI; 2005-057893/06.
XX
XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
XX Example; SEQ ID NO 2426; 265pp; English.
XX
XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
XX combo.
```

```
SQ Sequence 24 AA;
Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 15 CGPC 18

RESULT 65
ADV55148
ID ADV55148 standard; peptide; 24 AA.
XX
XX ADV55148;
AC
XX
XX 10-MAR-2005 (first entry)
DT
XX
DE G protein coupled receptor peptide SEQ ID NO 2645.
XX
XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.
XX
XX Unidentified.
XX
XX MO2004111636-A2.
XX
XX 23-DEC-2004.
XX
XX 17-JUN-2004; 2004MO-EP051158.
XX
XX 17-JUN-2003; 2003EP-00101775.
XX
XX 17-JUN-2003; 2003US-0479061P.
XX
XX (VIBV-) VIB VZW.
XX
XX (UYGE-) UNIV GENT.
XX
XX Kas K, Vandekerckhove J, Krols L;
XX
XX WPI; 2005-057893/06.
XX
XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.
XX
XX Example; SEQ ID NO 2645; 265pp; English.
XX
XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
XX combo.
```

Sequence 24 AA;

Query Match 100.0%; Score 31; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
15 CGPC 18

RESULT 66
AAB38027
ID AAB38027 standard; peptide; 25 AA.

XX AAB38027;
XX
XX 31-JAN-2001 (first entry)
XX
XX Fragment of human secreted protein encoded by gene 7 clone HMLH15.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiatherogenic; hepatotropic; antidiabetic; antiinflammatory; antitumor;
XX vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiac; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein.

OS Homo sapiens.

XX MO200055371-A1.

XX 21-SEP-2000.

XX 16-MAR-2000; 2000MO-US006783.

XX 18-MAR-1999; 99US-0125055P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruden SM, Ni J, Ebner R, Rosen CA, Shi Y, Birse C, Florence K;
XX Komatsoulis G, Lafleur DM, Moore PA, Olsen HS, Young PE;

XX WPI; 2000-594448/56.

XX New nucleic acid molecules encoding 27 human secreted proteins for
XX diagnosing, preventing, treating or ameliorating medical conditions and
XX used as food additives or preservatives.

XX Disclosure; Page 20; 453bp; English.

XX Sequences AAB37984-B38019 represent the amino acid sequences of 27 human
XX secreted proteins encoded by the genes AAC69084-C69119. The genes and
XX proteins are useful for preventing, ameliorating or treating medical
XX conditions, e.g. by protein or gene therapy. The genes are isolated from
XX a range of human tissues disclosed in the specification. The nucleic
XX acids, proteins, antibodies and (ant)agonists are useful in the
XX diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
XX ovarian cancer, and other cancers of the adrenal gland, bone, bone
XX marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b)
XX immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic
XX anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
XX multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
XX cardiovascular disorders such as myocardial ischemias; (d) wound healing
XX ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
XX infections

XX Sequence 25 AA;

Query Match 100.0%; Score 31; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 19 CGPC 22

RESULT 67
ADV55146
ID ADV55146 standard; peptide; 25 AA.

XX ADV55146;

XX 10-MAR-2005 (first entry)

XX G protein coupled receptor peptide SEQ ID NO 2643.

XX diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
XX food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

XX Unidentified.

XX MO2004111636-AZ.

XX 23-DEC-2004.

XX 17-JUN-2004; 2004MO-EP051158.

XX 17-JUN-2003; 2003EP-00101775.

XX 17-JUN-2003; 2003US-0479061P.

XX (VIBV-) VIB VZM.

XX (UYGB-) UNIV GENT.

XX Kas K, Vandekerckhove J, Krole L;

XX WPI; 2005-057893/06.

XX Identifying a peptide combo which corresponds with a family of proteins,
XX useful for diagnosing a variety of diseases, drug development or in
XX agriculture, comprises generating peptides by applying a digest on the
XX family of protein.

XX Example; SEQ ID NO 2643; 265bp; English.

XX The invention relates to a method of identifying a peptide combo which
XX corresponds with a family of proteins where each of the members of the
XX peptide combo is derived from a unique protein from the family. The
XX peptide combo is useful for quantifying specific known splice variants of
XX one or more particular proteins in a sample, for diagnosing complex
XX genetic diseases such as cancer, obesity, diabetes, asthma and
XX inflammation, neuropsychiatric disorders such as depression, for
XX quantifying one to several hundreds of protein disease markers
XX simultaneously leading to a more accurate diagnostic sub-classification,
XX for determining the extent of protein modification in a particular sample
XX of proteins, for tissue-typing analysis, for prenatal testing to detect
XX the presence of a congenital disease or for quantitating protein levels
XX diagnostic of a chromosomal abnormality, for diagnosing immune diseases
XX or neurological diseases, as biomarkers preclinical drug development,
XX development of improved animal models, biomarkers related with
XX toxicology, clinical drug development, guidance marketed drugs,
XX prognostic or diagnostic disease markers, drug target validation and
XX selection, monitoring protein splicing, drug lead profiling, pathway
XX analysis, answering basic disease biology questions, and in the fields of
XX food and feed, cosmetics, agriculture and animal breeding. The present
XX sequence represents a peptide from a G-protein coupled receptor peptide
XX combo.

XX Sequence 25 AA;

Query Match 100.0%; Score 31; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 8 CGPC 11

RESULT 68

ADV55040 ID ADV55040 standard; peptide; 25 AA.

AC ADV55040;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2537.

KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

OS Unidentified.

PN WO2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

PA (VIBV-) VIB VZW.
(UYGE-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krols L;

DR WPI; 2005-057893/06.

PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.

PS Example; SEQ ID NO 2537; 265pp; English.

CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

XX Sequence 25 AA;

SO Query Match 100.0%; Score 31; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5

Db 8 CGPC 11

RESULT 69

ADV54928 ID ADV54928 standard; peptide; 25 AA.

AC ADV54928;

DT 10-MAR-2005 (first entry)

DE G protein coupled receptor peptide SEQ ID NO 2425.

KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
food; feedstuff; cosmetics; agriculture; animal breeding; GPCR.

OS Unidentified.

PN WO2004111636-A2.

PD 23-DEC-2004.

PF 17-JUN-2004; 2004WO-EP051158.

PR 17-JUN-2003; 2003EP-00101775.

PR 17-JUN-2003; 2003US-0479061P.

PA (VIBV-) VIB VZW.
(UYGE-) UNIV GENT.

PI Kas K, Vandekerckhove J, Krols L;

DR WPI; 2005-057893/06.

PT Identifying a peptide combo which corresponds with a family of proteins,
PT useful for diagnosing a variety of diseases, drug development or in
PT agriculture, comprises generating peptides by applying a digest on the
PT family of protein.

PS Example; SEQ ID NO 2425; 265pp; English.

CC The invention relates to a method of identifying a peptide combo which
CC corresponds with a family of proteins where each of the members of the
CC peptide combo is derived from a unique protein from the family. The
CC peptide combo is useful for quantifying specific known splice variants of
CC one or more particular proteins in a sample, for diagnosing complex
CC genetic diseases such as cancer, obesity, diabetes, asthma and
CC inflammation, neuropsychiatric disorders such as depression, for
CC quantifying one to several hundreds of protein disease markers
CC simultaneously leading to a more accurate diagnostic sub-classification,
CC for determining the extent of protein modification in a particular sample
CC of proteins, for tissue-typing analysis, for prenatal testing to detect
CC the presence of a congenital disease or for quantitating protein levels
CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
CC or neurological diseases, as biomarkers preclinical drug development,
CC development of improved animal models, biomarkers related with
CC toxicology, clinical drug development, guidance marketed drugs,
CC prognostic or diagnostic disease markers, drug target validation and
CC selection, monitoring protein splicing, drug lead profiling, pathway
CC analysis, answering basic disease biology questions, and in the fields of
CC food and feed, cosmetics, agriculture and animal breeding. The present
CC sequence represents a peptide from a G-protein coupled receptor peptide
CC combo.

XX Sequence 25 AA;

SO Query Match 100.0%; Score 31; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5

Db 8 CGPC 11

RESULT 70
ADC89744

ID ADC89744 standard; peptide; 28 AA.

AC ADC89744;

DT 01-JAN-2004 (first entry)

DE Cyclic VEGF-165-derived peptide (residues 111-138), 3286.

KW Vascular endothelial growth factor; VEGF; VEGF-165 splice variant;
 KW neuropilin-1; NP-1; antagonist; competitive inhibitor; nerve growth;
 KW nerve repair; neurodegeneration; cancer; angiogenic condition;
 KW eye disease; rheumatoid arthritis; immunosuppressant; transplantation;
 KW antiangiogenic; neuroprotective; cytostatic; cerebroprotective;
 KW ophthalmological; antirheumatic; antithrombotic; immunosuppressive;
 KW cyclic.

OS Synthetic.
 OS Unidentified.

Key Location/Qualifiers
 FT Disulfide-bond 7..25
 FT Disulfide-bond 10..27

PN WO2003082918-A1.

PD 09-OCT-2003.

PF 28-MAR-2003; 2003WO-GB001375.

PR 02-APR-2002; 2002GB-00007644.

PA (ARKT-) ARK THERAPEUTICS LTD.

PI Selwood D, Loefer M, Zachary I;

DR WPI; 2003-804028/75.

PT New cyclic peptide derived from vascular endothelial growth factor,
 PT useful for treating e.g. neurodegeneration and cancer, antagonizes
 PT neuropilin-1.

PS Disclosure; Fig 1; 21pp; English.

CC The invention relates to a cyclic VEGF (vascular endothelial growth
 CC factor) peptide (ADC89740) with NP-1 (neuropilin-1) antagonist activity.
 CC The peptide corresponds to residues 138-165 of the VEGF-165 splice
 CC variant, but contains 2 disulfide bonds. It acts as a competitive
 CC inhibitor of NP-1, which plays an important role in angiogenesis
 CC (including VEGF-mediated tumour angiogenesis), neurodegeneration
 CC (involving interaction with semaphorin 3) and in immunosuppression. NP-1
 CC is a non-tyrosine kinase receptor for the VEGF-165 splice variant.
 CC Additionally, VEGF is known to promote the survival of tumour cells that
 CC express NP-1, including some breast carcinoma cells. The cyclic VEGF
 CC peptide of the invention can be used to stimulate nerve growth and
 CC repair, to treat neurodegeneration, and for anti-cancer therapy. It can
 CC also be used for treating other angiogenic conditions such as eye
 CC diseases and rheumatoid arthritis, and as an immunosuppressant for use in
 CC transplantation. The present sequence represents a cyclic VEGF-165
 CC derived peptide which was used in a study of VEGF-165 binding to NP-1
 CC expressing cells. The present sequence had no inhibitory effect on the
 CC binding of VEGF-165 to NP-1, unlike the cyclic peptide of the invention
 CC (ADC89740).

SQ Sequence 28 AA;

Query Match

100.0%; Score 31; DB 7; Length 28;

Best Local Similarity 100.0%; Pred.No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 7 CGPC 10

Search completed: February 23, 2006, 00:36:51
 Job time : 179 secs

THIS PAGE BLANK (USP10)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:38:49 ; Search time 23.5 Seconds
(without alignments)
24.566 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	35	1 NTSPRM	neurotoxin P2 - sc
2	31	100.0	35	2 A59356	neurotoxin Bmk 41-
3	31	100.0	55	2 S25774	testis-specific pr
4	31	100.0	56	1 WTRF	testis-specific pr
5	31	100.0	56	2 H81133	rubredoxin NMB0993
6	31	100.0	62	2 S15676	chorionic gonadotr
7	31	100.0	63	2 S25772	testis-specific pr
8	31	100.0	68	2 S25775	testis-specific pr
9	31	100.0	73	2 A60136	keratin, scale (cl
10	31	100.0	74	2 S25773	testis-specific pr
11	31	100.0	80	2 I65235	testicular luteini
12	31	100.0	88	2 B46264	chlorodoxin 2 - sl
13	31	100.0	89	2 E84409	chlorodoxin [impor
14	31	100.0	98	1 KRGLBS	keratin, feather -
15	31	100.0	102	1 G64213	chlorodoxin - Myco
16	31	100.0	102	2 H86572	chlorodoxin [impor
17	31	100.0	102	2 S73896	chlorodoxin - Myco
18	31	100.0	102	2 B71503	probable chlorodox
19	31	100.0	102	2 D72052	chlorodoxin CP0088
20	31	100.0	102	2 C81660	chlorodoxin TC0826
21	31	100.0	103	1 T8BY2	chlorodoxin II - y
22	31	100.0	103	2 T39085	chlorodoxin II - f
23	31	100.0	103	2 A11228	chlorodoxin [impor
24	31	100.0	103	2 AC1582	chlorodoxin [impor
25	31	100.0	104	1 A28086	chlorodoxin - rhod
26	31	100.0	104	1 A28215	chlorodoxin - Rhod
27	31	100.0	104	1 B37192	chlorodoxin - Baci
28	31	100.0	104	1 T8BY1	chlorodoxin I - ye
29	31	100.0	104	2 S77780	chlorodoxin - Myco
30	31	100.0	104	2 H95206	chlorodoxin [impor
31	31	100.0	104	2 H98071	chlorodoxin-disulf
32	31	100.0	104	2 A59394	chlorodoxin - Clos
33	31	100.0	104	2 C46264	chlorodoxin 3 - sl
34	31	100.0	104	2 B84037	chlorodoxin trxa l
35	31	100.0	104	2 B89885	chlorodoxin [impor
36	31	100.0	104	2 D86830	chlorodoxin [impor
37	31	100.0	104	2 C81432	chlorodoxin Cj0147
38	31	100.0	105	1 A30006	chlorodoxin - chic
39	31	100.0	105	1 A46264	chlorodoxin 1 - sl
40	31	100.0	105	1 JH0568	chlorodoxin [valid
41	31	100.0	105	1 J50667	chlorodoxin - rhes
42	31	100.0	105	1 S04107	chlorodoxin - mous
43	31	100.0	105	1 S04352	chlorodoxin - rat
44	31	100.0	105	1 TXRX	chlorodoxin - cory
45	31	100.0	105	2 S76386	chlorodoxin M-1 -
46	31	100.0	105	2 B97700	chlorodoxin [impor
47	31	100.0	105	2 AG2042	chlorodoxin [impor
48	31	100.0	105	2 D97279	chlorodoxin [impor
49	31	100.0	106	1 A35135	chlorodoxin - Rhod
50	31	100.0	106	2 S33357	chlorodoxin - Stre
51	31	100.0	106	2 H64622	chlorodoxin - Heli
52	31	100.0	106	2 A49888	chlorodoxin - Peni
53	31	100.0	106	2 AG2579	chlorodoxin C-1 tr
54	31	100.0	107	1 A32956	chlorodoxin m - Sy
55	31	100.0	107	1 TXAI	chlorodoxin 1 - An
56	31	100.0	107	1 A26622	chlorodoxin - Chro
57	31	100.0	107	1 S31915	chlorodoxin - red
58	31	100.0	107	1 S47867	chlorodoxin-like p
59	31	100.0	107	2 S73146	chlorodoxin A - re
60	31	100.0	107	2 S46521	chlorodoxin - Porp
61	31	100.0	107	2 T33843	hypothetical prote
62	31	100.0	107	2 S46958	chlorodoxin A - Sy
63	31	100.0	107	2 T02814	chlorodoxin TRXp1
64	31	100.0	107	2 B53307	chlorodoxin - Stre
65	31	100.0	107	2 AD1813	chlorodoxin [impor
66	31	100.0	107	2 AH3504	chlorodoxin C-1 f
67	31	100.0	107	2 B64047	chlorodoxin - Haem
68	31	100.0	108	2 G82991	chlorodoxin PA5240
69	31	100.0	108	2 B55124	chlorodoxin - Chlo
70	31	100.0	108	2 AD0471	chlorodoxin 1 [imp
71	31	100.0	108	2 AH2101	chlorodoxin [impor
72	31	100.0	108	2 D82338	chlorodoxin VC0306
73	31	100.0	109	1 A55124	chlorodoxin - Chlo
74	31	100.0	109	1 S35497	chlorodoxin - Salm
75	31	100.0	109	1 TXRC	chlorodoxin [valid
76	31	100.0	109	2 S27053	chlorodoxin - Emer
77	31	100.0	109	2 S77444	hypothetical prote
78	31	100.0	109	2 S46522	chlorodoxin A - Gr
79	31	100.0	110	2 AF0922	chlorodoxin [impor
80	31	100.0	110	2 T36576	chlorodoxin - Stre
81	31	100.0	110	2 T42061	chlorodoxin - Stre
82	31	100.0	110	2 AD2039	chlorodoxin [impor
83	31	100.0	110	2 A87688	chlorodoxin [impor
84	31	100.0	110	2 C81090	chlorodoxin NMB136
85	31	100.0	110	2 B81850	chlorodoxin I NMA1
86	31	100.0	111	1 A32233	chlorodoxin 2 [val
87	31	100.0	113	1 S57775	chlorodoxin h, cyt
88	31	100.0	114	1 J02242	chlorodoxin h - Ar
89	31	100.0	114	1 B64423	ychn protein homol
90	31	100.0	114	2 D75422	hypothetical prote
91	31	100.0	115	2 T29044	hypothetical prote
92	31	100.0	115	2 AF2098	chlorodoxin 2 [imp
93	31	100.0	116	2 T10739	chlorodoxin - comm
94	31	100.0	116	2 B70851	probable trxc prot
95	31	100.0	116	2 S09845	hypothetical prote
96	31	100.0	117	2 E70107	chlorodoxin (trxa)
97	31	100.0	118	2 S34812	chlorodoxin h2 - c
98	31	100.0	118	2 T10170	chlorodoxin - cast
99	31	100.0	118	2 PNO141	lutropin beta chai
100	31	100.0	118	2 PNO139	lutropin beta chai
101	31	100.0	119	2 T18644	hypothetical prote
102	31	100.0	119	2 T08271	probable chlorodox

103	31	100.0	119	2	T50867	176	31	100.0	194	2	T00482	probable thioredox
104	31	100.0	119	2	A61465	177	31	100.0	201	2	S16897	alanine-cRNA ligas
105	31	100.0	121	2	T93987	178	31	100.0	201	2	S16899	alanine-cRNA ligas
106	31	100.0	122	2	T04090	179	31	100.0	202	2	T50635	hypothetical prote
107	31	100.0	123	2	B70873	180	31	100.0	205	2	F71491	probable UDP-gluc
108	31	100.0	124	2	T13559	181	31	100.0	216	2	S72901	hypothetical prote
109	31	100.0	124	2	A83707	182	31	100.0	216	2	A70545	hypothetical prote
110	31	100.0	125	2	T50866	183	31	100.0	216	2	PT0375	natural killer cel
111	31	100.0	126	1	S16590	184	31	100.0	218	2	F81650	UDP-N-acetylglucos
112	31	100.0	127	1	S19498	185	31	100.0	220	2	T30688	hypothetical prote
113	31	100.0	127	2	B91218	186	31	100.0	220	2	G86164	protein F15K9.8 [f
114	31	100.0	127	2	C86064	187	31	100.0	222	2	A53263	tetraspan TSPAN-2
115	31	100.0	128	2	JQ1002	188	31	100.0	222	2	H87210	conserved hypotet
116	31	100.0	129	2	B96621	189	31	100.0	232	2	A41551	vascular endotheli
117	31	100.0	129	2	T08084	190	31	100.0	232	2	D96663	unknown protein, 5
118	31	100.0	130	2	D71707	191	31	100.0	233	2	D84797	hypothetical prote
119	31	100.0	131	2	T50862	192	31	100.0	241	2	C82852	competence protein
120	31	100.0	131	2	T50863	193	31	100.0	242	2	A66499	hypothetical prote
121	31	100.0	131	2	T50864	194	31	100.0	245	2	A43905	sperm outer dense
122	31	100.0	131	2	T50865	195	31	100.0	247	2	I48699	outer dense fiber
123	31	100.0	133	2	S58123	196	31	100.0	250	2	E87921	protein F56G4.5 [f
124	31	100.0	133	2	F97361	197	31	100.0	265	2	B48151	sperm tail protein
125	31	100.0	138	2	S00512	198	31	100.0	268	2	C38095	T-cell-specific tr
126	31	100.0	139	2	G70464	199	31	100.0	273	2	B31479	env polyprotein pr
127	31	100.0	139	2	H91059	200	31	100.0	277	2	I52825	gene M625 protein
128	31	100.0	139	2	G85904	201	31	100.0	281	2	S49353	protein S2 - phala
129	31	100.0	139	2	AB0831	202	31	100.0	282	2	S50031	proteacyclin-stimu
130	31	100.0	139	2	E65036	203	31	100.0	289	2	S49352	protein S1 - phala
131	31	100.0	139	2	IS2320	204	31	100.0	289	2	JCS938	thioredoxin-like p
132	31	100.0	140	1	S57774	205	31	100.0	290	2	T40552	thioredoxin-like p
133	31	100.0	140	1	G87183	206	31	100.0	296	2	T07367	thioredoxin-like p
134	31	100.0	141	1	UTBOB	207	31	100.0	299	2	E87262	thioredoxin [lmpor
135	31	100.0	141	1	UTHNB	208	31	100.0	302	2	A96789	protein T23E18.2 [
136	31	100.0	141	1	UTPCB	209	31	100.0	309	2	AB0838	virulence protein
137	31	100.0	141	1	UTRMB	210	31	100.0	321	2	AD0580	lipidic acid synthe
138	31	100.0	141	1	UTSHB	211	31	100.0	322	2	AH3011	thioredoxin trxA [
139	31	100.0	141	1	G75455	212	31	100.0	323	2	I48667	Mha3 (keratin acid
140	31	100.0	141	2	JC4527	213	31	100.0	329	2	AH3559	thioredoxin [lmpor
141	31	100.0	142	2	G75612	214	31	100.0	331	2	G98272	probable thioredox
142	31	100.0	145	2	S70356	215	31	100.0	332	2	I48691	regulatory protein
143	31	100.0	145	2	AD0397	216	31	100.0	334	2	A48151	sperm tail protein
144	31	100.0	148	2	B96721	217	31	100.0	340	1	C70538	probable 6-phospho
145	31	100.0	151	2	B96796	218	31	100.0	340	2	T33313	hypothetical prote
146	31	100.0	151	1	KRCHS	219	31	100.0	356	1	A35253	2-dehydro-3-deoxy-
147	31	100.0	156	2	T08086	220	31	100.0	356	1	ADECHY	2-dehydro-3-deoxy-
148	31	100.0	157	2	S16728	221	31	100.0	356	2	AB0833	2-dehydro-3-deoxy-
149	31	100.0	158	1	ZBBE11	222	31	100.0	356	2	H91061	hypothetical prote
150	31	100.0	160	2	A82020	223	31	100.0	356	2	D85906	hypothetical prote
151	31	100.0	160	2	D81247	224	31	100.0	356	2	AC0399	2-dehydro-3-deoxy-
152	31	100.0	161	2	T48767	225	31	100.0	357	2	S23526	cinnaamyl-alcohol d
153	31	100.0	162	2	T49420	226	31	100.0	357	2	S23525	cinnaamyl-alcohol d
154	31	100.0	167	2	T03957	227	31	100.0	357	2	D82292	phospho-2-dehydro-
155	31	100.0	169	1	KTHOB	228	31	100.0	362	2	I37459	keratin Ha3-II, ty
156	31	100.0	172	1	S38909	229	31	100.0	363	2	B97139	uncharacterized co
157	31	100.0	173	2	F84530	230	31	100.0	366	2	S61796	T-cell-specific tr
158	31	100.0	174	2	T29491	231	31	100.0	373	2	T33145	hypothetical prote
159	31	100.0	177	2	T09495	232	31	100.0	380	2	A71181	probable isomerase
160	31	100.0	179	2	T00893	233	31	100.0	380	2	H75159	3-isopropylmalate
161	31	100.0	179	2	A87654	234	31	100.0	380	2	G01639	transmembrane prot
162	31	100.0	181	1	TXSPM	235	31	100.0	381	2	A33477	protein-glutamine
163	31	100.0	182	2	T07837	236	31	100.0	386	2	T51171	homoaconitate hydr
164	31	100.0	182	2	S20929	237	31	100.0	392	2	A60777	keratin 2, type I,
165	31	100.0	182	2	S26539	238	31	100.0	395	1	J00396	nodulation protein
166	31	100.0	185	2	P75549	239	31	100.0	396	2	C84797	hypothetical prote
167	31	100.0	185	2	D95115	240	31	100.0	397	2	G97335	subtilisin-like se
168	31	100.0	186	2	F85044	241	31	100.0	398	1	S24802	polyferredoxin 6x2
169	31	100.0	186	2	T03808	242	31	100.0	399	2	F82657	beta-ketocacyl- (ACP
170	31	100.0	190	2	S04661	243	31	100.0	404	2	J50073	keratin, 47.6K tYP
171	31	100.0	190	2	S52130	244	31	100.0	412	1	KRSHTL1	keratin, 48K type
172	31	100.0	190	2	B40080	245	31	100.0	413	1	S34305	nodulation protein
173	31	100.0	191	2	T12261	246	31	100.0	415	2	S51977	FUN9 protein - yea
174	31	100.0	191	2	H97984	247	31	100.0	416	2	A61404	keratin A, type I
175	31	100.0	192	2	A72646	248	31	100.0	416	2	S60034	keratin Ha1, type

249	31	100.0	416	2	A46559	keratin, type I, h	322	31	100.0	835	2	T26086	hypothetical prote	
250	31	100.0	416	2	A99419	hypothetical prote	323	31	100.0	836	2	A56269	protein-glutamine	
251	31	100.0	416	2	G69524	3-isopropylmalate	324	31	100.0	837	2	T02761	outer arm dynein I	
252	31	100.0	417	2	H72362	3-isopropylmalate	325	31	100.0	842	2	C81396	alanine-tRNA ligas	
253	31	100.0	418	2	C72394	hypothetical prote	326	31	100.0	847	2	A64675	alanine-tRNA ligas	
254	31	100.0	419	2	D69051	3-isopropylmalate	327	31	100.0	847	2	F71842	alanine-tRNA ligas	
255	31	100.0	420	2	B64425	homoaconitate hydr	328	31	100.0	860	2	G82310	alanyl-tRNA synth	
256	31	100.0	422	2	C97290	3-isopropylmalate	329	31	100.0	873	2	H96503	protein Pgcl6.17 I	
257	31	100.0	423	2	B75045	probable 3-isoprop	330	31	100.0	874	2	H83533	alanyl-tRNA synth	
258	31	100.0	424	1	S12793	nodulation protein	331	31	100.0	874	2	F81063	alanyl-tRNA synth	
259	31	100.0	424	1	ZZZKCL	nodulation protein	332	31	100.0	874	2	C81804	alanine-tRNA ligas	
260	31	100.0	426	1	ZZZKRC4	nodulation protein	333	31	100.0	874	2	I64095	alanine-tRNA ligas	
261	31	100.0	426	2	A95321	NodC N-ACETYLGLUCO	334	31	100.0	875	2	AE0401	alanine-tRNA ligas	
262	31	100.0	428	2	A69085	3-isopropylmalate	335	31	100.0	876	1	SYECAT	alanine-tRNA ligas	
263	31	100.0	432	2	C70381	large subunit of l	336	31	100.0	876	2	AF0843	alanine-tRNA ligas	
264	31	100.0	433	2	B69495	aconitase (acn) ho	337	31	100.0	876	2	B91073	alanyl-tRNA synth	
265	31	100.0	434	2	D75373	3-isopropylmalate	338	31	100.0	877	2	S76394	hypothetical prote	
266	31	100.0	452	2	T36042	probable plasmid r	339	31	100.0	877	2	H71647	alanine-tRNA ligas	
267	31	100.0	454	2	T21358	hypothetical prote	340	31	100.0	878	2	B84977	alanine-tRNA ligas	
268	31	100.0	455	2	A55050	enigma - human	341	31	100.0	878	2	E85917	alanyl-tRNA synth	
269	31	100.0	458	1	S77662	thioredoxin-disulf	342	31	100.0	878	2	G97865	alanine-tRNA ligas	
270	31	100.0	458	2	D70325	hypothetical prote	343	31	100.0	880	2	AC2108	alanyl-tRNA synth	
271	31	100.0	463	2	T49460	hypothetical prote	344	31	100.0	880	2	H87562	alanyl-tRNA synth	
272	31	100.0	464	2	H90140	transcription regu	345	31	100.0	881	2	A97107	alanyl-tRNA synth	
273	31	100.0	464	2	T46333	hypothetical prote	346	31	100.0	885	2	AG3350	alanine-tRNA ligas	
274	31	100.0	483	2	AG1898	thioredoxin reduct	347	31	100.0	887	2	AC2806	alanyl-tRNA synth	
275	31	100.0	486	2	T39456	zinc finger protei	348	31	100.0	890	2	F75289	alanyl-tRNA synth	
276	31	100.0	508	1	KRSHL2	keratin type II, m	349	31	100.0	900	2	F97585	alanyl-tRNA synth	
277	31	100.0	525	2	T21357	hypothetical prote	350	31	100.0	900	2	C64232	alanine-tRNA ligas	
278	31	100.0	534	1	VCWSP	env polypeptide -	351	31	100.0	900	2	S73748	alanyl-tRNA synth	
279	31	100.0	535	2	T00824	probable thioredox	352	31	100.0	906	2	D82899	alanyl-tRNA synth	
280	31	100.0	574	1	H0CL1P	hydrogenase (EC 1,	353	31	100.0	916	2	C82844	alanyl-tRNA synth	
281	31	100.0	578	2	T02292	hypothetical prote	354	31	100.0	955	2	D96538	cytosolic tRNA-Ala	
282	31	100.0	584	1	C8HTA	complement C8 alpn	355	31	100.0	955	2	A45441	thrombospondin 4 -	
283	31	100.0	585	2	I46686	probable transcrip	356	31	100.0	956	1	A46016	thrombospondin 3 -	
284	31	100.0	597	2	S72468	hypothetical prote	357	31	100.0	956	2	A57121	alanyl-tRNA ligas	
285	31	100.0	604	2	T36966	hypothetical prote	358	31	100.0	958	2	S62065	alanyl-tRNA ligas	
286	31	100.0	606	2	T31557	hypothetical prote	359	31	100.0	959	2	T38247	probable alanyl-cr	
287	31	100.0	633	2	A75069	dipeptide transpor	360	31	100.0	961	1	TSHUP4	thrombospondin 4 p	
288	31	100.0	642	2	H97019	aconitase A [impor	361	31	100.0	965	2	S62935	hypothetical prote	
289	31	100.0	654	2	B56011	transcription fact	362	31	100.0	967	1	SYWTAT	alanine-tRNA ligas	
290	31	100.0	659	2	F70453	aconitase - Aquife	363	31	100.0	968	2	I60107	alanine-tRNA ligas	
291	31	100.0	662	1	VCWTLB	env polypeptide -	364	31	100.0	968	2	T29466	hypothetical prote	
292	31	100.0	662	1	VCWVGF	env polypeptide -	365	31	100.0	975	2	I48974	receptor-protein t	
293	31	100.0	662	2	A25982	env polypeptide -	366	31	100.0	976	2	A36355	protein-tyrosine k	
294	31	100.0	668	1	VCWVFP	env polypeptide pr	367	31	100.0	977	2	S49004	tyrosine kinase Mp	
295	31	100.0	670	2	T33304	hypothetical prote	368	31	100.0	989	2	S32671	alanine-tRNA ligas	
296	31	100.0	680	2	JC5133	protein-glutamine	369	31	100.0	1172	2	F96503	protein Pgcl6.13 I	
297	31	100.0	687	2	T39838	hypothetical prote	370	31	100.0	1178	1	A39804	thrombospondin pre	
298	31	100.0	693	1	S61067	homoaconitate hydr	371	31	100.0	1196	1	DNEBEF	DNA-binding protei	
299	31	100.0	695	2	S66662	protein-glutamine	372	31	100.0	1196	1	DNEBEK	DNA-binding protei	
300	31	100.0	712	2	A45638	immunodominant mlt	373	31	100.0	1196	1	DNEBEV1	major DNA-binding	
301	31	100.0	721	2	T38665	probable homoacon	374	31	100.0	1197	1	A48350	DNA-binding protei	
302	31	100.0	724	2	A48569	antigen Emi100 - E1	375	31	100.0	1364	2	T00250	MEG2 protein - hu	
303	31	100.0	744	2	A45622	surface antigen gp	376	31	100.0	1743	2	T15893	hypothetical prote	
304	31	100.0	755	2	A44315	cartilage oligomer	377	31	100.0	1786	1	MMMSB1	laminin beta-1 cha	
305	31	100.0	761	2	C64813	YbhJ protein - Bsc	378	31	100.0	2109	2	I38414	transcription fact	
306	31	100.0	761	2	G90728	probable enzyme I1	379	31	100.0	2148	2	AB6011	transcription fact	
307	31	100.0	761	2	H85579	RNA-directed RNA yb	380	31	100.0	2228	2	T14029	variant-specific s	
308	31	100.0	774	1	P31V50	basic directed RNA p	381	31	100.0	2282	2	T42717	DNA-binding protei	
309	31	100.0	774	2	S13670	aconitase hydratase 2	382	31	100.0	2630	2	T08868	polypeptide PI - A	
310	31	100.0	778	2	S50387	aconitase hydratase	383	31	100.0	3034	2	T14119	seven-pass transme	
311	31	100.0	778	2	T38347	aconitase hydratase	384	31	100.0	4302	2	A38971	polycyclic kidney	
312	31	100.0	779	2	S57805	aconitase hydratase	385	31	100.0	4357	2	T03455	ALR protein - huma	
313	31	100.0	780	2	T52543	aconitase hydratase	386	31	100.0	4526	2	T03454	ALR protein - huma	
314	31	100.0	781	2	A35544	aconitase hydratase	387	31	100.0	80.6	29	2	C61233	conceptus protein
315	31	100.0	781	2	S57528	aconitase hydratase	388	31	100.0	80.6	58	1	SMKD18	metallochionein 1
316	31	100.0	788	2	S44831	FS4H2.1 protein -	389	31	100.0	80.6	58	2	A37039	metallochionein 1
317	31	100.0	788	2	T26967	hypothetical prote	390	31	100.0	80.6	72	2	S59072	metallochionein 1s
318	31	100.0	789	2	S46631	aconitase hydratase	391	31	100.0	80.6	72	2	S15137	thioredoxin h2 - s
319	31	100.0	817	1	TGHUM1	protein-glutamine	392	31	100.0	80.6	74	1	SMBH1	metallochionein -li
320	31	100.0	824	2	B38423	protein-glutamine	393	31	100.0	80.6	74	2	S57768	metallochionein -li
321	31	100.0	832	2	A40205	Na+/H+-exchanging	394	31	100.0	80.6	75	2	JQ2358	wheat aluminum ind

395	25	80.6	77	2	S47158	metallochionein II	468	25	80.6	201	2	AC0255	probable phage pro
396	25	80.6	77	2	S57862	metallochionein 2b	469	25	80.6	208	2	E97094	ncharacterized con
397	25	80.6	77	2	S52636	metallochionein -	470	25	80.6	209	2	C71647	hypothetical prote
398	25	80.6	77	2	S31660	voltage-dependent	471	25	80.6	209	2	H97864	hypothetical prote
399	25	80.6	79	2	T17014	metallochionein-11	472	25	80.6	210	2	A87523	thiol-disulfide in
400	25	80.6	79	2	JQ2128	metallochionein -	473	25	80.6	212	2	H75148	hypothetical prote
401	25	80.6	80	2	T12928	thioredoxin - Bact	474	25	80.6	220	2	S48781	Li protein - human
402	25	80.6	80	2	T10087	metallochionein -	475	25	80.6	221	2	T29509	hypothetical prote
403	25	80.6	81	2	S27366	metallochionein B(476	25	80.6	222	2	S48786	Li protein - human
404	25	80.6	81	2	S27369	metallochionein B(477	25	80.6	222	2	D70866	hypothetical prote
405	25	80.6	82	2	T07114	metallochionein-11	478	25	80.6	224	2	S48779	Li protein - human
406	25	80.6	82	2	T07076	metallochionein-11	479	25	80.6	225	2	S19428	SKD1 protein - yea
407	25	80.6	82	2	T03727	metallochionein-11	480	25	80.6	227	2	B70790	hypothetical prote
408	25	80.6	84	2	C69499	virulence associat	481	25	80.6	228	2	S48783	Li protein - human
409	25	80.6	85	2	T00508	metallochionein-II	482	25	80.6	229	1	B43685	nonstructural prot
410	25	80.6	85	2	T07090	metallochionein-II	483	25	80.6	229	1	D43685	nonstructural prote
411	25	80.6	85	2	T05719	metallochionein-II	484	25	80.6	230	2	C84606	probable RAS type
412	25	80.6	87	2	A39439	small cysteine-ric	485	25	80.6	232	2	T16258	hypothetical prote
413	25	80.6	88	2	JC5203	outer membrane pro	486	25	80.6	233	2	H69611	phosphoadenylyl-su
414	25	80.6	88	2	JQ0514	cysteine-rich 9K p	487	25	80.6	236	2	G82578	conserved hypotet
415	25	80.6	88	2	S12126	cysteine-rich oute	488	25	80.6	240	2	H90064	conserved hypotet
416	25	80.6	88	2	S12125	cysteine-rich oute	489	25	80.6	241	2	F81835	hypothetical prote
417	25	80.6	88	2	E71513	probable ykda-cyst	490	25	80.6	241	2	B81129	conserved hypotet
418	25	80.6	88	2	D81671	cysteine rich oute	491	25	80.6	242	2	G86795	conserved hypotet
419	25	80.6	90	2	B86560	9 kDa-Cysteine-ric	492	25	80.6	242	2	T22915	hypothetical prote
420	25	80.6	90	2	A72064	cysteine rich oute	493	25	80.6	245	2	E64015	hypothetical prote
421	25	80.6	91	2	JN0140	insa protein - Esc	494	25	80.6	247	2	T31509	hypothetical prote
422	25	80.6	91	2	E90800	insa protein of in	495	25	80.6	247	2	T17311	hypothetical prote
423	25	80.6	98	2	S62346	L71-5 protein - fr	496	25	80.6	248	2	AD0394	hypothetical prote
424	25	80.6	101	2	S33514	13K prolamin - ric	497	25	80.6	250	2	S71522	outer dense fiber
425	25	80.6	106	2	AE1428	thioredoxin homolo	498	25	80.6	251	2	G84957	di-trans,poly-cis-
426	25	80.6	106	2	AD1802	thioredoxin homolo	499	25	80.6	254	2	C70682	probable cySH - My
427	25	80.6	108	1	S02802	thioredoxin C-2 -	500	25	80.6	255	2	I38426	lymphocyte activat
428	25	80.6	108	2	B84999	thioredoxin C-2 -	501	25	80.6	257	2	I38025	keratin-like prote
429	25	80.6	113	2	F82526	thioredoxin Xp2698	502	25	80.6	259	1	IC0H11	insulin-like growt
430	25	80.6	113	2	F65188	hypothetical 12.1	503	25	80.6	260	2	B71353	probable D,D-carbo
431	25	80.6	115	2	G84848	metallochionein-11	504	25	80.6	262	2	S56100	outer dense fiber
432	25	80.6	119	2	T17930	thioredoxin-like p	505	25	80.6	263	2	S56101	insulin-like growt
433	25	80.6	124	2	A70873	probable trxa prot	506	25	80.6	263	1	S23009	insulin-like growt
434	25	80.6	124	2	S25113	insulin-like growt	507	25	80.6	265	2	C70332	hypothetical prote
435	25	80.6	132	2	AI0543	probable secreted	508	25	80.6	266	2	C96913	sulfate adenylate
436	25	80.6	133	2	C90180	thioredoxin (trxa-	509	25	80.6	267	2	T13595	hypothetical prote
437	25	80.6	133	2	T37311	hypothetical prote	510	25	80.6	268	2	T20379	hypothetical prote
438	25	80.6	133	2	F72479	hypothetical prote	511	25	80.6	269	2	A89208	protein K10D6.2b l
439	25	80.6	134	2	AD2592	cytidine deaminase	512	25	80.6	270	2	T19207	hypothetical prote
440	25	80.6	134	2	G72678	hypothetical prote	513	25	80.6	272	1	A36082	insulin-like growt
441	25	80.6	135	2	C90393	thioredoxin (trxa-	514	25	80.6	272	2	I48600	insulin-like growt
442	25	80.6	140	2	H70809	probable thix prot	515	25	80.6	277	1	I37552	OX40 homolog - hum
443	25	80.6	141	2	T08790	hypothetical prote	516	25	80.6	279	1	B40731	alcohol dehydrogen
444	25	80.6	143	2	A72602	hypothetical prote	517	25	80.6	282	2	E83283	hypothetical prote
445	25	80.6	144	2	B82423	thioredoxin 2 VCA0	518	25	80.6	283	2	T26448	hypothetical prote
446	25	80.6	145	2	F97374	cytidine deaminase	519	25	80.6	286	2	C69100	conserved hypotet
447	25	80.6	145	2	S77736	probable zinc fing	520	25	80.6	286	2	S07533	puff II/9A-2 prote
448	25	80.6	150	2	A69551	conserved hypotet	521	25	80.6	286	2	S07532	puff II/9-1 proteI
449	25	80.6	150	2	A95388	protein [imported	522	25	80.6	287	2	T23579	hypothetical prote
450	25	80.6	151	2	AB3263	thiol:disulfide in	523	25	80.6	289	2	E83138	probable thioredox
451	25	80.6	154	2	H83526	hypothetical prote	524	25	80.6	290	1	D47468	cytochrome-c oxida
452	25	80.6	155	2	F87696	hypothetical prote	525	25	80.6	290	2	T23268	hypothetical prote
453	25	80.6	155	2	T30489	apoptosis inhibit	526	25	80.6	290	2	B88638	protein F58F6.2 [l
454	25	80.6	158	2	T25654	hypothetical prote	527	25	80.6	292	1	D55582	cytochrome-c oxida
455	25	80.6	161	2	T18498	hypothetical prote	528	25	80.6	294	2	E88640	protein F55A8.1 [l
456	25	80.6	170	2	H87704	thiol-disulfide in	529	25	80.6	297	2	T23909	hypothetical prote
457	25	80.6	176	1	A47384	cytochrome c bioge	530	25	80.6	304	2	T02125	chlorophyll a/b-bi
458	25	80.6	179	2	A13424	transcription regu	531	25	80.6	304	2	S04853	galactose 1-dehydr
459	25	80.6	180	2	S65026	finger protein XfG	532	25	80.6	307	2	F71294	hypothetical prote
460	25	80.6	185	2	A12991	conserved hypotet	533	25	80.6	310	2	T17980	hypothetical prote
461	25	80.6	185	2	A99292	hypothetical prote	534	25	80.6	314	2	AH3435	protein y1cc [limp
462	25	80.6	186	2	A45910	ultra-high-sulfur	535	25	80.6	317	2	G70313	lipopolysaccharide
463	25	80.6	187	2	G87521	HNH endonuclease f	536	25	80.6	319	2	T02454	hypothetical prote
464	25	80.6	189	2	T19559	hypothetical prote	537	25	80.6	321	2	A82070	transcription regu
465	25	80.6	190	2	AI3239	5-methylcytosine-s	538	25	80.6	322	2	PS0019	Ig gamma-2a chain
466	25	80.6	197	2	S22501	coat protein - And	539	25	80.6	322	2	T23580	hypothetical prote
467	25	80.6	199	2	S73702	hypothetical prote	540	25	80.6	325	2	B43692	t2 protein - rabbi

541	25	80.6	326	1	GOVZML	T2 protein - myxom	614	25	80.6	490	2	148189	cytochrome P450 II
542	25	80.6	327	2	A46484	apoptosis-mediated	615	25	80.6	490	2	149610	cytochrome P450 -
543	25	80.6	329	2	S32582	structural protein	616	25	80.6	490	2	A25954	cytochrome P450 2C
544	25	80.6	336	2	S61299	lipopolysaccharide	617	25	80.6	490	2	A32140	steroid 15beta-mon
545	25	80.6	336	2	C81073	ADP-hepoxe-LPS he	618	25	80.6	490	2	B28516	cytochrome P450 2C
546	25	80.6	336	2	B81869	lipopolysaccharide	619	25	80.6	490	2	F38462	S-mephenytoin 4'-h
547	25	80.6	337	2	S70125	PAS4 protein - yea	620	25	80.6	491	2	S05408	keratin, type II,
548	25	80.6	338	2	C82590	chlorodixin XP2174	621	25	80.6	491	2	T10930	3C3.21 protein - S
549	25	80.6	345	2	H83020	hepoxyltransferase	622	25	80.6	493	2	A31949	cytochrome P450 2E
550	25	80.6	346	2	S34165	keratin, type II -	623	25	80.6	493	2	A47350	cytochrome P450 II
551	25	80.6	348	2	T28623	hypothetical prote	624	25	80.6	493	2	A21231	cytochrome P450 2E
552	25	80.6	349	2	D36858	gene G4K protein -	625	25	80.6	493	2	A25341	cytochrome P450 2E
553	25	80.6	349	2	D72175	G2R protein - vari	626	25	80.6	494	2	S13101	cytochrome P450 c1
554	25	80.6	349	2	E71847	lipopolysaccharide	627	25	80.6	494	2	A46588	cytochrome P450 ar
555	25	80.6	349	2	G64668	Na/taurocholate co	628	25	80.6	494	2	G97496	integral membrane
556	25	80.6	351	2	T55601	site-specific DNA-	629	25	80.6	495	2	157463	keratin type II -
557	25	80.6	351	2	F81959	cinamyl-alcohol d	630	25	80.6	496	2	S55665	hypothetical prote
558	25	80.6	354	2	S60242	cinamyl-alcohol d	631	25	80.6	498	2	A47286	3',5'-cyclic-AMP p
559	25	80.6	354	2	JT0594	site-specific DNA-	632	25	80.6	500	2	A26685	cytochrome P450 2C
560	25	80.6	355	2	G83020	hepoxyltransferase	633	25	80.6	500	2	S62785	cytochrome P450 2C
561	25	80.6	356	2	S21423	cinamyl-alcohol d	634	25	80.6	502	2	A83029	conserved hypothet
562	25	80.6	357	2	T05413	hypothetical prote	635	25	80.6	506	2	S13720	coat protein - ara
563	25	80.6	357	2	T46690	cinamyl-alcohol d	636	25	80.6	513	2	A44150	structural protein
564	25	80.6	367	2	T02767	cinamyl-alcohol d	637	25	80.6	514	2	S48730	Cry j II protein -
565	25	80.6	367	2	T02990	cinamyl-alcohol d	638	25	80.6	514	2	JC2498	second major aller
566	25	80.6	368	2	T38901	probable dimeric d	639	25	80.6	517	2	S36496	L1 protein - human
567	25	80.6	369	2	T20505	hypothetical prote	640	25	80.6	518	2	S36472	hypothetical prote
568	25	80.6	370	2	G34462	cytochrome P450 2C	641	25	80.6	518	2	T00398	hypothetical prote
569	25	80.6	374	1	A53142	alcohol dehydrogen	642	25	80.6	519	2	T48498	hypothetical prote
570	25	80.6	378	1	B27718	cytochrome P450 2C	643	25	80.6	521	2	H69317	conserved hypothet
571	25	80.6	382	2	AB0945	alcohol dehydrogen	644	25	80.6	522	1	T42234	structural polypro
572	25	80.6	382	2	AI0040	probable methanol	645	25	80.6	530	2	GMWV1	fork head-related
573	25	80.6	396	2	T06102	heat shock protein	646	25	80.6	534	2	T15405	hypothetical prote
574	25	80.6	407	2	I48739	Mha2(keratin acid)	647	25	80.6	538	2	G69317	conserved hypothet
575	25	80.6	411	2	S41648	translation elonga	648	25	80.6	546	2	S36490	L1 protein - human
576	25	80.6	417	2	JC8000	N-acetylglactosam	649	25	80.6	550	2	JH0711	genome polyprotein
577	25	80.6	420	2	T00629	hypothetical prote	650	25	80.6	552	2	A33616	heterogeneous ribo
578	25	80.6	423	2	G71315	probable DNA polym	651	25	80.6	565	2	E91268	thiol disulfide in
579	25	80.6	429	2	T26192	hypothetical prote	652	25	80.6	565	2	C86109	thiol disulfide in
580	25	80.6	431	2	E96671	hypothetical prote	653	25	80.6	565	2	S56364	inner membrane cop
581	25	80.6	432	2	T28931	hypothetical prote	654	25	80.6	567	2	AE1044	thiol,disulfide in
582	25	80.6	434	2	C86331	P6F9.14 protein -	655	25	80.6	590	2	I46687	complement compone
583	25	80.6	435	2	E82753	D-amino acid dehyd	656	25	80.6	591	1	C8HUB	dreiprin - chicken
584	25	80.6	439	2	B81701	phospholipase D fa	657	25	80.6	593	2	151213	thiol,disulfide in
585	25	80.6	445	4	A28516	probable cytochrom	658	25	80.6	595	2	AI0042	inner membrane cop
586	25	80.6	448	2	F81703	phospholipase D fa	659	25	80.6	600	2	A82043	dreiprin E2 - chick
587	25	80.6	449	2	S28167	cytochrome P450 2B	660	25	80.6	607	2	A43776	hypothetical prote
588	25	80.6	450	2	T16259	hypothetical prote	661	25	80.6	616	2	T32131	hypothetical prote
589	25	80.6	454	2	JC7266	3',5'-cyclic-nucle	662	25	80.6	618	2	T26935	hypothetical prote
590	25	80.6	454	1	GOMST1	tumor necrosis fac	663	25	80.6	622	2	T37204	hypothetical prote
591	25	80.6	457	2	A37222	cytochrome P450 2C	664	25	80.6	627	2	T02610	probable YME1 ATP-
592	25	80.6	461	1	GQRTT1	tumor necrosis fac	665	25	80.6	629	2	T14776	hypothetical prote
593	25	80.6	466	2	JH0197	muscarinic acetylch	666	25	80.6	640	2	T08179	LK63 protein - Chl
594	25	80.6	466	2	S10126	muscarinic acetylch	667	25	80.6	640	2	T26820	hypothetical prote
595	25	80.6	466	2	A27386	muscarinic acetylch	668	25	80.6	645	2	T22178	hypothetical prote
596	25	80.6	466	2	S10856	muscarinic acetylch	669	25	80.6	647	2	T43952	hypothetical prote
597	25	80.6	466	2	F69331	conserved hypothet	670	25	80.6	647	2	T23814	hypothetical prote
598	25	80.6	468	2	I52418	cytochrome P450 -	671	25	80.6	651	2	JC7705	death receptor-6 -
599	25	80.6	468	2	T33857	hypothetical prote	672	25	80.6	658	2	F85024	probable GTP-rich
600	25	80.6	475	2	T24900	hypothetical prote	673	25	80.6	659	2	T01520	hypothetical prote
601	25	80.6	479	2	A61368	keratin type II, h	674	25	80.6	663	2	S21912	BrCore-Q1-21 prote
602	25	80.6	483	2	T47974	hypothetical prote	675	25	80.6	667	2	A48579	trophoblastic surfac
603	25	80.6	485	2	C86143	hypothetical prote	676	25	80.6	670	2	F88297	protein M28.1 lim
604	25	80.6	487	1	O4RBC6	cytochrome P450 2C	677	25	80.6	698	1	TRHUP	transferrin precur
605	25	80.6	487	1	O4RBP4	progestosterone mono	678	25	80.6	700	2	A86690	hypothetical prote
606	25	80.6	487	1	A26731	cytochrome P450 2C	679	25	80.6	709	2	C86648	ferrous ion transp
607	25	80.6	490	2	S28166	cytochrome P450 2C	680	25	80.6	713	2	A35502	major surface-labe
608	25	80.6	490	2	A29782	unspecific monooxy	681	25	80.6	723	2	E87706	prolyl oligopeptid
609	25	80.6	490	2	D28951	cytochrome P450 2C	682	25	80.6	726	2	H96689	hypothetical prote
610	25	80.6	490	2	A61269	cytochrome P450 2C	683	25	80.6	728	2	S21913	BrCore-TM1-Q1-21
611	25	80.6	490	2	B38462	S-mephenytoin 4-hy	684	25	80.6	737	2	P00219	RNA-2 polyprotein
612	25	80.6	490	2	I48162	cytochrome P450 -	685	25	80.6	755	2	S42462	structural polypro
613	25	80.6	490	2	I48163	cytochrome P450 -	686	25	80.6	759	2	T44142	DRI protein [impor

687	25	80.6	772	2	H84605	hypotheoretical prote		
688	25	80.6	794	1	KXHUJ	furin (EC 3.4.21.7		
689	25	80.6	797	2	A71267	hypotheoretical prote		
690	25	80.6	800	2	T01843	chloride channel p		
691	25	80.6	802	2	T24293	hypotheoretical prote		
692	25	80.6	835	2	A88238	protein T13H5.4 [l		
693	25	80.6	838	2	I45557	eyeless, long form		
694	25	80.6	889	2	A35679	rep protein - slim		
695	25	80.6	917	2	B85057	hypotheoretical prote		
696	25	80.6	934	1	A34372	complement C6 prec		
697	25	80.6	949	2	T24294	hypotheoretical prote		
698	25	80.6	975	2	T16073	hypotheoretical prote		
699	25	80.6	983	2	F86160	F1003.18 protein -		
700	25	80.6	985	2	I51549	receptor tyrosine		
701	25	80.6	987	2	A54092	protein-tyrosine k		
702	25	80.6	988	2	I50611	hypotheoretical prote		
703	25	80.6	989	2	T01519	RNA 1 protein - cu		
704	25	80.6	991	1	P1BVCV	RNA 1 protein - cu		
705	25	80.6	993	1	P1VXCM	RNA 1 protein - cu		
706	25	80.6	993	1	P1VXTA	RNA 1 protein - to		
707	25	80.6	993	2	E71392	ATP-dependent RNA		
708	25	80.6	993	2	JQ2169	RNA 1 protein - cu		
709	25	80.6	993	2	JA0074	RNA 1 protein - cu		
710	25	80.6	1005	1	P1VXBJ	RNA 1 protein - pe		
711	25	80.6	1006	2	JC5526	kinase-defective E		
712	25	80.6	1021	2	I39207	leukocyte surface		
713	25	80.6	1025	2	T42626	secreted leucine-r		
714	25	80.6	1025	2	A53121	peroxisome assembl		
715	25	80.6	1058	2	S08436	pol polyprotein -		
716	25	80.6	1119	2	A88481	protein C16A3.6 [l		
717	25	80.6	1145	2	S37136	structural polypro		
718	25	80.6	1164	2	T24806	hypotheoretical prote		
719	25	80.6	1221	2	T23472	hypotheoretical prote		
720	25	80.6	1223	2	T10365	helicase - Oryza		
721	25	80.6	1247	1	VHWN2	structural polypro		
722	25	80.6	1257	1	A41060	neural cell adhesi		
723	25	80.6	1257	2	S28764	neurocan precursor		
724	25	80.6	1259	2	S36126	neural cell adhesi		
725	25	80.6	1260	1	S05479	neural cell adhesi		
726	25	80.6	1268	2	S52781	neurocan - mouse		
727	25	80.6	1291	2	T21694	hypotheoretical prote		
728	25	80.6	1347	2	T02214	ubiquitous TPR mot		
729	25	80.6	1357	2	B96696	protein FIN21.4 [l		
730	25	80.6	1401	2	T02255	probable ubiquitou		
731	25	80.6	1408	2	S16148	gene serrate prote		
732	25	80.6	1531	2	T42218	slit-1 protein hom		
733	25	80.6	1541	2	T02831	RNA protein I4171.		
734	25	80.6	1573	2	S01845	DNA (cytosine-5-)		
735	25	80.6	1607	1	MMMSB2	laminin gamma-1 ch		
736	25	80.6	1646	1	MMTMS2	186K protein - cuc		
737	25	80.6	1680	2	A43434	furin (EC 3.4.21.7		
738	25	80.6	1681	2	A55138	sodium channel mna		
739	25	80.6	1682	2	A45380	sodium channel pro		
740	25	80.6	1790	1	MMFEB1	laminin beta-1 cha		
741	25	80.6	1808	2	T15099	hypotheoretical prote		
742	25	80.6	1820	2	A55494	latent transformin		
743	25	80.6	1846	2	T10670	hypotheoretical prote		
744	25	80.6	2049	2	T43161	sodium channel pro		
745	25	80.6	2052	2	T37711	probable n-end-rec		
746	25	80.6	2109	1	ZLVN	genome polyprotein		
747	25	80.6	2175	1	GNNYBE	genome polyprotein		
748	25	80.6	2215	2	T30870	myosin VIIa - mous		
749	25	80.6	2274	2	T30258	adenomatous polypro		
750	25	80.6	2813	1	VWNU	von Willebrand fac		
751	25	80.6	2823	2	F87908	protein T22A3.8 [l		
752	25	80.6	2823	2	T23064	hypotheoretical prote		
753	25	80.6	2824	2	T22759	hypotheoretical prote		
754	25	80.6	2894	2	T42214	ocogelin - mouse		
755	25	80.6	3075	2	S14458	laminin alpha-1 ch		
756	25	80.6	3084	1	MMMSA	laminin alpha-1 ch		
757	25	80.6	3102	2	T43291	laminin alpha chn		
758	25	80.6	3635	2	T10053	laminin alpha 5 ch		
759	25	80.6	3672	2	T23433	hypotheical prote		
760	25	80.6	760	25	3704	2	T37316	probable laminin a
761	25	80.6	761	25	3712	2	S18253	laminin alpha-1 ch
762	25	80.6	762	25	3766	2	T29165	hypotheical prote
763	24	77.4	763	24	45	2	T12318	metallothionein -
764	24	77.4	764	24	45	2	T12322	metallothionein -
765	24	77.4	765	24	68	2	AD2481	hypotheical prote
766	24	77.4	766	24	71	2	T09587	metallothionein-11
767	24	77.4	767	24	72	2	T07073	metallothionein ty
768	24	77.4	768	24	72	2	T07105	metallothionein-11
769	24	77.4	769	24	72	2	A34131	metallothionein I
770	24	77.4	770	24	73	2	T07109	metallothionein-11
771	24	77.4	771	24	74	2	T16979	metallothionein-11
772	24	77.4	772	24	75	2	S09098	metallothionein -
773	24	77.4	773	24	75	2	S37240	metallothionein-11
774	24	77.4	774	24	75	2	T12188	metallothionein -
775	24	77.4	775	24	76	2	S17560	metallothionein-11
776	24	77.4	776	24	77	2	S37239	metallothionein-11
777	24	77.4	777	24	77	2	T12187	metallothionein, t
778	24	77.4	778	24	78	2	S48038	metallothionein-11
779	24	77.4	779	24	80	2	T12326	metallothionein-11
780	24	77.4	780	24	80	2	T14387	metallothionein -
781	24	77.4	781	24	81	1	SMWUL	metallothionein-11
782	24	77.4	782	24	81	2	S57861	metallothionein 2a
783	24	77.4	783	24	84	2	T07115	metallothionein-11
784	24	77.4	784	24	119	2	S14292	transcription acti
785	24	77.4	785	24	130	1	KRSH3A	keratin high-sulfu
786	24	77.4	786	24	131	1	KRG3M	keratin high-sulfu
787	24	77.4	787	24	131	1	KRSH3A	keratin high-sulfu
788	24	77.4	788	24	131	1	A46298	pigment deposition
789	24	77.4	789	24	132	1	KRG3J	keratin high-sulfu
790	24	77.4	790	24	132	2	T37143	agouti protein
791	24	77.4	791	24	134	2	A54002	pollen allergen Lo
792	24	77.4	792	24	135	2	F82551	hypotheical prote
793	24	77.4	793	24	137	2	T22308	hypotheical prote
794	24	77.4	794	24	140	2	I38232	gene SMA3 protein
795	24	77.4	795	24	140	2	I38233	gene SMA4 protein
796	24	77.4	796	24	140	2	I38234	gene SMA5 protein
797	24	77.4	797	24	205	2	T31489	hypotheical prote
798	24	77.4	798	24	244	2	H81905	probable phosphad
799	24	77.4	799	24	246	2	C81111	phosphodensome P
800	24	77.4	800	24	250	1	A49053	CD27 antigen precu
801	24	77.4	801	24	250	1	T30502	hypotheical prote
802	24	77.4	802	24	260	1	A46517	CD27 antigen precu
803	24	77.4	803	24	265	2	T47537	pollen allergen ho
804	24	77.4	804	24	265	2	T05668	hypotheical prote
805	24	77.4	805	24	293	2	T51522	hypotheical prote
806	24	77.4	806	24	314	2	I37383	FAS soluble protei
807	24	77.4	807	24	335	2	A40036	apoptosis-mediati
808	24	77.4	808	24	363	3	S42386	major outer membra
809	24	77.4	809	24	372	2	S11009	major outer membra
810	24	77.4	810	24	372	2	B60756	major outer membra
811	24	77.4	811	24	374	2	S11006	major outer membra
812	24	77.4	812	24	375	2	S11007	major outer membra
813	24	77.4	813	24	377	2	B64428	formate hydrogenly
814	24	77.4	814	24	381	2	D69032	formate hydrogenly
815	24	77.4	815	24	387	2	C81747	major outer membra
816	24	77.4	816	24	387	2	JT0947	mouse pneumonitis
817	24	77.4	817	24	387	2	E82777	phage-related inte
818	24	77.4	818	24	387	2	S16034	major outer membra
819	24	77.4	819	24	389	1	MMCMP3	major outer membra
820	24	77.4	820	24	389	1	I40864	major outer membra
821	24	77.4	821	24	389	2	A60109	major outer membra
822	24	77.4	822	24	389	2	A43587	major outer membra
823	24	77.4	823	24	389	2	D86577	major outer membra
824	24	77.4	824	24	389	2	I40739	major outer membra
825	24	77.4	825	24	392	2	A75593	alcohol dehydrogen
826	24	77.4	826	24	392	2	A40371	major outer membra
827	24	77.4	827	24	393	1	MMCWTE	major outer membra
828	24	77.4	828	24	393	2	J71484	probable major out
829	24	77.4	829	24	393	2	JC1432	major outer membra
830	24	77.4	830	24	393	2	S06259	major outer membra
831	24	77.4	831	24	393	2	T01645	major outer membra
832	24	77.4	832	24	394	1	MMCWTEB	major outer membra

833	24	77.4	394	2	S11012	major outer membra	906	23	74.2	55	2	S36791	ferredoxin 2[4Fe-4
834	24	77.4	395	1	MMCWTF	major outer membra	907	23	74.2	55	2	A24932	ferredoxin 2[4Fe-4
835	24	77.4	396	2	S12799	major outer membra	908	23	74.2	56	1	FECLCP	ferredoxin 2[4Fe-4
836	24	77.4	397	1	MMCWTC	major outer membra	909	23	74.2	56	2	I37970	zinc finger protei
837	24	77.4	397	1	MMCWTH	major outer membra	910	23	74.2	56	2	S31198	metallochionein -
838	24	77.4	397	1	JEO413	major outer membra	911	23	74.2	56	2	P90059	hypothetical prote
839	24	77.4	402	1	MMCWPM	major outer membra	912	23	74.2	56	2	B64366	ferredoxin 2[4Fe-4
840	24	77.4	402	2	I40740	major outer membra	913	23	74.2	56	2	F69517	ferredoxin (fdx-8)
841	24	77.4	402	2	B60109	major outer membra	914	23	74.2	56	2	B69135	ferredoxin - Metha
842	24	77.4	402	2	A60341	major outer membra	915	23	74.2	56	2	B69337	ferredoxin [import
843	24	77.4	404	2	I40741	major outer membra	916	23	74.2	57	1	SMK025	metallochionein 2
844	24	77.4	408	2	S33683	site-specific DNA-	917	23	74.2	57	2	S59073	metallochionein 1s
845	24	77.4	433	2	C82713	polysaccharide bio	918	23	74.2	58	2	S43367	zinc finger protei
846	24	77.4	455	2	AH2055	hypothetical prote	919	23	74.2	58	2	A43284	RNA polymerase II
847	24	77.4	463	2	S75889	hypothetical prote	920	23	74.2	58	2	I37558	ferredoxin [import
848	24	77.4	469	2	A90166	conserved hypotet	921	23	74.2	58	2	B97333	hypothetical prote
849	24	77.4	480	2	JC7812	BCL6 homologous z1	922	23	74.2	58	2	G36953	ferredoxin 2[4Fe-4
850	24	77.4	511	2	UC7682	spermatogenesis as	923	23	74.2	58	2	B42960	ferredoxin (fdx-5)
851	24	77.4	524	2	A29677	complement C9 prec	924	23	74.2	58	2	C69365	ferredoxin (fdx-5)
852	24	77.4	537	2	B84772	probable DnaJ prot	925	23	74.2	59	1	FEDV2N	ferredoxin 2[4Fe-4
853	24	77.4	539	2	S58287	J-domain protein D	926	23	74.2	59	1	FEWZB	ferredoxin 2[4Fe-4
854	24	77.4	559	1	C9HU	complement C9 prec	927	23	74.2	59	2	F69315	conserved hypotet
855	24	77.4	633	1	C98321	C4-dicarboxylate t	928	23	74.2	59	2	T08149	metallochionein-1i
856	24	77.4	709	2	T28712	hypothetical prote	929	23	74.2	60	1	A54516	ferredoxin 2[4Fe-4
857	24	77.4	712	2	JC4935	peroxidase (EC 1.1	930	23	74.2	60	1	A64349	riboseomal protei
858	24	77.4	746	2	G84605	hypothetical prote	931	23	74.2	60	1	FEC1	ferredoxin 2[4Fe-4
859	24	77.4	930	2	B84505	probable retroelem	932	23	74.2	60	2	T09258	metallochionein-1i
860	24	77.4	1008	2	T18832	probable RNA helic	933	23	74.2	60	2	S42374	hypothetical prote
861	24	77.4	1040	2	E71412	hypothetical prote	934	23	74.2	60	2	S42375	hypothetical prote
862	24	77.4	1188	2	D86236	protein F14N23.5 f	935	23	74.2	60	2	A42960	ferredoxin 2[4Fe-4
863	24	77.4	1296	2	T16859	hypothetical prote	936	23	74.2	61	2	F69270	ferredoxin (fdx-2)
864	24	77.4	1403	2	S64142	hypothetical prote	937	23	74.2	61	1	FRCP	ferredoxin 2[4Fe-4
865	24	77.4	1441	2	T39636	probable cleavage	938	23	74.2	61	2	S14049	metallochionein pr
866	24	77.4	1530	2	B82085	glutamate synthase	939	23	74.2	61	2	B66577	hypothetical prote
867	24	77.4	1786	1	MMHUB1	laminin beta-1 cha	940	23	74.2	62	2	T21305	bacterioferritin-a
868	24	77.4	1955	1	AGCH	agrin precursor -	941	23	74.2	62	2	F82332	ORF MSY185 hypot
869	24	77.4	1959	1	AGRT	agrin - rat	942	23	74.2	62	2	T28346	ferredoxin 2[4Fe-4
870	24	77.4	2182	2	T28634	erythrocyte membra	943	23	74.2	62	2	B97344	FECLCP
871	24	77.4	2212	2	T28157	polymerase - Berne	944	23	74.2	63	1	FECLCP	ferredoxin [4Fe-4S
872	24	77.4	2291	2	S11238	hypothetical prote	945	23	74.2	63	1	FERFIP	ferredoxin 2[4Fe-4
873	24	77.4	2647	2	T28161	variant-specific s	946	23	74.2	64	1	C69303	ferredoxin (fdx-4)
874	24	77.4	3078	2	T28432	arylsulfatase A -	947	23	74.2	64	1	QOECB7	Yhea protein - Bac
875	23	74.2	20	2	I54283	neurotoxin Bt-II -	948	23	74.2	64	1	FERMN	ferredoxin 2[4Fe-4
876	23	74.2	24	2	A53357	alpha-conotoxin p	949	23	74.2	64	2	ARI005	bacterioferritin-a
877	23	74.2	25	2	A58647	CAPS protein - ant	950	23	74.2	64	2	A85998	hypothetical prote
878	23	74.2	27	2	S55030	erythrocyte chemok	951	23	74.2	64	2	AG0025	probable bacteriof
879	23	74.2	28	2	I52627	toxin-like protein	952	23	74.2	64	2	A95317	FdxN ferredoxin 1f
880	23	74.2	35	2	S06667	hypothetical prote	953	23	74.2	65	1	S09280	ferredoxin 2[4Fe-4
881	23	74.2	36	2	S33435	riboseomal protei	954	23	74.2	65	2	FERFIC	ferredoxin 2[4Fe-4
882	23	74.2	37	2	T07519	spike protein - po	955	23	74.2	65	2	A38739	metallochionein -
883	23	74.2	37	2	A49591	metallochionein -	956	23	74.2	65	2	AT1251	conserved hypotet
884	23	74.2	38	2	T12331	hypothetical prote	957	23	74.2	65	2	B25103	ferredoxin 2[4Fe-4
885	23	74.2	40	2	B69408	hypothetical prote	958	23	74.2	65	2	B35405	ferredoxin 2[4Fe-4
886	23	74.2	42	2	A71265	riboseomal protei	959	23	74.2	66	2	S78705	protein YB056w-a
887	23	74.2	44	1	S27036	hypothetical prote	960	23	74.2	67	2	T11547	metallochionein -
888	23	74.2	44	2	F82363	hypothetical prote	961	23	74.2	68	1	A41608	riboseomal protei
889	23	74.2	47	2	T05661	Ig gamma heavy cha	962	23	74.2	68	2	A31490	phosphoprotein p2
890	23	74.2	48	2	A30504	DNA-directed RNA p	963	23	74.2	69	2	C69294	ferredoxin (fdx-3)
891	23	74.2	48	2	C90189	riboseomal protei	964	23	74.2	70	2	AE0938	50S ribosomeal prot
892	23	74.2	51	2	G69133	cysteine proteinas	965	23	74.2	71	2	AE0014	50S ribosomeal prot
893	23	74.2	53	2	F32946	ferredoxin 2[4Fe-4	966	23	74.2	71	2	C53306	ferredoxin - pia
894	23	74.2	54	1	PEME	ferredoxin 2[4Fe-4	967	23	74.2	73	2	H83204	conserved hypotet
895	23	74.2	55	1	PECLCB	ferredoxin 2[4Fe-4	968	23	74.2	74	1	GSRF7	salivary glue prot
896	23	74.2	55	1	PECLCB	ferredoxin 2[4Fe-4	969	23	74.2	74	2	I47084	BlitB high-sulfur
897	23	74.2	55	1	PECLCT	ferredoxin 2[4Fe-4	970	23	74.2	74	2	C82919	hypothetical prote
898	23	74.2	55	1	PECLCT	ferredoxin 2[4Fe-4	971	23	74.2	74	2	G82810	hypothetical prote
899	23	74.2	55	1	FEPE	ferredoxin 2[4Fe-4	972	23	74.2	74	2	A69097	ferredoxin - Metha
900	23	74.2	55	1	PEOFR	ferredoxin 2[4Fe-4	973	23	74.2	74	2	AH1317	ferredoxin homolo
901	23	74.2	55	2	H69388	SSU ribosomeal prot	974	23	74.2	74	2	AH1689	ferredoxin homolo
902	23	74.2	55	2	A82464	hypothetical prote	975	23	74.2	75	2	H90187	SSU ribosomeal prot
903	23	74.2	55	2	S17805	hypothetical prote	976	23	74.2	76	1	S76753	hypothetical prote
904	23	74.2	55	2	JU0126	ferredoxin 2[4Fe-4	977	23	74.2	76	2	I83048	FSH beta-subunit -
905	23	74.2	55	2	JX0144	ferredoxin - Clost	978	23	74.2	76	2	AB1970	hypothetical prote

979 23 74.2 76 2 F83930 hypothetical prote
980 23 74.2 77 2 T09815 expansin (clone pd
981 23 74.2 77 2 D69432 iron-sulfur cluster
982 23 74.2 77 2 C89878 conserved hypochet
983 23 74.2 78 2 JC2496 ferredoxin [3Fe-4S
984 23 74.2 78 2 A70026 hypothetical prote
985 23 74.2 79 2 F84076 hypothetical prote
986 23 74.2 79 2 C84077 nitrogen fixation
987 23 74.2 79 2 C82740 hypothetical prote
988 23 74.2 80 2 T43368 ribosomal protein
989 23 74.2 80 2 T43625 ribosomal protein
990 23 74.2 80 2 T02063 metallochionein-11
991 23 74.2 80 2 A89860 hypothetical prote
992 23 74.2 80 2 B64307 ferredoxin - Metha
993 23 74.2 81 1 A55790 ferredoxin [4Fe-4S
994 23 74.2 81 1 FEBSFP ferredoxin [4Fe-4S
995 23 74.2 81 2 I48749 s-laminin - mouse
996 23 74.2 81 2 T30482 zink finger protei
997 23 74.2 82 1 CCP55M cytochrome c551 [v
998 23 74.2 82 2 D69621 ferredoxin fer - B
999 23 74.2 82 2 E83944 ferredoxin [4Fe-4S
1000 23 74.2 82 2 A83676 ferredoxin [4Fe-4S

ALIGNMENTS

RESULT 1

NTSRPM neurotoxin P2 - scorpion (Androctonus mauretanicus)

C/Species: Androctonus mauretanicus mauretanicus

C/Date: 15-Oct-1982 #sequence_revision 15-Oct-1982 #text_change 09-Jul-2004

C/Accession: A01758

R/Rosao, J.P.; Rochat, H.

Toxicol 23, 113-125, 1985

A/Title: Characterization of ten proteins from the venom of the Moroccan scorpion Androc

A/Reference number: A94318; MUID:85193276; PMID:3992595

A/Accession: A01758

A/Molecule type: protein

A/Residues: 1-35 <ROS>

A/Cross-references: UNIPROT:P01498; UNIPARC:UPI0000036305

C/Superfamily: scorpion neurotoxin

C/Keywords: neurotoxin; venom

F/1-18,4-25,15-30,19-32/Diulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 35;

Best Local Similarity 100.0%; Pred. No. 59;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 1 CGPC 4

RESULT 2

A59356 neurotoxin Bmk 41-2 - scorpion (Butus Martensii Karsch)

C/Species: Butus Martensii Karsch

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 19-Apr-2002

C/Accession: A59356

R/Xu, C.

submitted to the Protein Sequence Database, October 2000

A/Description: Purification and Sequence determination of a new neurotoxin from scorpion

A/Reference number: A59356

A/Accession: A59356

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-35 <XUC>

A/Cross-references: UNIPARC:UPI00001766C6

C/Superfamily: scorpion neurotoxin

C/Keywords: venom

F/1-35/Product: neurotoxin Bmk 41-2 #status experimental <MAT>

F/1-18,4-25,15-30,19-32/Diulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 1 CGPC 4

RESULT 3

S25774 testis-specific protein Mat84dc - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: S25774; C5655

R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.

Mech. Dev. 35, 143-151, 1991

A/Title: A cluster of four genes selectively expressed in the male germ line of Drosoph

A/Reference number: A56565; MUID:92102953; PMID:1684716

A/Molecule type: DNA

A/Residues: 1-55 <KUH>

A/Cross-references: UNIPROT:Q01644; UNIPARC:UPI00001246FE; EMBL:X67703; NID:g11072; PID

A/Note: the authors translated the codon TGC for residue 55 as Thr

A/Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBIPI:74222)

C/Genetics:

A/Gene: Mat84dc

A/Cross-references: FlyBase:FBgn0004174

A/Map position: 3

C/Superfamily: fruit fly testis-specific protein

C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 55;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 3 CGPC 6

RESULT 4

WTFP testis-specific protein (clone msc(3)gl-9) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C/Accession: S00340

R/Kuhn, R.; Schaefer, U.; Schaefer, M.

EMBO J. 7, 447-454, 1988

A/Title: Cis-acting regions sufficient for spermatocyte-specific transcriptional and sp

A/Reference number: S00340; MUID:88211557; PMID:2835228

A/Accession: S00340

A/Molecule type: DNA

A/Residues: 1-56 <KUH>

A/Cross-references: UNIPROT:P08175; UNIPARC:UPI0000124701; EMBL:Y00831; NID:98650; PID

C/Genetics:

A/Gene: FlyBase:Mat87F

A/Cross-references: FlyBase:FBgn0002862

C/Superfamily: fruit fly testis-specific protein

C/Keywords: sex-specific protein; testis

Query Match 100.0%; Score 31; DB 1; Length 56;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 3 CGPC 6

RESULT 5

H81133

rubredoxin NMB0993 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain C/Species: Neisseria meningitidis
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: H81133; B81888
 R/RefSeq: H. J. Saunders, N. J. Heidelberg, J. J. Jeffries, A. C. Nelson, K. E. Eisen, J. A. Hickey, E. K. Hatt, D. H. Salberg, S. L. White, O. Fleischmann, R. D. Dougherty, B. A. J. H. Qun, H. Vamathavan, J. Gill, J. Scarlato, V. Maignani, V. Pizzo, M. Science 287, 1809-1815, 2000
 A/Authors: Grandi, G.; Sun, L.; Smith, H. O.; Fraser, C. M.; Moxon, E. R.; Rappelli, R.; V. A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A/Reference number: A81000; MUID:2015755; PMID:10710307
 A/Status: preliminary
 A/Accession: H81133
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-56 <TEXT>
 A/Cross-references: UNIPROT:Q9JQN3; UNIPARC:UP100000C4E89; GB:AE02450; GB:AE02098; NID: A/Experimental source: serogroup B, strain MC58
 R/RefSeq: H. J. Achman, M. J. James, K. D. Bentley, S. D. Churcher, C. J. Klee, S. R. Morel; Holroyd, S. J. Jørgensen, K. J. Leather, S. J. Mouton, S. J. Mungall, K. J. Quail, M. A. Rajandream, Nature 404, 502-506, 2000
 A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A/Reference number: A81775; MUID:2022556; PMID:10761919
 A/Accession: B81888
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-56 <PAR>
 A/Cross-references: UNIPARC:UP100000C4E89; GB:AL162755; GB:AL157959; NID:G7379742; PIDN: A/Experimental source: serogroup A, strain Z2491
 C/Genetics:
 A/Accession: NMB0993; NMA1201
 C/Suprafamily: rubredoxin; rubredoxin homology
 C/Keywords: iron; metalloprotein
 F/3-49/Domain: rubredoxin homology <RUB>
 F/3-9,39,42/Binding site: iron (Cys) #status predicted

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 6 CGPC 9

RESULT 6
 S15676
 chorionic gonadotropin beta chain - donkey (fragment)
 C/Species: Equus asinus (donkey)
 C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C/Accession: S15676
 R/RefSeq: S. E. A. Stewart, F. J. M. Mol. Endocrinol. 4, 143-150, 1990
 A/Title: Partial cDNA sequence for the donkey chorionic gonadotropin-beta subunit
 A/Reference number: S15676; MUID:90262634; PMID:2344391
 A/Accession: S15676
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-62 <LEI>
 A/Cross-references: UNIPROT:P19794; UNIPARC:UP10000165CA; EMBL:X53669
 C/Suprafamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 31; DB 2; Length 62;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 6 CGPC 9

RESULT 7
 S25772
 testis-specific protein Mat84da - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S25772; A56565
 R/RefSeq: R. J. Kuh, C. J. Boersch, D. J. Glaetzer, K. H. J. Schaefer, U. J. Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosoph
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25772
 A/Molecule type: DNA
 A/Residues: 1-63 <KUH>
 A/Cross-references: UNIPROT:Q01642; UNIPARC:UP100001246FP; EMBL:X67703; NID:G11072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74219, NCBI:74224)
 C/Genetics:
 A/Accession: Mat84da
 A/Cross-references: FlyBase:FBgn0004172
 A/Map position: 3
 A/Intons: 13/3
 C/Suprafamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 63;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 17 CGPC 20

RESULT 8
 S25775
 testis-specific protein Mat84d - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C/Accession: S25775; D56565
 R/RefSeq: R. J. Kuh, C. J. Boersch, D. J. Glaetzer, K. H. J. Schaefer, U. J. Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: A cluster of four genes selectively expressed in the male germ line of Drosoph
 A/Reference number: A56565; MUID:92102953; PMID:1684716
 A/Accession: S25775
 A/Molecule type: DNA
 A/Residues: 1-68 <KUH>
 A/Cross-references: UNIPROT:Q01645; UNIPARC:UP1000012EA57; EMBL:X67703; NID:G11072; PIDN: A/Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBI:74223)
 C/Genetics:
 A/Accession: Mat84d
 A/Cross-references: FlyBase:FBgn0004175
 A/Map position: 3
 C/Suprafamily: fruit fly testis-specific protein
 C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 10 CGPC 13

RESULT 9
 A60136
 keratin, scale (clone CSK9) - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 30-Jan-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
 C/Accession: A60136
 R/RefSeq: R. J. Kuh, C. J. Boersch, D. J. Glaetzer, K. H. J. Schaefer, U. J. Schaefer, M. Mech. Dev. 35, 143-151, 1991
 A/Title: Isolation and characterization of keratin mRNA from the scale epidermis of the
 A/Reference number: A60136; MUID:85122780; PMID:2578818
 A/Accession: A60136
 A/Molecule type: mRNA
 A/Residues: 1-73 <WIL>

A/Cross-references: UNIPROT:Q9YH54; UNIPARC:UPI00000FB20A; GB:M25641; NID:g212233; PIDN:
C/Superfamily: feather keratin
C/Keywords: tandem repeat
F/1-49/Region: 13-residue repeats (G-G-S-S-L-G-Y-G-G-L-Y-G-Y)

Query Match 100.0%; Score 31; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 70 CGPC 73

RESULT 10
S25773
testis-specific protein Mat84Db - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: S25773; B56565

R/Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991

A/Title: A cluster of four genes selectively expressed in the male germ line of *Drosophi*
A/Reference number: A56565; MUID:92102953; PMID:1684716
A/Accession: S25773

A/Molecule type: DNA
A/Residues: 1-74 <KDH>
A/Cross-references: UNIPROT:Q01643; UNIPARC:UPI000012EAB6; EMBL:X67703; NID:g11072; PIDN:
A/Note: sequence extracted from NCBI backbone (NCBIN:74217, NCBI:P:74220)
C/Genetics:

A:Gene: Mat84Db
A/Cross-references: FlyBase:FBgn0004173
A/Map position: 3

C/Superfamily: fruit fly testis-specific protein
C/Keywords: spermatogenesis; tandem repeat

Query Match 100.0%; Score 31; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 9 CGPC 12

RESULT 11

I65235
testicular luteinizing hormone beta subunit - rat
C/Species: *Rattus norvegicus* (Norway rat)

C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C/Accession: I65235

R/Zhang, P.P.; Rannikko, A.; Huhtaniemi, I.
Biochem. Biophys. Res. Commun. 210, 858-865, 1995

A/Title: Isolation and characterization of testis-specific cDNAs for luteinizing hormone
A/Reference number: I52320; MUID:95283549; PMID:7763258
A/Accession: I65235

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-80 <RES>

A/Cross-references: UNIPROT:Q63013; UNIPARC:UPI00000E74EB; EMBL:U25803; NID:g904025; PIDN:
C/Genetics:

A:Gene: TLHB3
C/Superfamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 49 CGPC 52

RESULT 12
B46264
thioredoxin 2 - slime mold (*Dictyostelium discoideum*) (fragment)

C/Species: *Dictyostelium discoideum*
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C/Accession: B46264

R/Wetterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992

A/Title: Thioredoxin from *Dictyostelium discoideum* are a developmentally regulated mult
A/Reference number: A46264; MUID:92250653; PMID:1577820
A/Accession: B46264

A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-88 <MET>

A/Cross-references: UNIPROT:P29446; UNIPARC:UPI0000136D74; GB:M91382; NID:g167930; PIDN:
C/Superfamily: thioredoxin; thioredoxin homology
F/8-88/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 31 CGPC 34

RESULT 13

B84409
thioredoxin [imported] - *Halobacterium* sp. NRC-1

C/Species: *Halobacterium* sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 05-Oct-2004
C/Accession: B84409

R/Ng, W.V.; Kennedy, S.P.; Mahapatra, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laeky, S.
; Leitauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; L
A/Title: Genome sequence of *Halobacterium* species NRC-1.
A/Reference number: A84160; MUID:20504483; PMID:11016950
A/Accession: B84409

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-89 <STO>

A/Cross-references: UNIPROT:Q9HMD0; UNIPARC:UPI0000063B9A; GB:AE04437; NID:g10581982; I
C/Genetics:

A:Gene: trxA2
C/Superfamily: thioredoxin

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 13 CGPC 16

RESULT 14

KRGLBS
keratin, feather - silver gull

C/Species: *Larus novaehollandiae* (silver gull)
C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C/Accession: A02850

R/O'Donnell, I.U.; Inglis, A.S.
Aust. J. Biol. Sci. 27, 369-382, 1974

A/Title: Amino acid sequence of a feather keratin from silver gull (*Larus novaeholland*
A/Reference number: A02850; MUID:75054009; PMID:4429491
A/Accession: A02850

A/Molecule type: protein
A/Residues: 1-98 <ODO>

A/Cross-references: UNIPROT:P02451; UNIPARC:UPI000012E06F
A/Experimental source: calamus of wing feathers from a single bird

A>Note: the sequence of the region 75-83 is tentative due to carry-over of residues from
A>Note: 4-Asp and 27-Glu may be amidated in the original feather
A>Note: the alternatives 39-Gln, 48-Thr, 55-Val, 56-Ala, 62-Ala, 63-Ala, 76-Ile, 78-Ser,
C:Superfamily: feather keratin
C:Keywords: blocked amino end; epidermis, feather, fibrous protein, horn, integument
F:1/Modified site: blocked amino end (Ala) (probably acetylated) #status experimental

Query Match 100.0%; Score 31; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 6 CGPC 9

RESULT 15
G64213
thioredoxin - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 16-Aug-1996 #text_change 05-Oct-2004
C:Accession: G64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
, C.A.; Venter, J.C.
Science 270, 397-403, 1995

A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; WUID:96026346; PMID:7569993
A:Accession: G64213
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-102 <TR>
A:Cross-references: UNIPROT:P47370; UNIPARC:UPI0000136E89; GB:U39691; GB:L43967; NID:GLD
A:Experimental source: strain G-37
C:Genetics:

A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-90/Domain: thioredoxin homology <THR>
F:30-33/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 16
H65572
thioredoxin (imported) - Chlamydomonas pneumoniae (strain J138)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H65572
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
Nucleic Acids Res. 28, 2311-2314, 2000

A>Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A66491; WUID:20330349; PMID:10871362
A:Accession: H65572
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <STO>
A:Cross-references: UNIPROT:Q9Z7P5; UNIPARC:UPI00004461A; GB:BA000008; NID:98979031; PI
A:Experimental source: strain J138
C:Genetics:

A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 17
S73896
thioredoxin - Mycoplasma pneumoniae (strain ATCC 29342)
N:Alternate names: hypothetical protein A65_orf102
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C>Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S73896
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirk, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996

A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A:Reference number: S73327; WUID:97105885; PMID:8948633
A:Accession: S73896
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-102 <HN>
A:Cross-references: UNIPROT:P75512; UNIPARC:UPI0000136E8A; EMBL:AE000056; GB:U00089; NIT
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:

A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
F:9-90/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 18
B71503
probable thioredoxin - Chlamydia trachomatis (serotype D, strain WJ3/Cx)
C:Species: Chlamydia trachomatis
C>Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 05-Oct-2004
C:Accession: B71503
R:Stephens, R.S.; Kalan, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998

A>Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.
A:Reference number: A71570; WUID:99000809; PMID:9784136
A:Accession: B71503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <ARN>

A:Cross-references: UNIPROT:O84544; UNIPARC:UPI0000136E75; GB:AE001324; GB:AE001273; NID
A:Experimental source: serotype D, strain WJ-3/Cx
C:Genetics:

A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 19
D72052
thioredoxin CP0088 (imported) - Chlamydomonas pneumoniae (strains CWL029 and AR39)
C:Species: Chlamydomonas pneumoniae, Chlamydia pneumoniae
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C:Accession: D72052; E81614

R;Kalan, S.; Mitchell, W.; Marathe, R.; Lamme, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999

A;Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: D72052

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <ARN>

A;Cross-references: UNIPROT:Q927P5; UNIPARC:UPI000004461A; GB:AE001648; GB:AE001363; NID:91107668; PMID:1988444

A;Experimental source: strain CWL029

R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81614

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <REA>

A;Cross-references: UNIPARC:UPI000004461A; GB:AE002172; GB:AE002161; NID:97189018; PIDN:CAA97572.1; PMID:10684935

A;Experimental source: strain AR39, HL cells

C;Genetics: trxA; CP0088

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
DB 28 CGPC 31

RESULT 20

C81660

Chlorodioxin TC0826 [imported] - *Chlamydia muridarum* (strain N195)

C;Species: *Chlamydia muridarum*, *Chlamydia trachomatis* Mopn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C;Accession: C81660

R;Read: T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: C81660

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-102 <TET>

A;Cross-references: UNIPROT:Q9PUK3; UNIPARC:UPI0000057A90; GB:AE002349; GB:AE002160; NID:91107668; PMID:1988444

A;Experimental source: strain N195 (Mopn)

C;Genetics:

A;Gene: TC0826

C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
DB 28 CGPC 31

RESULT 21

TXB2

thioredoxin II - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein L1933; protein YLR043C

C;Species: *Saccharomyces cerevisiae*

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C;Accession: S15048; A39847; S15360; S64870; B38665

R;Gen, Z.R.

J. Biol. Chem. 266, 1692-1696, 1991

A;Title: Yeast thioredoxin genes.

A;Reference number: A38669; MUID:91107668; PMID:1988444

A;Accession: S15048

A;Molecule type: DNA

A;Residues: 1-103 <GAN>

A;Cross-references: UNIPROT:P22217; UNIPARC:UPI000004F943; EMBL:M59169; NID:9173027; PIDN:CAA97572.1; PMID:10684935

R;Miller, E.G.D.

J. Biol. Chem. 266, 9194-9202, 1991

A;Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval

A;Reference number: A39847; MUID:91225027; PMID:2026619

A;Accession: A39847

A;Molecule type: DNA

A;Residues: 1-103 <MUL>

A;Cross-references: UNIPARC:UPI000004F943; GB:M62647; NID:9173047; PIDN:AAA35177.1; PIDN:CAA97572.1; PMID:10684935

R;Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.

Eur. J. Biochem. 23, 328-335, 1971

A;Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of tr

A;Reference number: S05793; MUID:72100583; PMID:4945270

A;Accession: S15360

A;Molecule type: protein

A;Residues: 26-34 <HAL>

A;Cross-references: UNIPARC:UPI0000171E21

R;Koetter, P.; Rose, M.; Entian, K.D.

submitted to the Protein Sequence Database, May 1996

A;Reference number: S64863

A;Accession: S64870

A;Molecule type: DNA

A;Residues: 1-103 <NOE>

A;Cross-references: UNIPARC:UPI000004F943; EMBL:Z73215; NID:91360372; PIDN:CAA97572.1; PMID:10684935

A;Note: experimental_source strain S288C

C;Genetics:

A;Gene: SGD:TRX1; TR-II; MIPS:YLR043C

A;Cross-references: SGD:S0004033; MIPS:YLR043C

A;Map position: 12R

C;Superfamily: thioredoxin; thioredoxin homology

C;Keywords: redox-active disulfide

F/2-103/Product: thioredoxin II #status predicted <MAT>

F/9-90/Domain: thioredoxin homology <THR>

F/30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
DB 30 CGPC 33

RESULT 22

T39085

thioredoxin II - fission yeast (*Schizosaccharomyces pombe*)

N;Alternate names: thioredoxine 2

C;Species: *Schizosaccharomyces pombe*

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T39085; T46567

R;Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21826

A;Accession: T39085

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-103 <GEN>

A;Cross-references: UNIPROT:O14463; UNIPARC:UPI000016205F; EMBL:Z99532; PIDN:CAB16724.1

R;Jennings, G.; Perret, E.; Bonin, O.; Picard, A.; Caput, D.

submitted to the EMBL Data Library, October 1997

A;Description: TRX2, a fission yeast stress protein.

A;Reference number: Z23075

A;Accession: T46567

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: mRNA

A;Residues: 1-103 <LEN>

A:Cross-references: UNIPARC:UPI000016205F; EMBL:AA003819; PIDN:CAA06033.1
A:Experimental source: strain 972(-)
C:Genetics:
A:Gene: trx2: SPAC7D4.07c
A:Map position: 1
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 30 CGPC 33

RESULT 23
A11228
thioredoxin [imported] - *Listeria monocytogenes* (strain EGD-e)
C:Species: *Listeria monocytogenes*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: A11228
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltounnam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <GLA>
A:Cross-references: UNIPROT:Q9S386; UNIPARC:UPI000005509E; GB:NC_003210; PIDN:CAC99311.1
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 28 CGPC 31

RESULT 24
AC1582
thioredoxin [imported] - *Listeria innocua* (strain C1p11262)
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AC1582
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blecker, .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltounnam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tlerez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1582
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <GLA>
A:Cross-references: UNIPROT:Q9S386; UNIPARC:UPI000005509E; GB:AL592022; PIDN:CAC96427.1;
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 28 CGPC 31

RESULT 25
A28086
thioredoxin - rabbit
C:Species: *Oryctolagus cuniculus* (domestic rabbit)
C>Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
C:Accession: A28086
R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S. J. Biol. Chem. 263, 9589-9597, 1988
A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined
A:Reference number: A28086; MUID:88257078; PMID:3164311
A:Accession: A28086
A:Molecule type: protein
A:Residues: 1-104 <JOH>
A:Cross-references: UNIPROT:P08628; UNIPARC:UPI0000136B36
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:8-91/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 31 CGPC 34

RESULT 26
A28215
thioredoxin - *Rhodospirillum rubrum*
C:Species: *Rhodospirillum rubrum*
C>Date: 28-Aug-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
C:Accession: A28215
R:Johnson, T.C.; Yee, B.C.; Carlson, D.E.; Buchanan, B.B.; Johnson, R.S.; Mathews, W.R. J. Bacteriol. 170, 2406-2408, 1988
A:Title: Thioredoxin from *Rhodospirillum rubrum*: primary structure and relation to chior
A:Reference number: A28215; MUID:88198045; PMID:3129411
A:Accession: A28215
A:Molecule type: protein
A:Residues: 1-104 <JOH>
A:Cross-references: UNIPROT:P10473; UNIPARC:UPI0000171E24
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:7-90/Domain: thioredoxin homology <THR>
F:29-32/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 29 CGPC 32

RESULT 27
B37192
thioredoxin - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C>Date: 31-Jan-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
C:Accession: B37192; H69726
R:Chen, N.Y.; Zhang, J.J.; Paulus, H. J. Gen. Microbiol. 135, 2931-2940, 1989

A>Title: Chromosomal location of the *Bacillus subtilis* aspartokinase II gene and nucleot
A/Reference number: A37192; MUID:9012525; PMID:2559145
A/Accession: B37192
A/Molecule type: DNA
A/Residues: 1-104 <CHE>
A/Cross-references: UNIPARC:UPI00006087B; GB:U03294; GB:M26384; NID:g14
R/Kuner, S.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Allioni, G.; Azevedo, V.; Berth
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gallier
A.; Koch, J.; Harwood, C.R.; Hanaul, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsreith, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A/Authors: Schlögl, S.; Schreier, R.; Scollone, F.; Sekiguchi, J.; Sekowska, A.; Serch
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A/Reference number: A69580; MUID:9804403; PMID:9384377
A/Accession: H69726
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-104 <KUN>
A/Cross-references: UNIPARC:UPI000006087B; GB:299118; GB:AL009126; NID:g2635200; PIDN:CA
A/Experimental source: strain 168
A/Genetics: trxA
A/Map position: 70 min
A/Cross-family: thiorodoxin; thiorodoxin homology
A/Keywords: redox-active disulfide
F/9-90/Domain thiorodoxin homology <THR>
F/29-32/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||||
Db 29 CGPC 32

RESULT 28
TXB1
thiorodoxin I - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein G7746; protein YGR209C; thiorodoxin 2
C/Species: *Saccharomyces cerevisiae*
C/Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text change 05-Oct-2004
C/Accession: S15049; B39847; S05793; S53932; S61947; S64551; S63858; A38669
R/Gan, Z.R.
J. Biol. Chem. 266, 1692-1696, 1991
A>Title: Yeast thiorodoxin genes.
A/Reference number: A38669; MUID:91107668; PMID:1988444
A/Accession: S15049
A/Molecule type: DNA
A/Residues: 1-104 <GAN>
A/Cross-references: UNIPROT:P22803; UNIPARC:UPI000004F91C; GB:M59166; NID:g173025; PIDN:
R/Muller, E.G.D.
J. Biol. Chem. 266, 9194-9202, 1991
A>Title: Thiorodoxin deficiency in yeast prolongs S phase and shortens the G1 interval
A/Reference number: A39847; MUID:91225027; PMID:2026619
A/Accession: B39847
A/Molecule type: DNA
A/Residues: 1-104 <MDL>
A/Cross-references: UNIPARC:UPI000004F91C; GB:M62648; NID:g173049; PIDN:AAA5178.1; PID:
R/Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.
Eur. J. Biochem. 23, 328-335, 1971
A>Title: Yeast thiorodoxin. Amino-acid sequence around the active-center disulfide of th
A/Reference number: S05793; MUID:72100583; PMID:4945270
A/Accession: S05793

A/Molecule type: protein
A/Residues: 2;27-43;98-104 <HAL>
A/Cross-references: UNIPARC:UPI0000118C95; UNIPARC:UPI0000171E1F; UNIPARC:UPI0000171E20
A/Note: the sequence from the summary and from Fig. 5 is inconsistent with that from pag
R/Guerreiro, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa
submitted to the EMBL Data Library, April 1995
A/Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII
es, of the human.
A/Reference number: S53922
A/Accession: S53932
A/Molecule type: DNA
A/Residues: 1-104 <GUB>
A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; PT
A/Experimental source: strain S288C
A/Experimental source: strain S288C
R/Song, J.M.; Cheung, E.; Rabinowitz, J.C.
submitted to the EMBL Data Library, November 1995
A/Description: Analysis of the 15.6-kb fragment encompassing the ADE3 gene.
A/Reference number: S61947
A/Accession: S61947
A/Molecule type: DNA
A/Residues: 1-104 <SON>
A/Cross-references: UNIPARC:UPI000004F91C; EMBL:U40843; NID:g1165213; PIDN:AAA85584.1;
A/Experimental source: strain GR88
R/Guerreiro, P.; Barreiros, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pous
submitted to the Protein Sequence Database, May 1996
A/Reference number: S64517
A/Accession: S64531
A/Molecule type: DNA
A/Residues: 1-104 <GUM>
A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z72994; NID:g1323374; PIDN:CAA97236.1;
A/Experimental source: strain S288C
R/Guerreiro, P.; Barreiros, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pous
Yeast 12, 273-280, 1996
A/Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII reveal
terial electron-transferring flavoproteins (beta-chain) and of the *Escherichia coli* pho
A/Reference number: S63848; MUID:97060019; PMID:8904340
A/Accession: S63858
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-104 <GUF>
A/Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; P
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
A/Genetics: trpX2; trpI; MIPS:YGR209C
A/Map position: 7R
A/Cross-references: SGD:S0003441; MIPS:YGR209C
A/Suprafamily: thiorodoxin; thiorodoxin homology
C/Keywords: redox-active disulfide
F/2-104/Product: thiorodoxin I #status experimental <MAT>
F/9-91/Domain thiorodoxin homology <THR>
F/31-34/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 29
S77780
thiorodoxin - *Mycoplasma capricolum* (fragment)
N/Alternate names: protein MC064
C/Species: *Mycoplasma capricolum*
C/Date: 09-Oct-1997 #sequence revision 24-Oct-1997 #text change 09-Jul-2004
C/Accession: S77780; S46921
R/Bork, P.; Ouzounis, C.; Casati, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.
Mol. Microbiol. 16, 955-967, 1995
A>Title: Exploring the *Mycoplasma capricolum* genome: a minimal cell reveals its physiol
A/Reference number: S77739; MUID:96059641; PMID:7476192
A/Accession: S77780

A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-104 <BOR>
A:Cross-references: UNIPROT:Q48985; UNIPARC:UPI0000083213; EMBL:233053; NID:G514449; PID
A:Experimental source: ATCC 27343
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:13-93/Domain: thioredoxin homology <THR>
F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 33 CGPC 36

RESULT 30
H95206
thioredoxin [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Jul-2004
C:Accession: H95206
R:Retellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzaple,
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21557209; PMID:11463916
A:Accession: H95206
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <KUR>
A:Cross-references: UNIPROT:Q97P88; UNIPARC:UPI00000519A5; GB:AE005672; PIDN:AAK75849.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SP1776
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 28 CGPC 31

RESULT 31
H98071
thioredoxin-disulfide reductase (EC 1.8.1.9) [imported] - Streptococcus pneumoniae (stra
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: H98071
R:Hoshino, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Buggett, S.; Dehoff, B.S.; H
e, R.; LeBlanc, D.J.; Lee, L.N.; Letkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5703-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: H98071
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-104 <KUR>
A:Cross-references: UNIPROT:Q8DNP9; UNIPARC:UPI00000836A4; GB:AE007317; PIDN:AAL00405.1;
C:Genetics:

A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: oxidoreductase

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 28 CGPC 31

RESULT 32
A59394
thioredoxin - Clostridium pasteurianum
C:Species: Clostridium pasteurianum
C>Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 05-Oct-2004
C:Accession: B59394; A59394
R:Reynolds, C.M.; Meyer, J.; Poole, L.B.
Biochemistry 41, 1990-2001, 2002
A:Title: NADH-dependent bacterial thioredoxin reductase-like protein, in conjunction wit
A:Reference number: B59394
A:Accession: B59394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <RE1>
A:Cross-references: UNIPARC:UPI0000174DEF
R:Reynolds, C.M.; Poole, L.B.; Hammel, K.E.; Wada, K.; Buchanan, B.B.
submitted to the Protein Sequence Database, September 2001
A:Reference number: A59394
A:Accession: A59394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <RE2>
A:Cross-references: UNIPARC:UPI0000174DEF
R:Hammel, K.E.; Cornwell, K.L.; Buchanan, B.B.
Proc. Natl. Acad. Sci. USA 80, 3681-3685, 1983
A:Title: Ferredoxin/flavoprotein-linked pathway for the reduction of thioredoxin.
A:Reference number: A59432
A:Contents: annotation; purification and characterization of the protein
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 28 CGPC 31

RESULT 33
C46264
thioredoxin 3 - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C:Accession: C46264
R:Welterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992
A:Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult
A:Reference number: A46264; MUID:92250653; PMID:1577820
A:Accession: C46264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-104 <ME1>
A:Cross-references: UNIPROT:P29447; UNIPARC:UPI0000136D7B; GB:M91383; NID:G167932; PIDN:
F:8-91/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 31 CGPC 34

RESULT 34

B84037
thioredoxin trxa [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004

C/Accession: B84037

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; PMID:20512582; PMID:11058132

A/Accession: B84037

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <STO>

A/Cross-references: UNIPROT:Q9K6A8; UNIPARC:UPI00000C40CD; GB:AE001517; GB:BA000004; NIT

A/Experimental source: strain C-125

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 29 CGPC 32

RESULT 35

B89885

thioredoxin [imported] - Staphylococcus aureus (strain N315)

C/Species: Staphylococcus aureus

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C/Accession: B89885

R/Kuroda, M.; Oheta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaio, C.; Sekimizu, K.;

C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A/Reference number: A89758; PMID:21311952; PMID:11418146

A/Accession: B89885

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <KUR>

A/Cross-references: UNIPROT:Q9ZEH4; UNIPARC:UPI00000D78B6; GB:BA000018; PID:g13700945; F

A/Experimental source: strain N315

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 29 CGPC 32

RESULT 36

D86830

thioredoxin [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 05-Oct-2004

C/Accession: D86830

R/Bolotin, A.; Winkler, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss

A/Reference number: A86625; PMID:21235186; PMID:11337471

A/Accession: D86830

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <STO>

A/Cross-references: UNIPROT:Q9CF37; UNIPARC:UPI00000C6AAD; GB:AE005176; PID:g12724655; F

A/Experimental source: strain IL1403

C/Genetics:

A/Gene: trxa

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 28 CGPC 31

RESULT 37

C81432

thioredoxin Cj0147c [imported] - Campylobacter jejuni (strain NCTC 11168)

C/Species: Campylobacter jejuni

C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C/Accession: C81432

R/Ferhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

Nature 403, 665-668, 2000

A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy

A/Reference number: A81250; PMID:20150912; PMID:10688204

A/Accession: C81432

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104 <PAR>

A/Cross-references: UNIPROT:Q9PIY0; UNIPARC:UPI00000C205F; GB:AL139074; GB:AL111168; NI

A/Experimental source: serotype O2, strain NCTC 11168

C/Genetics:

A/Gene: trxa; Cj0147c

C/Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 29 CGPC 32

RESULT 38

A30006

thioredoxin - chicken

C/Species: Gallus gallus (chicken)

C/Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A30006

R/Jones, S.W.; Luk, K.C.

J. Biol. Chem. 263, 9607-9611, 1988

A/Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is diferencia

A/Reference number: A30006; PMID:88257080; PMID:2838473

A/Accession: A30006

A/Molecule type: mRNA

A/Residues: 1-105 <JON>

A/Cross-references: UNIPROT:P08629; UNIPARC:UPI00001713BC; GB:J03882; NID:g212765; PIDN

C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide

F:9-92/Domain1: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 32 CGPC 35

RESULT 39

A46264

thioredoxin 1 - slime mold (Dictyostelium discoideum)

C/Spectrum: Dictyostelium discoideum

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #ext_change 05-Oct-2004

C/Accession: A46264

R/Wetterauer, B.; Jacquot, J.P.; Veron, M.

J. Biol. Chem. 267, 9895-9904, 1992

A/Title: Thioredoxins from Dictyostelium discoideum are a developmentally regulated mult

A/Reference number: A46264; MWID:92250553; PMID:1577820

A/Accession: A46264

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-105 <MET>

A/Cross-references: UNIPARC:P29445; UNIPARC:UPI0000136DA; GB:M91384; NID:g167928; PIDN:

C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide

F/9-92/Domain: thioredoxin homology <THR>

F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 ||||
 Db 32 CGPC 35

RESULT 40

JH0568

thioredoxin [validated] - human

N/Alternate names: ATL-derived factor (ADF); eosinophil cytotoxicity-enhancing factor; C/Species: Homo sapiens (man)

C/Date: 30-Jun-1992 #sequence_revision 26-May-1994 #ext_change 05-Oct-2004

C/Accession: JH0568; S04106; S44375; A31993; P00709; A60749; A38922; S53453; A60870

R/Tonissen, K.F.; Wells, J.R.E.

Gene 102, 221-228, 1991

A/Title: Isolation and characterization of human thioredoxin-encoding genes.

A/Reference number: JH0568; MWID:91340156; PMID:1874447

A/Accession: JH0568

A/Molecule type: DNA

A/Residues: 1-105 <TON>

A/Cross-references: UNIPARC:P10599; UNIPARC:UPI000011065C; EMBL:X54539; NID:g37455; PIDN:

R/Ragaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 8, 757-764, 1989

A/Title: ATL-derived factor (ADF), an IL-2 receptor/γac inducer homologous to thioredox

A/Reference number: S04106; MWID:89251607; PMID:2785919

A/Accession: S04106

A/Molecule type: mRNA

A/Residues: 1-105 <TAG1>

A/Cross-references: UNIPARC:UPI000011065C; GB:X77584; NID:g453963; PIDN:CAAS4687.1; PID:

A/Note: this sequence has been revised in reference S44375

R/Ragaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,

EMBO J. 13, 2244, 1994

A/Reference number: S44375; MWID:94244626; PMID:8187776

A/Contents: erratum

A/Accession: S44375

A/Molecule type: mRNA

A/Residues: 1-105 <TAG2>

A/Cross-references: UNIPARC:UPI000011065C; EMBL:X77584; NID:g453963; PIDN:CAAS4687.1; PI

R/Wollman, B.E.; d'Aurion, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Grabe

J. Biol. Chem. 263, 15506-15512, 1988

A/Title: Cloning and expression of a cDNA for human thioredoxin.

A/Reference number: A31993; MWID:89008454; PMID:3170595

A/Accession: A31993

A/Molecule type: mRNA
 A/Residues: 1-38, 'N', 40-73, 'T', 75-105 <MOU>
 A/Cross-references: UNIPARC:UPI000003066B; GB:J04026; NID:g339648; PIDN:AAV74596.1; PID

R/Martin, H.; Dean, M.

Biochem. Biophys. Res. Commun. 175, 123-128, 1991

A/Title: Identification of a thioredoxin-related protein associated with plasma membran

A/Reference number: P00709; MWID:91151337; PMID:1998498

A/Accession: P00709

A/Molecule type: protein

A/Residues: 2-13, 'X', 15 <MAR>

A/Cross-references: UNIPARC:UPI0000171E19

R/Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.

J. Immunol. 143, 979-983, 1989

A/Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical charact

A/Reference number: A60749; MWID:89309777; PMID:2745979

A/Accession: A60749

A/Molecule type: protein

A/Residues: 2-12, 'K', 14-15, 'XX', 18-19, 'X', 21-22 <STL>

A/Cross-references: UNIPARC:UPI0000171E1A

A/Note: the abstract is inconsistent with figure 4 in having one undetermined residue a

R/Rimsky, L.; Makasugi, H.; Ferrara, P.; Robin, P.; Capdevielle, J.; Turcz, T.; Fradel

J. Immunol. 136, 3304-3310, 1986

A/Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel i

A/Reference number: A38922; MWID:86169684; PMID:3485686

A/Accession: A38922

A/Molecule type: protein

A/Residues: 2-16 <MAK>

A/Cross-references: UNIPARC:UPI0000171E1B

R/Dean, M.F.; Martin, H.; Sansom, P.A.

Biochem. J. 304, 861-867, 1994

A/Title: Characterization of a thioredoxin-related surface protein.

A/Reference number: S53453; MWID:95118305; PMID:7818492

A/Accession: S53453

A/Molecule type: protein

A/Residues: 1-21, 38-57 <DEA>

A/Cross-references: UNIPARC:UPI00000353C5; UNIPARC:UPI0000171E1C

A/Note: described to be a surface-associated thioredoxin

R/Makasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fzadelizi, D.; Turcz, T.; Bertoglio,

Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987

A/Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it use

A/Reference number: A60870; MWID:87118252; PMID:3027706

A/Contents: annotation

A/Reference number: A65533; PDB:1ERT

A/Contents: annotation

A/Reference number: A50924; PDB:4TRX

A/Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', 75-105

R/Forman-Kay, J.D.; Clore, G.M.; Gronenborn, A.M.

submitted to the Brookhaven Protein Data Bank, December 1990

A/Reference number: A50924; PDB:4TRX

A/Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', 75-105

R/Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.

Biochemistry 30, 2685-2698, 1991

A/Title: High-resolution three-dimensional structure of reduced recombinant human thior

A/Reference number: A38953; MWID:91159399; PMID:2001356

A/Contents: annotation; conformation by (1)H- and (15)N-NMR

C/Comment: This small ubiquitous protein functions in many intracellular biological path

C/Genetics:

A/Gene: GDB:TXN

A/Cross-references: GDB:120475; OMIM:187700

A/Map position: 9q31-9q31

A/Intons: 8/3; 43/3; 63/3; 85/3

C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide

F/2-105/Product: thioredoxin #status experimental <MAT>

F/9-92/Domain: thioredoxin homology <THR>

F/32-35/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 41

thioredoxin - rhesus macaque
 C/Species: Macaca mulatta (rhesus macaque)
 C/Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C/Accession: J50667
 R/An, G.; Wu, R.
 Biochem. Biophys. Res. Commun. 183, 170-175, 1992
 A/Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in mon
 A/Reference number: J50667; MUID:92181438; PMID:1543487
 A/Accession: J50667
 A/Molecule type: mRNA
 A/Residues: 1-105 <ANG>
 A/Cross-references: UNIPROT:P29451; UNIPARC:UPI000016C493; GB:M64643; NID:G342338; PIDN:
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/3-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 42

S04107
 thioredoxin - mouse
 N/Alternate names: ATL-derived factor (ADF)
 C/Species: Mus musculus (house mouse)
 C/Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 05-Oct-2004
 C/Accession: J04068; S44376; S04107
 R/Matsui, M.; Taniguchi, Y.; Hirota, K.; Takeo, M.; Yodoi, J.
 Gene 152, 165-171, 1995
 A/Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.
 A/Reference number: J04068; MUID:55137382; PMID:7835655
 A/Accession: J04068
 A/Molecule type: DNA
 A/Residues: 1-105 <MAT>
 A/Cross-references: UNIPROT:P10639; UNIPARC:UPI0000163891; DDBJ:D21855; NID:G517128
 R/Tagaya, Y.; Maeda, Y.; Matsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMBL J. 13, 2244, 1994
 A/Reference number: S44375; MUID:94244626; PMID:8187776
 A/Contents: extratum

A/Accession: S44376
 A/Molecule type: mRNA
 A/Residues: 1-105 <TG1>
 A/Cross-references: UNIPARC:UPI0000163891; EMBL:X77585; NID:G453971; PIDN:CA54688.1; PI
 R/Tagaya, Y.; Maeda, Y.; Matsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMBL J. 8, 757-764, 1989
 A/Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxi
 A/Reference number: S04106; MUID:89251607; PMID:2785919
 A/Accession: S04107
 A/Molecule type: mRNA
 A/Residues: 1-93, 'N', '94-96, 'ALT', 100-104, 'S', <TG2>
 A/Cross-references: UNIPARC:UPI0000171E1E; GB:X77585
 C/Comment: This small ubiquitous protein functions in many intracellular biological path
 C/Genetic: A/Gene: MGI:Txn
 A/Cross-references: MGI:36258
 A/Map position: 4:24.6
 A/Intons: 29/2; 44/1; 84/2
 C/Superfamily: thioredoxin; thioredoxin homology

C/Keywords: redox-active disulfide
 F/3-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 43

S04352
 thioredoxin - rat
 N/Alternate names: thioredoxin-related surface protein SASP
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C/Accession: S04352; S66372
 R/Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.
 Nucleic Acids Res. 17, 3973, 1989
 A/Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.
 A/Reference number: S04352; MUID:89282399; PMID:2734107
 A/Accession: S04352
 A/Molecule type: mRNA
 A/Residues: 1-105 <TON>
 A/Cross-references: UNIPROT:P11232; UNIPARC:UPI000003066A; EMBL:X14878; NID:G57385; PIDN:
 R/Dean, M.F.; Martin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A/Title: Characterization of a thioredoxin-related surface protein.
 A/Reference number: S53453; MUID:95118305; PMID:7818492
 A/Accession: S66372
 A/Molecule type: protein

A/Residues: 2-21 <DRA>
 A/Cross-references: UNIPARC:UPI0000171E1D
 A/Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found
 A/Note: described to be a surface-associated thioredoxin
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/2-105/Product: thioredoxin #status experimental <MAT>
 F/2-92/Domain: thioredoxin homology <THR>
 F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 44

TXFK
 thioredoxin - coryneform bacterium ATCC11425
 C/Species: coryneform bacterium ATCC11425
 C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
 C/Accession: A00281
 R/Meng, M.; Hogenkamp, H.P.C.
 J. Biol. Chem. 256, 9174-9182, 1981
 A/Title: Purification, characterization, and amino acid sequence of thioredoxin from Co
 A/Reference number: A00281; MUID:81264365; PMID:7021558
 A/Accession: A00281
 A/Molecule type: protein

A/Residues: 1-105 <MEN>
 A/Cross-references: UNIPROT:P00275; UNIPARC:UPI0000136D69
 A/Note: the source was designated as Corynebacterium nephridii
 C/Comment: Thioredoxins are ubiquitous small hydrogen carrier proteins that participate
 C/Superfamily: thioredoxin; thioredoxin homology
 C/Keywords: redox-active disulfide
 F/8-91/Domain: thioredoxin homology <THR>
 F/30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 45

thioredoxin M-1 - Synechocystis sp. (strain PCC 6803)

N:Alternate names: protein slr0233

C:Species: Synechocystis sp.

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

A:Accession: S76386

R:Kaneko, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis

A:Reference number: S74322; PMID:97061201; PMID:8905231

A:Accession: S76386

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-105 <KAN>

A:Cross-references: UNIPROT:P52232; UNIPARC:UPI0000136D6; EMBL:D64000; GB:AE001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Gene: trxm-1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 46

thioredoxin [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

A:Accession: B97700

R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; PMID:21442074; PMID:11557893

A:Accession: B97700

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q92JRS; UNIPARC:UPI0000136E9A; GB:AE006914; PIDN:AAI02540.1;

C:Gene: trxA

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 47

AG2042

thioredoxin [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004

A:Accession: AG2042

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; PMID:21595285; PMID:11759840

A:Accession: AG2042

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <KUR>

A:Cross-references: UNIPROT:Q8VYU1; UNIPARC:UPI00000CE247; GB:BA000019; PIDN:BAW73592.1,

A:Experimental source: strain PCC 7120

C:Gene: slr1893

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 48

thioredoxin [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

A:Accession: D97279

R:Dally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc

A:Reference number: A96900; PMID:21359325; PMID:21359325

A:Accession: D97279

A:Status: preliminary

A:Molecule type: DNA

A:Cross-references: UNIPROT:Q97EM7; UNIPARC:UPI00000CA715; GB:AE001437; PIDN:AAK81023.1,

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Gene: slr1893

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 30 CGPC 33

RESULT 49

thioredoxin - Rhodospirillum rubrum

C:Species: Rhodospirillum rubrum

C:Date: 27-Jul-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

A:Accession: A35135; A30508

R:Fillie, S.; Breton, A.M.; Clement-Metral, J.D.; Galibert, F.

J. Bacteriol. 172, 1556-1561, 1990

A:Title: Cloning, nucleotide sequence, and expression of the Rhodospirillum rubrum

A:Reference number: A35135; PMID:90170874; PMID:2137818

A:Accession: A35135

A:Molecule type: DNA

A:Residues: 1-106 <PII>

A:Cross-references: UNIPROT:P08058; UNIPARC:UPI000016FF78; GB:M33806; NID:G152044; PIDN

A:Experimental source: strain Y
R:Clemet-Metral, J.D.; Holmgren, A.; Cambillau, C.; Joernvall, H.; Eklund, H.; Thomas, Eur. J. Biochem. 172, 413-419, 1998
A:Title: Amino acid sequence determination and three-dimensional modelling of thioredoxin
A:Reference number: A30508; MUID:86166714; PMID:3280308
A:Accession: A30508
A:Molecule type: Protein
A:Residues: 2-63, 'Z', 65-106 <CLE>
A:Cross-references: UNIPARC:UPI0000171E23
C:Experimental source: strain Y
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 50
S33357
thioredoxin - Streptomyces aureofaciens (fragment)
C:Species: Streptomyces aureofaciens
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33357
R:Labudova, O.; Nemethova, M.; Turna, J.; Kollarova, M.
Submitted to the EMBL Data Library, April 1993
A:Description: PCR cloning of a protein-coding part of the thioredoxin gene from Streptococcus
A:Reference number: S33357
A:Accession: S33357
A:Molecule type: DNA
A:Residues: 1-106 <LAB>
A:Cross-references: UNIPROT:P33791; UNIPARC:UPI0000136E9D; EMBL:X72799; NID:9297872; P1
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 51
H64622
thioredoxin - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variety: strains J99, 26695
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64622; C71890
R:Tombo, J.F.; White, O.; Kellavag, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalek, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64622
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-106 <TOM>
A:Cross-references: UNIPROT:P56430; UNIPARC:UPI0000136E82; GB:AE000594; GB:AE000511; NIT
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: C71890
A:Molecule type: DNA
A:Residues: 1-106 <ARN>
A:Cross-references: UNIPARC:UPI0000136E82; GB:AE001507; GB:AE001439; NID:94155326; PIDN
C:Experimental source: strain J99
C:Genetics:
A:Gene: trxA; HP0824
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 30 CGPC 33

RESULT 52
A49888
thioredoxin - Penicillium chrysogenum
C:Species: Penicillium chrysogenum
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 05-Oct-2004
C:Accession: A49888; S3886
R:Cohen, G.; Argaman, A.; Schreiber, R.; Mslowati, M.; Aharonowitz, Y.
J. Bacteriol. 176, 973-984, 1994
A:Title: The thioredoxin system of Penicillium chrysogenum and its possible role in peni
A:Reference number: A49888; MUID:94148789; PMID:8106340
A:Accession: A49888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <COH>
A:Cross-references: UNIPROT:P34723; UNIPARC:UPI0000136E91; EMBL:X76120; NID:9426468; PI
C:Genetics:
A:Gene: trxA
A:Introns: 8/2
C:Superfamily: thioredoxin; thioredoxin homology
F:10-92/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 53
AG2579
thioredoxin C-1 trxA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004
C:Accession: AG2579
R:Wood, D.W.; Serubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-106 <KUR>
A:Cross-references: UNIPROT:Q8UJ46; UNIPARC:UPI0000164451; GB:AE008688; PIDN:AL41053.1
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: trxA
A:Map position: circular chromosome
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 31 CGPC 34

RESULT 54

A32956
thioredoxin m - Synechococcus sp.

C:Species: Synechococcus sp.
C>Date: 17-Jul-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A32956; A30842
R/Muller, E.G.D.; Buchanan, B.B.

J. Biol. Chem. 264, 4008-4014, 1989

A>Title: Thioredoxin is essential for photosynthetic growth. The thioredoxin m gene of A

A/Reference number: A32956; MUID:89139466; PMID:2492995

A/Residues: 1-107 <MUL>
A/Molecule type: DNA

A/Cross-references: UNIPARC:UPI000001823; GB:J04475; NID:g142153; PIDN:AAA23057.1; PID:

A/Note: the source is designated as Anacystis nidulans R2, which is also called Synechoc

C/Genetics:
A:Gene: trxm
C:Superfamily: thioredoxin; thioredoxin homology
C/Keywords: redox-active disulfide
F/10-93/Domain: thioredoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 55

TXAI
thioredoxin 1 - Anabaena sp.

C:Species: Anabaena sp.
C>Date: 31-Dec-1988 #sequence_revision 11-Apr-1997 #text_change 05-Oct-2004

C/Accession: I39624; A23910
R/Hlm, C.

J. Bacteriol. 168, 1258-1264, 1986

A>Title: Cloning, expression, and characterization of the Anabaena thioredoxin gene in E

A/Reference number: I39624; MUID:87057030; PMID:3096973

A/Status: preliminary; translated from GB/EMBL/DBD

A/Molecule type: DNA
A/Residues: 1-107 <RES>

A/Cross-references: UNIPARC:UPI00001655B5; GB:M14736; NID:g142117; PIDN:AAA22049.1; PID:

J. Biol. Chem. 260, 9567-9573, 1985

A/Title: The primary structure of thioredoxin from the filamentous cyanobacterium Anaba

A/Reference number: A23910; MUID:85261357; PMID:3926769

A/Accession: A23910
A/Molecule type: protein
A/Residues: 2-107 <GLB>

A/Cross-references: UNIPARC:UPI0000136D66
A/Experimental source: PCC 7119, ATCC 29151
C:Superfamily: thioredoxin; thioredoxin homology
C/Keywords: heat-stable protein; redox-active disulfide
F/2-107/Product: thioredoxin #status experimental <MAT>
F/10-93/Domain: thioredoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 56

A26622
thioredoxin - Chromatium vinosum

C:Species: Chromatium vinosum
C>Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: A26622
R/Johnson, R.S.; Blemann, K.

Biochemistry 26, 1209-1214, 1987

A>Title: The primary structure of thioredoxin from Chromatium vinosum determined by hig

A/Reference number: A26622; MUID:87185419; PMID:3567166

A/Accession: A26622
A/Molecule type: protein

A/Residues: 1-107 <JOH>
A/Cross-references: UNIPROT:P09857; UNIPARC:UPI0000136E76

A/Note: unidentified residues are Ile or Leu
C:Superfamily: thioredoxin; thioredoxin homology
C/Keywords: heat-stable protein; redox-active disulfide
F/10-93/Domain: thioredoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 57

S31915
thioredoxin - red alga (Cyanidium caldarium)

C:Species: Cyanidium caldarium
C>Date: 03-Mar-1994 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C/Accession: S31915; S45488
R/Jangsdorf, A.; Emich, A.; Zetsche, K.

submitted to the EMBL Data Library, February 1993

A/Description: A thioredoxin gene is located upstream of rbcLs in the unicellular red al

A/Reference number: S31915
A/Accession: S31915

A/Molecule type: DNA
A/Residues: 1-107 <LAN>

A/Cross-references: UNIPROT:P37395; UNIPARC:UPI0000136E7B; EMBL:Z21723; NID:g14402; PIDN:

R/Ohta, N.; Kawano, S.; Kuroiwa, T.
Curr. Genet. 26, 136-138, 1994

A>Title: Physical map of the plastid genome of the unicellular red alga Cyanidium calda

A/Reference number: S45488; MUID:95094309; PMID:8001167

A/Accession: S45488
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 'M', '6', 'IDEU', '11-12', 'DT', '15-16', 'LQ', '19', 'HQ', '22-38', 'A', '40', 'IL', '43-44', 'I', '46-4

A/Cross-references: UNIPARC:UPI000000A275B
C/Genetics:
A:Gene: trx
C:Superfamily: thioredoxin; thioredoxin homology
C/Keywords: redox-active disulfide
F/10-93/Domain: thioredoxin homology <THR>
F/32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 58

thioredoxin-like protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: S47867
R:Salz, H.K.; Flickinger, T.W.; Mitterdorf, E.; Pellicena-Palle, A.; Peteschek, J.P.; Bro
Genetics 136, 1075-1086, 1994
A>Title: The *Drosophila* maternal effect locus *deadhead* encodes a thioredoxin homolog req
A:Reference number: S47867, PMID:94274010; PMID:7516301
A:Accession: S47867
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <SAL>
A:Cross-references: UNIPROT:P47938; UNIPARC:UPI0000124A52; EMBL:L27072; NID:G435591; P
C:Genetics:
A:Gene: FlyBase:dhd
A:Cross-references: FlyBase:FBgn0011761
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:8-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 59

thioredoxin A - red alga (*Porphyra purpurea*) chloroplast
C:Species: *Porphyra purpurea*
C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C:Accession: S73146
R:Reich, M.; Munholland, J.
Plant Mol. Biol. Rep. 13, 333-335, 1995
A>Title: Complete nucleotide sequence of the *Porphyra purpurea* chloroplast genome.
A:Reference number: S73108
A:Accession: S73146
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <REI>
A:Cross-references: UNIPROT:P51225; UNIPARC:UPI0000136E93; EMBL:U8804; NID:G1276652; P
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C:Genetics:
A:Gene: trxA
A:Genome: chloroplast
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 60
S46521
thioredoxin - *Porphyra yezoensis* chloroplast

C:Species: chloroplast *Porphyra yezoensis*
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S46521
R:Reynolds, A.E.; Chesnick, J.M.; Woolford, J.; Catcolico, R.A.
Plant Mol. Biol. 25, 13-21, 1994
A>Title: Chloroplast encoded thioredoxin genes in the red alga *Porphyra yezoensis* and C
A:Reference number: S46521; PMID:94272009; PMID:8003693
A:Accession: S46521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <REV>
A:Cross-references: UNIPROT:P50254; UNIPARC:UPI0000136B94; EMBL:X76612; NID:G509276; P
C:Genetics:
A:Genome: chloroplast
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 61

hypothetical protein Y44E3A.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33843
R:Woesner, J.; Graves, T.; Keppler, D.
submitted to the EMBL Data Library, November 1998
A>Description: The sequence of C. elegans cosmid Y44E3A.
A:Reference number: Z21422
A:Accession: T33843
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-107 <MOE>
A:Cross-references: UNIPROT:Q9TXV8; UNIPARC:UPI0000077021; EMBL:AF106589; PIDN:AACT8230
A:Experimental source: strain Bristol N2; clone Y44E3A
C:Genetics:
A:Gene: CESP:Y44E3A.3
A:Map position: 1
A:introns: 31/2
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 62

S46958
thioredoxin A - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein slr0623
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S46958; S76679
R:Navarro, F.; Florencio, F.J.
submitted to the EMBL Data Library, July 1994
A>Description: The gene encoding for thioredoxin (trxA) in the cyanobacterium *Synechoc*
A:Reference number: S46957
A:Accession: S46958
A:Molecule type: DNA

A;Residues: 1-107 <NAV>
A;Cross-references: UNIPROT:P52231; UNIPARC:UPI0000164C7C; EMBL:X80486; NID:G515939; PID: R;Taneke, T.; Sato, S.; Kocani, H.; Tanaka, A.; Asamiu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76679
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <RAN>
A;Cross-references: UNIPARC:UPI0000164C7C; EMBL:D64004; GB:AB001339; NID:G1001701; PID: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: trxA
C;Superfamily: thioredoxin; thioredoxin homology
C;Keywords: redox-active disulfide
F;10-93/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 32 CGPC 35

RESULT 63
T02814
thioredoxin TRXRPI [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: B81458; T02814
R;Wyle, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: B81458
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <PYL>
A;Cross-references: UNIPROT:Q25345; UNIPARC:UPI000007DADA; GB:AE001274; NID:G3264850; PID: A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: TRXRPI
A;Map position: 1
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 31 CGPC 34

RESULT 64
B53307
thioredoxin - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 05-Oct-2004
C;Accession: B53307
R;Cohen, G.; Yanko, M.; Mislavici, M.; Arzaman, A.; Schreiber, R.; Av-Gay, Y.; Aharonov, J. Bacteriol. 175, 5159-5167, 1993
A;Title: Thioredoxin-thioredoxin reductase system of *Streptomyces clavuligerus*: sequence
A;Reference number: A53307; MUID:93352422; PMID:8349555
A;Accession: B53307
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-107 <COH>
A;Cross-references: UNIPROT:Q05739; UNIPARC:UPI0000136E9E; GB:Z21946; NID:G287916; PID: C;Genetics:
A;Gene: trxA
A;Start codon: GTG
C;Superfamily: thioredoxin; thioredoxin homology
F;11-93/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 33 CGPC 36

RESULT 65
AD1813
thioredoxin [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C;Accession: AD1813
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena*
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD1813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:P06544; UNIPARC:UPI00001655B5; GB:BA000019; PID:BA877576.1
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: trxA
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 32 CGPC 35

RESULT 66
AH3504
thioredoxin C-1 [imported] - *Brucella melitensis* (strain 16M)
C;Species: *Brucella melitensis*
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004
C;Accession: AH3504
R;Dzuvich, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3504
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <KUR>
A;Cross-references: UNIPROT:Q8YB56; UNIPROT:Q8FYX9; UNIPARC:UPI00000582C9; GB:AE008917; A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI2022
A;Map position: 1
C;Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 31 CGPC 34

RESULT 67

E64047
Chloredoxin - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: E64047
R:Flaeschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gockyne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fitchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A:Author: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; PMID:95350630; PMID:7542800
A:Accession: E64047
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-107 <TIGR>
A:Cross-references: UNIPROT:P43785; UNIPARC:UPI0000136E81; GB:U32693; GB:I42023; NID:915
A:Note: named as homolog to a protein from Anacyetis nidulans
C:Superfamily: Chloredoxin; thioedoxin homology
C:Keywords: redox-active disulfide
F:10-93/Domain: thioedoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 68

G82991
Chloredoxin PA5240 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: G82991
R:Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Braham, S.; Van, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, .; Loty, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: G82991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <STO>
A:Cross-references: UNIPROT:Q9X2T1; UNIPARC:UPI0000136E95; GB:AE004936; GB:AE004091; NID:10984043
A:Experimental source: strain PA01
C:Genetics:
A:Gene: trxA; PA5240
C:Superfamily: thioedoxin; thioedoxin homology

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 33 CGPC 36

RESULT 69

B55124
Chloredoxin - Chloredoxin limicola f.sp. thiosulfatophilum

C:Species: Chloredoxin limicola f.sp. thiosulfatophilum
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Oct-2004
C/Accession: B55124; A27801
R:Biemann, K.; Papayanopoulos, I.A. Acc. Chem. Res. 27, 370-378, 1994
A:Title: Amino acid sequencing of proteins.
A:Reference number: A55124
A:Accession: B55124
A:Molecule type: protein
A:Residues: 1-108 <BIR>

A:Cross-references: UNIPARC:UPI0000174DEC
A:Note: unidentified residues are Ile or Leu
A:Note: the species is identified as Chloredoxin thiosulfatophilum
R:Matthews, W.R.; Johnson, R.S.; Corwell, K.L.; Johnson, T.C.; Buchanan, B.B.; Biemann, J. Biol. Chem. 262, 7537-7545, 1987
A:Title: Mass spectrometrically derived amino acid sequence of thioedoxin from Chloredoxin
A:Reference number: A27801; PMID:87222370; PMID:3294835
A:Accession: A27801
A:Molecule type: protein
A:Residues: 1-15, 'XX', 18-41, 'X', 43-44, 'X', 46-53, 'XX', 56-65, 'X', 67-74, 'X', 76-78, 'XX', 81-107
A:Cross-references: UNIPARC:UPI0000174DBD
A:Experimental source: strain Tassajara
A:Note: unidentified residues are Ile or Leu
A:Note: the species is identified as Chloredoxin thiosulfatophilum
C:Superfamily: Chloredoxin; thioedoxin homology
C:Keywords: photosynthesis; redox-active disulfide
F:10-93/Domain: thioedoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 32 CGPC 35

RESULT 70

AD0471
Chloredoxin 1 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: AD0471
R:Parhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: AD0471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8ZAD9; UNIPARC:UPI00000DC66C; GB:AL590842; PIDN:CAC93336.1
A:Genetics:
A:Gene: trxA
C:Superfamily: thioedoxin; thioedoxin homology

Query Match 100.0%; Score 31; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 33 CGPC 36

Search completed: February 23, 2006, 00:42:24
Job time : 40.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:42 ; Search time 146.5 Seconds
(without alignments)
28.895 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	35	1 SCXP_ANDMA	P01498 androcyon
2	31	100.0	36	1 BS14_BUTSI	P59887 buthus sind
3	31	100.0	38	2 O46620_TAPIN	O46620 tapirus ind
4	31	100.0	42	2 O46620_EQUAS	O46620 equus asinu
5	31	100.0	49	2 Q23947_DROHY	Q23947 drosophila
6	31	100.0	49	2 Q23948_DROHY	Q23948 drosophila
7	31	100.0	51	2 Q8MLN5_DROME	Q8MLN5 drosophila
8	31	100.0	52	2 Q6QAU0_DROMA	Q6QAU0 drosophila
9	31	100.0	55	1 MS84C_DROME	O01644 drosophila
10	31	100.0	55	2 Q6QAT9_DROSI	Q6QAT9 drosophila
11	31	100.0	55	2 Q6QAU1_DROMA	Q6QAU1 drosophila
12	31	100.0	56	1 MS87F_DROME	P08175 drosophila
13	31	100.0	56	2 Q595V9_NEILA	Q595V9 neisseria l
14	31	100.0	56	2 Q5F8A3_NEIGL	Q5F8A3 neisseria g
15	31	100.0	56	2 Q7DDJ1_NEIMB	Q7DDJ1 neisseria m
16	31	100.0	56	2 Q9UCN3_NEIMA	Q9UCN3 neisseria m
17	31	100.0	58	2 Q6QAT8_DROSI	Q6QAT8 drosophila
18	31	100.0	59	1 SCCR_MESMA	Q99420 mesobuthus
19	31	100.0	59	1 SCCX_MESMA	Q99420 mesobuthus
20	31	100.0	60	2 Q7IDA0_DROYA	Q7IDA0 drosophila
21	31	100.0	60	2 Q8MSH6_DROME	Q8MSH6 drosophila
22	31	100.0	61	2 Q8T4O3_DROME	Q8T4O3 drosophila
23	31	100.0	62	1 SCIT_MESTA	P81161 mesobuthus
24	31	100.0	63	1 MS84A_DROME	P01642 mesobuthus
25	31	100.0	64	2 Q8MI19_SHEEP	Q8MI19 ovis aries
26	31	100.0	66	2 Q6IMK3_PIG	Q6IMK3 sus scrofa
27	31	100.0	67	2 Q9VW83_DROME	Q9VW83 drosophila
28	31	100.0	69	2 Q6ERU8_ORYSA	Q6ERU8 oryza sativ
29	31	100.0	71	2 Q7PK85_ANOGA	Q7PK85 anopheles g
30	31	100.0	72	1 MS84D_DROME	Q01645 drosophila
31	31	100.0	72	2 Q5TSU4_ANOGA	Q5TSU4 anopheles g

32	31	100.0	72	2 Q4V3L2_DROME	Q4V3L2 drosophila
33	31	100.0	72	2 Q74DK8_GEOSL	Q74DK8 geobacter s
34	31	100.0	72	2 Q4KKV5_MUSCUL	Q4KKV5 mus musculu
35	31	100.0	73	2 Q6ERU3_ORYSA	Q6ERU3 oryza sativ
36	31	100.0	73	2 Q9YH54_GALLI	Q9YH54 gallus gall
37	31	100.0	74	1 MS84B_DROME	Q01643 drosophila
38	31	100.0	75	2 Q5YWM2_NOCFA	Q5YWM2 nocardia fa
39	31	100.0	75	2 Q82DM2_STREPT	Q82DM2 streptococ
40	31	100.0	75	2 Q4RP51_TETRAO	Q4RP51 tetraodon n
41	31	100.0	76	2 Q6UYH8_9CAUD	Q6UYH8 burkholderi
42	31	100.0	76	2 Q74114_MYCPA	Q74114 mycobacteri
43	31	100.0	77	2 Q8XHP3_CLOPE	Q8XHP3 clostridium
44	31	100.0	77	2 Q4S147_TETNG	Q4S147 tetraodon n
45	31	100.0	80	2 Q9VJMS_DROME	Q9VJMS drosophila
46	31	100.0	80	2 Q95JG5_BOVIN	Q95JG5 bos taurus
47	31	100.0	80	2 Q95JG6_BOVIN	Q95JG6 bos taurus
48	31	100.0	80	2 Q63013_RAT	Q63013 rattus norv
49	31	100.0	80	2 Q4T7B7_TETNG	Q4T7B7 tetraodon n
50	31	100.0	82	2 Q46622_CERSI	Q46622 ceratotheri
51	31	100.0	83	2 Q4ZC47_9VIRU	Q4ZC47 bacterioph
52	31	100.0	84	2 Q60744_HUMAN	Q60744 homo sapien
53	31	100.0	84	2 Q6J821_9VIRU	Q6J821 actinoplane
54	31	100.0	84	2 Q6MWE8_ORYSA	Q6MWE8 oryza sativ
55	31	100.0	85	2 Q16275_HUMAN	Q16275 homo sapien
56	31	100.0	85	2 Q5T936_HUMAN	Q5T936 homo sapien
57	31	100.0	87	2 Q8W710_9CAUD	Q8W710 cyanophag
58	31	100.0	87	2 Q9C922_ARATH	Q9C922 arabidopsis
59	31	100.0	88	1 THIO2_DICDI	P29446 dictyosteli
60	31	100.0	88	2 Q5V0J2_HALMA	Q5V0J2 haloarcula
61	31	100.0	88	2 Q8P2Q6_METMA	Q8P2Q6 methanosarc
62	31	100.0	88	2 Q71UV5_HORSE	Q71UV5 equus cabal
63	31	100.0	88	2 Q6ZHP3_BURMA	Q6ZHP3 burkholderi
64	31	100.0	89	2 Q9HMD0_HALSA	Q9HMD0 halobacteri
65	31	100.0	89	2 Q46618_EQUZE	Q46618 equus zebra
66	31	100.0	89	2 Q46619_EQUHM	Q46619 equus hemio
67	31	100.0	89	2 Q4HCJ2_9EBIO	Q4HCJ2 deinococcus
68	31	100.0	89	2 Q4LEN8_PAROL	Q4LEN8 paraliichthy
69	31	100.0	89	2 Q4LEP0_PAROL	Q4LEP0 paraliichthy
70	31	100.0	90	2 Q7R522_GIALA	Q7R522 giardia lam
71	31	100.0	91	1 THIO_THIRO	P96132 thiocapsa r
72	31	100.0	92	2 Q5S2Z0_HUMAN	Q5S2Z0 homo sapien
73	31	100.0	93	2 Q8TL30_METAC	Q8TL30 methanosarc
74	31	100.0	94	2 Q4HC04_9EBIO	Q4HC04 deinococcus
75	31	100.0	95	2 Q4KXV3_PLACH	Q4KXV3 plasmodium
76	31	100.0	96	2 Q4Z518_PLABE	Q4Z518 plasmodium
77	31	100.0	96	2 Q8GMS1_ARATH	Q8GMS1 arabidopsis
78	31	100.0	98	1 KRF1_LARNO	P02451 latius novae
79	31	100.0	98	2 Q25549_NAEFO	Q25549 naegleria f
80	31	100.0	98	2 Q5UB12_BACFN	Q5UB12 bacteroides
81	31	100.0	98	2 Q64RG1_BACFR	Q64RG1 bacteroides
82	31	100.0	99	2 Q8AB91_BACTN	Q8AB91 bacteroides
83	31	100.0	100	1 THIO_MYCGA	Q92EP9 mycoplasma
84	31	100.0	100	2 Q9UN64_MYCGA	Q9UN64 mycoplasma
85	31	100.0	100	2 Q6KIE8_MYCPA	Q6KIE8 mycoplasma
86	31	100.0	101	1 THIO1_CHLTE	Q8K44 chlorobium
87	31	100.0	101	2 Q4N2X5_THRPA	Q4N2X5 thiereria p
88	31	100.0	101	2 Q22031_CYACA	Q22031 cyanidium c
89	31	100.0	101	2 Q6KIE7_MYCWO	Q6KIE7 mycoplasma
90	31	100.0	102	1 THIO_CHLYC	P52227 chlamydomon
91	31	100.0	102	1 THIO_CHLMU	Q9ZPK3 chlamydia m
92	31	100.0	102	1 THIO_CHLNP	Q9ZPK3 chlamydia p
93	31	100.0	102	1 THIO_CHLNR	Q84544 chlamydia t
94	31	100.0	102	1 THIO_CVAME	Q22022 cyanidiosch
95	31	100.0	102	1 THIO_MYCGB	P47370 mycoplasma
96	31	100.0	102	1 THIO_MYCPN	P75512 mycoplasma
97	31	100.0	102	1 THIO_SCHPO	P14463 schizosacch
98	31	100.0	102	1 TRX1_YEAST	P22217 saccharomyc
99	31	100.0	102	2 Q9XT61_MACFA	Q9XT61 macaca fasc
100	31	100.0	102	2 Q61731_CHLAB	Q61731 chlamydomon
101	31	100.0	102	2 Q6F1T8_MESFL	Q6F1T8 mecoplasma
102	31	100.0	102	2 Q6MUG0_MYCWS	Q6MUG0 mycoplasma
103	31	100.0	103	1 THIO_BACSV	P14949 bacillus su
104	31	100.0	103	1 THIO_LISIN	P04414 listeria in

105	31	100.0	103	1	THIO_LRSMO	P0A413	listeria mo	178	31	100.0	104	2	Q72ZM0	BACCI	Q72ZM0	bacillus ce	
106	31	100.0	103	1	TRX2_YEAST	P22A03	saccharomyc	179	31	100.0	104	2	Q72QY0	LEPIC	Q72QY0	leptospira	
107	31	100.0	103	2	Q75C00_ASHCO	P75C00	ashbya goss	180	31	100.0	104	2	Q6HD04	BACFR	Q6HD04	bacillus th	
108	31	100.0	103	2	Q6FND5_CANGA	Q6FND5	candida gla	181	31	100.0	104	2	Q6AYG6	BACFR	Q6AYG6	bacteroides	
109	31	100.0	103	2	Q6BJ80_DEBHA	Q6BJ80	debaromyces	182	31	100.0	104	2	Q63S80	BACCC	Q63S80	bacillus ce	
110	31	100.0	103	2	Q5ACN1_CANAL	Q5ACN1	candida alb	183	31	100.0	104	2	Q5WEK7	BACSC	Q5WEK7	bacillus cl	
111	31	100.0	103	2	Q7QC45_AMOGA	Q7QC45	anopheles h	184	31	100.0	104	2	Q5M212	STR12	Q5M212	streptococ	
112	31	100.0	103	2	Q5IER4_ENTHI	Q5IER4	entamoeba g	185	31	100.0	104	2	Q5LY08	STR11	Q5LY08	streptococ	
113	31	100.0	103	2	Q6Z832_ORISA	Q6Z832	crya seriv	186	31	100.0	104	2	Q5HX18	CAMJR	Q5HX18	campylobact	
114	31	100.0	103	2	Q7P4M8_FUSNV	Q7P4M8	fusobacteri	187	31	100.0	104	2	Q5HQ29	STABO	Q5HQ29	staphylococ	
115	31	100.0	103	2	Q5FLM1_LACAC	Q5FLM1	lactobacilli	188	31	100.0	104	2	Q5HGT9	STAC	Q5HGT9	staphylococ	
116	31	100.0	103	2	Q8RH23_FUSNN	Q8RH23	fusobacteri	189	31	100.0	104	2	Q81L73	BACAN	Q81L73	bacillus an	
117	31	100.0	103	2	Q8BVI7_LACPL	Q8BVI7	lactobacilli	190	31	100.0	104	2	Q6S6E9	BACLD	Q6S6E9	bacillus l1	
118	31	100.0	103	2	Q7AKU7_LACJO	Q7AKU7	lactobacilli	191	31	100.0	105	1	THI01_CORNE		THI01_CORNE		
119	31	100.0	103	2	Q720U6_LISMP	Q720U6	listeria mo	192	31	100.0	105	1	THI01_DICDI		THI01_DICDI		
120	31	100.0	104	1	THI03_DICDI	P29447	dictyostell	193	31	100.0	105	1	THI01_ALIAC		THI01_ALIAC		
121	31	100.0	104	1	THIO_BOVIN	Q97680	bos taurus	194	31	100.0	105	1	THIO_PONPY		THIO_PONPY		
122	31	100.0	104	1	THIO_CALJA	Q9bd13	callithrix	195	31	100.0	105	1	THIO_RHOSH		THIO_RHOSH		
123	31	100.0	104	1	THIO_CHICK	P08629	gallus gall	196	31	100.0	105	1	THIO_RICCN		THIO_RICCN		
124	31	100.0	104	1	THIO_HORSE	P10599	equus caball	197	31	100.0	105	1	THIO_RICCN		THIO_RICCN		
125	31	100.0	104	1	THIO_HUMAN	P10599	homo sapien	198	31	100.0	105	1	THIO_RICCN		THIO_RICCN		
126	31	100.0	104	1	THIO_MACMU	P29451	macaca mula	199	31	100.0	105	2	Q519H9	ENTHI	Q519H9	entamoeba h	
127	31	100.0	104	1	THIO_MOOSE	P10639	mus musculus	200	31	100.0	105	2	Q54KN7	DICDI	Q54KN7	dictyostell	
128	31	100.0	104	1	THIO_OPHHA	Q98TX1	ophiophagus	201	31	100.0	105	2	Q5CR91	CRYPV	Q5CR91	cryptospori	
129	31	100.0	104	1	THIO_PIG	P82460	sus scrofa	202	31	100.0	105	2	Q7PAB0	RICSI	Q7PAB0	ricketsia	
130	31	100.0	104	1	THIO_RABIT	P08628	cricetulus	203	31	100.0	105	2	Q6BY00	RICCY	Q6BY00	ricketsia	
131	31	100.0	104	1	THIO_RAT	P11222	rattus norv	204	31	100.0	105	2	Q97EM7	CLOAB	Q97EM7	clostridium	
132	31	100.0	104	1	THIO_RHORU	P10473	rhodospirill	205	31	100.0	105	2	Q8YV11	ANASP	Q8YV11	anaebana sp	
133	31	100.0	104	1	THIO_SHEEP	P50413	ovis aries	206	31	100.0	105	2	Q8XMF0	CLOE	Q8XMF0	clostridium	
134	31	100.0	104	1	THIO_STAM	P0A0R4	staphylococ	207	31	100.0	105	2	Q8X0T2	CLOE	Q8X0T2	clostridium	
135	31	100.0	104	1	THIO_STAN	P99122	staphylococ	208	31	100.0	105	2	Q7VKR2	HAEDU	Q7VKR2	haemophilus	
136	31	100.0	104	1	THIO_STAN	Q6ghu0	staphylococ	209	31	100.0	105	2	Q7U534	SYNXX	Q7U534	synecococ	
137	31	100.0	104	1	THIO_STAS	Q6gae9	staphylococ	210	31	100.0	105	2	Q5KMG6	GEOXA	Q5KMG6	geobacillus	
138	31	100.0	104	1	THIO_STAU	P0A0K6	staphylococ	211	31	100.0	105	2	Q5ZKC4	MOUSE	Q5ZKC4	mus musculu	
139	31	100.0	104	1	THIO_STAW	P0A0K5	staphylococ	212	31	100.0	105	2	Q80ZD7	MELUD	Q80ZD7	melospirita	
140	31	100.0	104	1	THIO_STAP	Q6Cp15	staphylococ	213	31	100.0	105	2	Q6GQ64	XENIA	Q6GQ64	xenopus lae	
141	31	100.0	104	2	Q6CN03_KLUUA	Q6CN03	kluyveromyc	214	31	100.0	105	2	Q5XGB5	XENIR	Q5XGB5	xenopus tiro	
142	31	100.0	104	2	Q6C399_YARLI	Q6C399	varicowia li	215	31	100.0	105	2	Q5U566	XENIR	Q5U566	xenopus lae	
143	31	100.0	104	2	Q5KKS5_RRYNE	Q5KKS5	cryptococcu	216	31	100.0	106	1	THI01_ANASO		THI01_ANASO		
144	31	100.0	104	2	Q5WJ88_RRYNE	Q5WJ88	cryptococcu	217	31	100.0	106	1	THI01_ANASO		THI01_ANASO		
145	31	100.0	104	2	Q9U1G7_FASHE	Q9U1G7	fasciola he	218	31	100.0	106	1	THI01_SINP7		THI01_SINP7		
146	31	100.0	104	2	Q9U544_FASHE	Q9U544	fasciola he	219	31	100.0	106	1	THI01_SINP7		THI01_SINP7		
147	31	100.0	104	2	Q9NIR2_PLAFA	Q9NIR2	plasmodium	220	31	100.0	106	1	THI02_DROYA		THI02_DROYA		
148	31	100.0	104	2	Q962B7_BRABE	Q962B7	branchiosto	221	31	100.0	106	1	THIO_COBCM		THIO_COBCM		
149	31	100.0	104	2	Q9NFK9_PLARA	Q9NFK9	plasmodium	222	31	100.0	106	1	THIO_HELPU		THIO_HELPU		
150	31	100.0	104	2	Q7RH10_PLAFO	Q7RH10	plasmodium	223	31	100.0	106	1	THIO_HELPU		THIO_HELPU		
151	31	100.0	104	2	Q7KQL8_PLAFA	Q7KQL8	plasmodium	224	31	100.0	106	1	THIO_PASMU		THIO_PASMU		
152	31	100.0	104	2	Q6B963_SCHMA	Q6B963	schistosoma	225	31	100.0	106	1	THIO_PENCH		THIO_PENCH		
153	31	100.0	104	2	Q5DAX8_SCHMA	Q5DAX8	schistosoma	226	31	100.0	106	1	THIO_PENCH		THIO_PENCH		
154	31	100.0	104	2	Q48985_MYCCA	Q48985	mycoplasma	227	31	100.0	106	1	THIO_STRAU		THIO_STRAU		
155	31	100.0	104	2	Q4HFK4_CAMCO	Q4HFK4	campylobact	228	31	100.0	106	2	THIO_SYNY3		THIO_SYNY3		
156	31	100.0	104	2	Q4HUN3_CAMLA	Q4HUN3	campylobact	229	31	100.0	106	2	Q9U515_MANSE		Q9U515_MANSE		
157	31	100.0	104	2	Q4HNN5_CAMOP	Q4HNN5	campylobact	230	31	100.0	106	2	Q4PNB0_IXOSC		Q4PNB0_IXOSC		
158	31	100.0	104	2	Q7M0Y9_CLOPA	Q7M0Y9	clostridium	231	31	100.0	106	2	Q963B4_AEDAE		Q963B4_AEDAE		
159	31	100.0	104	2	Q5LHJ1_BACFN	Q5LHJ1	bacteroides	232	31	100.0	106	2	Q8T9N5_SCHNA		Q8T9N5_SCHNA		
160	31	100.0	104	2	Q4LSFO_STRAHJ	Q4LSFO	staphylococ	233	31	100.0	106	2	Q9U8F3_SCHNA		Q9U8F3_SCHNA		
161	31	100.0	104	2	Q8DNP9_STRRS	Q8DNP9	streptococ	234	31	100.0	106	2	Q9GMW8_MACRA		Q9GMW8_MACRA		
162	31	100.0	104	2	Q817L8_BACCR	Q817L8	bacillus ce	235	31	100.0	106	2	Q5VAN9_RHITT		Q5VAN9_RHITT		
163	31	100.0	104	2	Q9K8A8_BACHD	Q9K8A8	bacillus ha	236	31	100.0	106	2	Q4TMB6_GSPEN		Q4TMB6_GSPEN		
164	31	100.0	104	2	Q9PIY0_CAMJE	Q9PIY0	campylobact	237	31	100.0	106	2	Q8KVV0_9PROT		Q8KVV0_9PROT		
165	31	100.0	104	2	Q9CFJ7_LACLA	Q9CFJ7	lactococcus	238	31	100.0	106	2	Q5NNI9_ZYMOO		Q5NNI9_ZYMOO		
166	31	100.0	104	2	Q97P68_STRPN	Q97P68	streptococcus	239	31	100.0	106	2	Q6NDN2_RHOJA		Q6NDN2_RHOJA		
167	31	100.0	104	2	Q8XHX1_CLOPE	Q8XHX1	clostridium	240	31	100.0	106	2	Q8UTJ6_AGRP5		Q8UTJ6_AGRP5		
168	31	100.0	104	2	Q8NZ17_STRPB	Q8NZ17	streptococ	241	31	100.0	106	2	Q89WD9_BRAJA		Q89WD9_BRAJA		
169	31	100.0	104	2	Q99Y75_STRPY	Q99Y75	streptococ	242	31	100.0	106	2	Q8EMN2_SYLCP		Q8EMN2_SYLCP		
170	31	100.0	104	2	Q8EP16_OCEIH	Q8EP16	oceanobacill	243	31	100.0	106	2	Q5LLP8_SILIC		Q5LLP8_SILIC		
171	31	100.0	104	2	Q8E3J7_STRPA3	Q8E3J7	streptococ	244	31	100.0	106	2	Q8DGN0_SYNBL		Q8DGN0_SYNBL		
172	31	100.0	104	2	Q8DXX8_STRPA5	Q8DXX8	streptococ	245	31	100.0	106	2	Q7MSG6_WOLNU		Q7MSG6_WOLNU		
173	31	100.0	104	2	Q8DSD2_STRPMU	Q8DSD2	streptococ	246	31	100.0	106	2	Q6MS96_PARWU		Q6MS96_PARWU		
174	31	100.0	104	2	Q835H2_ENTFA	Q835H2	enterococcus	247	31	100.0	106	2	Q4S0R5_TETNG		Q4S0R5_TETNG		
175	31	100.0	104	2	Q8A5L0_BACTN	Q8A5L0	bacteroides	248	31	100.0	107	1	THI01_DROME		THI01_DROME		
176	31	100.0	104	2	Q7MXW5_PORGI	Q7MXW5	porphyromon	249	31	100.0	107	1	THI01_DROYA		THI01_DROYA		
177	31	100.0	104	2	Q7CET1_STRP3	Q7CET1	streptococ	250	31	100.0	107	1	THIO_CHRVI		THIO_CHRVI		
																Q72ZM0	bacillus ce
																Q72QY0	leptospira
																Q6HD04	bacillus th
																Q6AYG6	bacteroides
																Q63S80	bacillus ce
																Q5WEK7	bacillus cl
																Q5M212	streptococ
																Q5LY08	streptococ
																Q5HX18	campylobact
																Q5HQ29	staphylococ
																Q5HGT9	staphylococ
																Q81L73	bacillus an
																Q6S6E9	bacillus l1
																P00275	corynebacte
																P29445	dictyostell
																P52332	syncocyst
																P80519	alicyclobac

251	31	100.0	107	1	THIO_CYACA	P37395 cyanidium c	324	31	100.0	108	2	O8YU9 ANASP	O8YU9 anabaena sp
252	31	100.0	107	1	THIO_BOHR	O17485 echinococcu	325	31	100.0	108	2	O8Y056 RALSO	O8Y056 ralestonia s
253	31	100.0	107	1	THIO_HAEN	P43785 haemophilus	326	31	100.0	108	2	O8EJ06 SHEON	O8EJ06 shewanella
254	31	100.0	107	1	THIO_ICTPU	O9d613 icetalurus p	327	31	100.0	108	2	O8DDN7 VIBVU	O8DDN7 vibrio vuln
255	31	100.0	107	1	THIO_PORPU	P51225 porphyra pu	328	31	100.0	108	2	O8YKH6 VIBPA	O8YKH6 vibrio para
256	31	100.0	107	1	THIO_PORPE	P50254 porphyra ye	329	31	100.0	108	2	O8ZVN2 NITEU	O8ZVN2 nitrosomona
257	31	100.0	107	1	THIO_STRCL	O05739 streptomyces	330	31	100.0	108	2	O7UJ35 RHODA	O7UJ35 rhodospirillum
258	31	100.0	107	2	O7RXV8 NEUCR	O7RXV8 neuropeira	331	31	100.0	108	2	O7XN22 CHRVO	O7XN22 chromobacter
259	31	100.0	107	2	O9C1L1 NEUCR	O9C1L1 neuropeira	332	31	100.0	108	2	O6MKD2 BDEBA	O6MKD2 bdellovibrio
260	31	100.0	107	2	O5EN23 MAGGR	O5EN23 magnaportia	333	31	100.0	108	2	O6A034 DESPS	O6A034 desulfobacter
261	31	100.0	107	2	O51V99 MAGGR	O51V99 magnaportia	334	31	100.0	108	2	O6ABW1 LEXIX	O6ABW1 leifsonia x
262	31	100.0	107	2	O7PM26 ANOGA	O7PM26 anopheles g	335	31	100.0	108	2	O63U09 BURMA	O63U09 burkholderi
263	31	100.0	107	2	O81PJO DROME	O81PJO drosophila	336	31	100.0	108	2	O62UJ6 BIPMA	O62UJ6 burkholderi
264	31	100.0	107	2	O9NG21 ANOGA	O9NG21 anopheles g	337	31	100.0	108	2	O5ZRE7 LEGSPA	O5ZRE7 legionella
265	31	100.0	107	2	O9NG23 TRYBA	O9NG23 trypanosoma	338	31	100.0	108	2	O5X0U3 LEGPA	O5X0U3 legionella
266	31	100.0	107	2	O25345 LEXIA	O25345 leishmania	339	31	100.0	108	2	O5W5L4 LEGPL	O5W5L4 legionella
267	31	100.0	107	2	O9IXY8 CAEBL	O9IXY8 caenorhabd	340	31	100.0	108	2	O5QYF9 IDILO	O5QYF9 idiomaticina
268	31	100.0	107	2	O6B343 TRYCR	O6B343 trypanosoma	341	31	100.0	108	2	O5P1K8 AZOSE	O5P1K8 azotarcus sp
269	31	100.0	107	2	O617H0 CAEBR	O617H0 caenorhabd	342	31	100.0	108	2	O5NG78 FRATT	O5NG78 francisella
270	31	100.0	107	2	O5S1X7 IXOSC	O5S1X7 ixodes scap	343	31	100.0	108	2	O7ZUI4 BRARE	O7ZUI4 brachydanio
271	31	100.0	107	2	O67UL8 ORYSA	O67UL8 oryza sativ	344	31	100.0	109	1	THIO2_SYNY3	THIO2 syny3
272	31	100.0	107	2	O57AF5 BRUBA	O57AF5 bruceella ab	345	31	100.0	109	1	THIO_CHIAN	THIO chian
273	31	100.0	107	2	O5FGA3 ENRG	O5FGA3 enrichtia r	346	31	100.0	109	1	THIO_EMENT	THIO ementi
274	31	100.0	107	2	O9AUR5 ACTAC	O9AUR5 actinobacill	347	31	100.0	109	1	THIO_GRIPA	THIO gripa
275	31	100.0	107	2	O79N44 SYNP7	O79N44 synchococc	348	31	100.0	109	2	O4W214 ASPFU	O4W214 aspergillus
276	31	100.0	107	2	O6M1C7 CORGL	O6M1C7 corynebacte	349	31	100.0	109	2	O8MIN1 CAPHI	O8MIN1 capra hircu
277	31	100.0	107	2	O4ORG1 HARBH	O4ORG1 haemophilus	350	31	100.0	109	2	O84XS1 CHLRE	O84XS1 chlamydomon
278	31	100.0	107	2	O6NEA2 CORDI	O6NEA2 corynebacte	351	31	100.0	109	2	O4K3Z3 PSEFS	O4K3Z3 pseudomonas
279	31	100.0	107	2	O92TCS RHIME	O92TCS rhizobium m	352	31	100.0	109	2	O5FKX3 SALPA	O5FKX3 salmonella
280	31	100.0	107	2	O6G1B7 BARQU	O6G1B7 bartonella	353	31	100.0	109	2	O8ECG6 PSEPK	O8ECG6 pseudomonas
281	31	100.0	107	2	O6G588 BARHE	O6G588 bartonella	354	31	100.0	109	2	O87UQ3 PSESM	O87UQ3 pseudomonas
282	31	100.0	107	2	O8FYX9 BRUSU	O8FYX9 bruceella su	355	31	100.0	109	2	O60CP8 METCA	O60CP8 methylococc
283	31	100.0	107	2	O98CM9 RHILIO	O98CM9 rhizobium l	356	31	100.0	109	2	O4S0R6 TETNG	O4S0R6 tetradodon n
284	31	100.0	107	2	O73GQ5 WOJPM	O73GQ5 wolbachia p	357	31	100.0	110	1	THIO2_ANASP	THIO2 anasp
285	31	100.0	107	2	O8IE56 BRDME	O8IE56 bruceella me	358	31	100.0	110	1	THIO_STRCO	THIO strco
286	31	100.0	107	2	O8FSW0 COREF	O8FSW0 corynebacte	359	31	100.0	110	2	O4WV97 ASPFU	O4WV97 aspergillus
287	31	100.0	107	2	O8DKP7 SYNEL	O8DKP7 synchococc	360	31	100.0	110	2	O6QUK5 PAXIN	O6QUK5 paxillus in
288	31	100.0	107	2	O7VBF6 PROMA	O7VBF6 prochloroc	361	31	100.0	110	2	O5BH10 EMENT	O5BH10 ementi
289	31	100.0	107	2	O7VGM6 PROMA	O7VGM6 prochloroc	362	31	100.0	110	2	O6ZYLO 9METZ	O6ZYLO 9metz
290	31	100.0	107	2	O7V126 PROMP	O7V126 prochloroc	363	31	100.0	110	2	O4H9D7 9PEIO	O4H9D7 9peio
291	31	100.0	107	2	O7U898 SYNPX	O7U898 synchococc	364	31	100.0	110	2	O879K6 STRP3	O879K6 streptococ
292	31	100.0	107	2	O72B01 DESVH	O72B01 desulfocvibr	365	31	100.0	110	2	O5F8V8 NEIG1	O5F8V8 neisseria g
293	31	100.0	107	2	O65827 MANSMT	O65827 manheimia	366	31	100.0	110	2	O9A218 CAUCR	O9A218 caulobacter
294	31	100.0	107	2	O5NF09 FRATT	O5NF09 francisella	367	31	100.0	110	2	O9UYI9 NEIMB	O9UYI9 neisseria m
295	31	100.0	107	2	O5MZR6 SYNP6	O5MZR6 synchococ	368	31	100.0	110	2	O9UTV5 NEISSEA	O9UTV5 neisseria m
296	31	100.0	107	2	O5HAC8 EHRBM	O5HAC8 ehrlichia r	369	31	100.0	110	2	O8YVY7 ANASP	O8YVY7 anabaena sp
297	31	100.0	107	2	O6D616 BRARE	O6D616 brachydanio	370	31	100.0	110	2	O88ZK9 LACPL	O88ZK9 lactobacill
298	31	100.0	108	1	THIO2_CHLRE	O8E449 chlorobium	371	31	100.0	110	2	O82FE7 STRAM	O82FE7 streptomyces
299	31	100.0	108	1	THIO2_CHLRE	P10472 chlorobium	372	31	100.0	110	2	O7NM87 GLOVI	O7NM87 gloeobacter
300	31	100.0	108	1	THIO_ECOLI	P00274 escherichia	373	31	100.0	110	2	O5YMS6 NOCPA	O5YMS6 nocardiella fa
301	31	100.0	108	1	THIO_PSEAE	P09271 pseudomonas	374	31	100.0	111	2	O5TVVO ANOGA	O5TVVO anopheles g
302	31	100.0	108	1	THIO_THIFE	P52233 thiodacillu	375	31	100.0	111	2	O9ALM7 SYNP7	O9ALM7 synp7
303	31	100.0	108	2	O4WMD4 ASPFU	O4WMD4 aspergillus	376	31	100.0	111	2	O5EUB4 9ENTR	O5EUB4 buchneria ap
304	31	100.0	108	2	O5JRY2 HDWAN	O5JRY2 homo sapien	377	31	100.0	111	2	O5N064 SYNP6	O5N064 synchococ
305	31	100.0	108	2	O5T933 HDWAN	O5T933 homo sapien	378	31	100.0	111	2	O6NUC1 XENIA	O6NUC1 xenopus lae
306	31	100.0	108	2	O9S5J2 DROME	O9S5J2 drosophila	379	31	100.0	112	1	THIO_MYCSM	THIO mycsm
307	31	100.0	108	2	O41OD7 9BIVA	O41OD7 chlamys far	380	31	100.0	112	1	TRXH_CHIRE	TRXH chire
308	31	100.0	108	2	O5TY47 ANOGA	O5TY47 anopheles g	381	31	100.0	112	2	O9U2Z9 CAEBL	O9U2Z9 caenorhabd
309	31	100.0	108	2	O6VH15 1POBA	O6VH15 ipomoea bat	382	31	100.0	112	2	O8IEV4 TRIVA	O8IEV4 trichomonas
310	31	100.0	108	2	O6IVR6 9GAMM	O6IVR6 uncultured	383	31	100.0	112	2	O6IVS9 TRIVA	O6IVS9 trichomonas
311	31	100.0	108	2	O7BEF7 PRB01	O7BEF7 gamma-prote	384	31	100.0	112	2	O6IVS8 TRIVA	O6IVS8 trichomonas
312	31	100.0	108	2	O4NK10 9MICC	O4NK10 arthrobacte	385	31	100.0	112	2	O5YBBI 9CLOI	O5YBBI helicospori
313	31	100.0	108	2	O4IH05 9BURK	O4IH05 burkholderi	386	31	100.0	112	2	O7MGP8 VIBVY	O7MGP8 vibrio vuln
314	31	100.0	108	2	O4O108 AZOVI	O4O108 azotobacter	387	31	100.0	112	2	O6ILL6 PHOPR	O6ILL6 photobacter
315	31	100.0	108	2	O6Q926 9GAMM	O6Q926 uncultured	388	31	100.0	112	2	O67LQ7 STRTH	O67LQ7 streptobacte
316	31	100.0	108	2	O5EBU4 9VIBF1	O5EBU4 vibrio fisc	389	31	100.0	113	2	O8MI20 SHEEP	O8MI20 ovis aries
317	31	100.0	108	2	O4FQ72 9GAMM	O4FQ72 psychrobact	390	31	100.0	113	2	O6B8P1 GRATL	O6B8P1 graciilaria
318	31	100.0	108	2	O7MYL3 PHOHL	O7MYL3 photorhabd	391	31	100.0	113	2	O8GUR9 PPA	O8GUR9 pium sativ
319	31	100.0	108	2	O8ZAD9 YERPE	O8ZAD9 yerinia pe	392	31	100.0	113	2	O4UPY4 XANCP	O4UPY4 xanthomonas
320	31	100.0	108	2	O6G618 YERPE	O6G618 yerinia ps	393	31	100.0	113	2	O5GUR7 XANOR	O5GUR7 xanthomonas
321	31	100.0	108	2	O6CZ80 ERMCT	O6CZ80 erwinia car	394	31	100.0	113	2	O6OB26 METCA	O6OB26 methylococ
322	31	100.0	108	2	O5FT93 GLOOX	O5FT93 gluconobact	395	31	100.0	113	2	O8PFZ2 XANAC	O8PFZ2 xanthomonas
323	31	100.0	108	2	O9KV51_VIBCH	O9KV51 vibrio choi	396	31	100.0	113	2	O8P4D3_XANCP	O8P4D3 xanthomonas

397	31	100.0	113	2	0879Y5_XYLEFT	0879Y5 xylella fas	470	31	100.0	124	2	06M1N0_CORGL	06m1n0 corynebacte
398	31	100.0	114	1	TH1O2_DROME	09v429 drosophila	471	31	100.0	124	2	08N1S8_CORGL	08n1s8 corynebacte
399	31	100.0	114	1	TRX12_ARATH	P29414 arthropoda	472	31	100.0	124	2	09KFM2_BACDH	09kfm2 bacillus ha
400	31	100.0	114	1	Y989_METUA	058396 methanococc	473	31	100.0	124	2	05YVL7_NOCFA	05yvl7 nocardia fa
401	31	100.0	114	2	06M0G2_METMP	06m0g2 methanococc	474	31	100.0	125	1	TRXH_PICMA	065049 picea maria
402	31	100.0	114	2	051FJ8_ENTHI	051fj8 entamoeba h	475	31	100.0	125	2	05FYH5_PINTA	05fyh5 pinus taeda
403	31	100.0	114	2	07YZF7_CABEL	07yze7 caenorhabdi	476	31	100.0	125	2	05FYH8_PINTA	05fyh8 pinus taeda
404	31	100.0	114	2	09RY12_DEIRA	09ry12 drosococcus	477	31	100.0	125	2	05FYI9_PINTA	05fyi9 pinus taeda
405	31	100.0	114	2	067SM1_SYMTH	067sm1 symbiodacte	478	31	100.0	125	2	05FYJ1_PINTA	05fyj1 pinus taeda
406	31	100.0	115	2	TH1O1_CABEL	009433 caenorhabdi	479	31	100.0	125	2	05FYJ5_PINTA	05fyj5 pinus taeda
407	31	100.0	115	1	TH1O_MYCBO	P0a617 mycobacteri	480	31	100.0	125	2	05FYU8_PINTA	05fyj8 pinus taeda
408	31	100.0	115	1	TH1O_MYCTU	P0a616 mycobacteri	481	31	100.0	125	2	05FYK2_PINTA	05fyk2 pinus taeda
409	31	100.0	115	2	0751D5_ASHGO	P0a615 ashyba goss	482	31	100.0	125	2	05L1V9_ORYSA	05l1v9 oryza sativ
410	31	100.0	115	2	05P8S9_ANAMM	05p8s9 anaplaasma m	483	31	100.0	125	2	09LXD4_WHEAT	09lxd4 triticum ae
411	31	100.0	115	2	05MZN0_SYMP6	05mzn0 synecchococ	484	31	100.0	125	2	04SLD3_TETNG	04slld3 tetradon n
412	31	100.0	116	1	TRXH_FAGES	096419 fagopyrum e	485	31	100.0	126	1	TRXH1_TOBAC	096419 nicotiana t
413	31	100.0	116	2	ULB1_HCMVA	P16625 human cytom	486	31	100.0	126	1	TRXH_WHEAT	087GH7_PODAN
414	31	100.0	116	2	04WB53_ASPFU	04wb53 aspergillus	487	31	100.0	126	2	08TGH7_PODAN	08tgh7 podospora a
415	31	100.0	116	2	06U838_PARB	06u838 paracoccidi	488	31	100.0	126	2	0685T8_9SCOR	0685t8 mesobuthus
416	31	100.0	116	2	04ZZP9_PSESY	04zzp9 pseudomonas	489	31	100.0	126	2	0685V0_9SCOR	0685v0 mesobuthus
417	31	100.0	117	1	TH1O_BORBU	051088 borrelia bu	490	31	100.0	126	2	0685V4_9SCOR	0685v4 mesobuthus
418	31	100.0	117	2	0740Z6_MYCPA	0740z6 mycobacteri	491	31	100.0	126	2	0685X1_9SCOR	0685x1 mesobuthus
419	31	100.0	117	2	0662V3_BORGA	0662v3 borrelia ga	492	31	100.0	126	2	0685X8_9SCOR	0685x8 mesobuthus
420	31	100.0	117	2	093AQ3_MYCPA	093aq3 mycobacteri	493	31	100.0	126	2	0685Y5_9SCOR	0685y5 mesobuthus
421	31	100.0	118	1	LSHB_BALAC	P33088 balaenopter	494	31	100.0	126	2	0685Y8_9SCOR	0685y8 mesobuthus
422	31	100.0	118	1	LSHB_PHYCA	P25330 physelet ca	495	31	100.0	126	2	0685Y9_9SCOR	0685y9 buthus eup
423	31	100.0	118	1	TRXH2_TOBAC	007090 nicotiana t	496	31	100.0	126	2	0685X9_9SCOR	0685x9 mesobuthus
424	31	100.0	118	1	TRXH_RICCO	043636 ricinus com	497	31	100.0	126	2	0685W5_9SCOR	0685w5 mesobuthus
425	31	100.0	118	2	064BN2_9ARCH	064bn2 unclutured	498	31	100.0	126	2	067412_9ORTO	067412 influenza c
426	31	100.0	118	2	08WT16_DROME	08wt16 drosophila	499	31	100.0	126	2	067413_INCNB	067413 influenza c
427	31	100.0	118	2	093X24_PEA	093x24 pisum sativ	500	31	100.0	126	2	067414_9ORTO	067414 influenza c
428	31	100.0	118	2	08GVD3_WHEAT	08gvd3 triticum ae	501	31	100.0	127	1	KRCL_CHICK	P25692 gallus gall
429	31	100.0	118	2	07XKX3_HORVD	07xkx3 hordeum vul	502	31	100.0	127	1	TH1O_NEUCR	P42115 neosporea
430	31	100.0	118	2	05XA57_STRP6	05xa57 streptococc	503	31	100.0	127	1	TRX3_YEAST	P25372 saccharomyc
431	31	100.0	119	1	TH1O2_CABEL	017424 caenorhabdi	504	31	100.0	127	1	TXND8_HUMAN	06a555 homo sapien
432	31	100.0	119	2	05V6K7_HALMA	05v6k7 halocactula	505	31	100.0	127	1	TXND8_MOUSE	069bd2 mus musculu
433	31	100.0	119	2	046709_HALSA	046709 halobacteri	506	31	100.0	127	1	TXND8_RAT	069bd1 rattus norv
434	31	100.0	119	2	07M3C7_RABIT	07m3c7 oryctolagus	507	31	100.0	127	2	08MMQ4_PIG	08mmq4 sus scrofa
435	31	100.0	119	2	09SP36_SECCO	09sp36 secale cere	508	31	100.0	127	2	06NEDJ_CORDI	06nedj corynebacte
436	31	100.0	119	2	05ZF48_PLAMJ	05zf48 plantago ma	509	31	100.0	127	2	07W131_BORBA	07w131 borstetella
437	31	100.0	119	2	08F4W0_LEPIN	08f4w0 leptospira	510	31	100.0	127	2	07W665_BORBA	07w665 borstetella
438	31	100.0	120	2	05JRY3_HUMAN	05jry3 homo sapien	511	31	100.0	127	2	07VXN6_BORPE	07vxn6 borstetella
439	31	100.0	120	2	04R1O4_CABEL	04r1o4 caenorhabdi	512	31	100.0	128	1	LSHB_PHOSU	09q7a9 phodopus eu
440	31	100.0	120	2	09AR82_PEA	09ar82 pisum sativ	513	31	100.0	128	1	08SP15_HORSE	08sp15 equus cabal
441	31	100.0	120	2	04NLS3_9MICC	04nls3 arthropacte	514	31	100.0	129	1	DYLA_CHIRE	039591 chlamydomon
442	31	100.0	120	2	06SKX3_ARTNU	06skx3 arthropacte	515	31	100.0	129	2	09XIF4_ARATH	09xif4 arabidopsis
443	31	100.0	121	1	Y008_METKA	P94948 methanopyru	516	31	100.0	129	2	0825V1_STRPW	0825v1 streptomyc
444	31	100.0	121	2	0945O4_SCHPO	0945o4 schizosacch	517	31	100.0	130	2	064395_TRTTU	064395 triticum tu
445	31	100.0	121	2	08IKL4_PLAF7	08ikl4 plasmodium	518	31	100.0	130	2	08GUR8_PEA	08gur8 pisum sativ
446	31	100.0	121	2	07R8F6_PLAYO	07r8f6 plasmodium	519	31	100.0	131	2	07FR21_WHEAT	07fr21 triticum ae
447	31	100.0	121	2	06ICG9_CABER	06icg9 caenorhabdi	520	31	100.0	131	2	08MJB6_CARCA	08mjb6 capreolus c
448	31	100.0	121	2	04YYYS_PLABE	04yyys plasmodium	521	31	100.0	131	2	09SMG4_LOLPR	09smg4 lolium pere
449	31	100.0	121	2	09FR13_ORYSA	09fr13 oryza sativ	522	31	100.0	131	2	09SMG4_SECCO	09smg5 secale cere
450	31	100.0	121	2	06L4X5_ORYSA	06l4x5 oryza sativ	523	31	100.0	131	2	09SMG6_HORBU	09smg6 hordeum bul
451	31	100.0	121	2	06AAH7_PROAC	06aah7 propionibac	524	31	100.0	131	2	08HEX0_WHEAT	08hex0 triticum ae
452	31	100.0	121	2	04TDS8_TETNG	04tds8 tetradon n	525	31	100.0	131	2	08GZK4_HORVD	08gzk4 hordeum vul
453	31	100.0	122	1	TRXH_ORYSA	042443 oryza sativ	526	31	100.0	131	2	084X91_9POLA	084x91 leymus chin
454	31	100.0	122	2	07EXZ7_ORYSA	07exz7 oryza sativ	527	31	100.0	131	2	09AS75_ORYSA	09as75 oryza sativ
455	31	100.0	122	2	07XZX2_HORVD	07xzx2 hordeum vul	528	31	100.0	131	2	09S753_9POLA	09s753 phalaris co
456	31	100.0	122	2	04W1F6_MAIZE	04w1f6 zeae mays (m	529	31	100.0	131	2	04NT79_9DELT	04nt79 anaeromyxob
457	31	100.0	123	2	09N1S1_CAPCA	09n1s1 capreolus c	530	31	100.0	132	2	08HEX4_ORYSA	08hex4 oryza sativ
458	31	100.0	123	2	07XJ63_ARATH	07xj63 arabidopsis	531	31	100.0	133	1	TRXH2_ARATH	038849 arabidopsis
459	31	100.0	123	2	06VH14_IPOBA	06vh14 ipomoea bat	532	31	100.0	133	2	08HEX5_MAIZE	08hex5 zeae mays (m
460	31	100.0	123	2	05JMR9_ORYSA	05jmr9 oryza sativ	533	31	100.0	133	2	08GZT3_BRACM	08gzt3 brassica ca
461	31	100.0	123	2	04JSG8_CORUK	04jsg8 corynebacte	534	31	100.0	133	2	07D2B9_AGRYS	07d2b9 agrobacteri
462	31	100.0	123	2	07U0U5_MYCBO	07u0u5 mycobacteri	535	31	100.0	134	2	08L9A6_ARATH	08l9a6 arabidopsis
463	31	100.0	123	2	07DBE1_MYCTU	07dbe1 mycobacteri	536	31	100.0	134	2	08S1R5_ORYSA	08s1r5 oryza sativ
464	31	100.0	123	2	08G4Z3_BIFPO	08g4z3 bifidobacte	537	31	100.0	134	2	09RD25_STRCO	09rd25 streptomyce
465	31	100.0	124	2	04V6C1_DROME	04v6c1 drosophila	538	31	100.0	135	2	070YJ4_HORVN	070yj4 hordeum vul
466	31	100.0	124	2	08SP29_PIG	08sp29 sus scrofa	539	31	100.0	135	2	06PY94_SOYBN	06py94 glycine max
467	31	100.0	124	2	09GKU0_CALUA	09gku0 callithrix	540	31	100.0	135	2	057HT5_SALCH	057ht5 salmonella
468	31	100.0	124	2	038456_BPPI1	038456 bacterioph	541	31	100.0	135	2	04LGT1_9BUNK	04lgt1 burkholderi
469	31	100.0	124	2	06RJ27_CAPAN	06rj27 capsicum an	542	31	100.0	135	2	09DEQ1_MOUSE	09deg1 mus musculu

543	31	100.0	135	2	Q9D6R7	MOUSE	Q9D6R7	mus musculus	616	31	100.0	142	2	Q9BD19	PANTHA	Q9BD19	panthera t
544	31	100.0	135	2	Q9D7C0	MOUSE	Q9D7C0	mus musculus	617	31	100.0	142	2	Q5ZF46	PLAMU	Q5ZF46	plantaago m
545	31	100.0	136	2	Q5UW65	HALMA	Q5UW65	haloarcula	618	31	100.0	142	2	Q4W5X2	BACCE	Q4W5X2	baclillus ce
546	31	100.0	136	2	Q8WK10	HUMAN	Q8WK10	homo sapien	619	31	100.0	142	2	Q81FMO	BACCR	Q81FMO	baclillus ce
547	31	100.0	136	2	Q8WN99	PETRY	Q8WN99	pteropus ly	620	31	100.0	142	2	Q9RYV9	DEIRA	Q9RYV9	delinococcus
548	31	100.0	136	2	Q8WNA0	CYNVA	Q8WNA0	cynoccephalu	621	31	100.0	142	2	Q5QZV7	IDIL0	Q5QZV7	idolomarina
549	31	100.0	136	2	Q8WNA1	LORTA	Q8WNA1	loris tardi	622	31	100.0	142	2	Q8R3V1	MOUSE	Q8R3V1	mus musculus
550	31	100.0	136	2	Q8WNA2	GALSE	Q8WNA2	galago sene	623	31	100.0	143	1	LSHB	FELCA	LSHB	felis silve
551	31	100.0	136	2	Q8WNA5	TARBA	Q8WNA5	tarsius ban	624	31	100.0	143	2	Q6VB16	IPOBA	Q6VB16	ipomoea bat
552	31	100.0	136	2	Q8WNB5	TARBA	Q8WNB5	colobus gue	625	31	100.0	143	2	Q8S3L2	PROST	Q8S3L2	populus tre
553	31	100.0	136	2	Q8WNB6	PREOB	Q8WNB6	presbytis o	626	31	100.0	144	2	Q51010	ENTHI	Q51010	entamoeba h
554	31	100.0	136	2	Q8WNB7	MACMU	Q8WNB7	macaca mula	627	31	100.0	144	2	Q41UJ1	AZCVI	Q41UJ1	azotobacter
555	31	100.0	136	2	Q9JWZ3	PRUPE	Q9JWZ3	prunus pers	628	31	100.0	144	2	Q4KJF7	PSEF5	Q4KJF7	pseudomonas
556	31	100.0	136	2	Q4SEK3	TETNG	Q4SEK3	tetrarodon n	629	31	100.0	144	2	Q7UFC1	PHROA	Q7UFC1	rhodopirell
557	31	100.0	137	2	Q4PLX7	TXOSC	Q4PLX7	ixodes scap	630	31	100.0	144	2	Q8BFW1	PSEBK	Q8BFW1	pseudomonas
558	31	100.0	137	2	Q4NF78	9M1CC	Q4NF78	arthrobacte	631	31	100.0	145	1	THIO3	CORRE	THIO3	cornebace
559	31	100.0	137	2	Q5UR29	MIMIV	Q5UR29	mimivirus	632	31	100.0	145	2	Q61JZ7	CABER	Q61JZ7	caenorhabdi
560	31	100.0	138	1	LSHB	CANFA	LSHB	canis fam1	633	31	100.0	145	2	Q7XV06	ORYSA	Q7XV06	oryza sativ
561	31	100.0	138	2	Q64MX0	ORYSA	Q64MX0	oryza sativ	634	31	100.0	145	2	Q84XR9	CHLRE	Q84XR9	chlamydomon
562	31	100.0	138	2	Q624I3	ORYSA	Q624I3	oryza sativ	635	31	100.0	145	2	Q6NCU6	RHOPA	Q6NCU6	rhodopseudo
563	31	100.0	138	2	Q7ZWM1	CHICK	Q7ZWM1	gallus gall	636	31	100.0	145	2	Q8ZBM4	YERPS	Q8ZBM4	yersinia pe
564	31	100.0	139	1	THIO2	ECOLI	THIO2	escherichia	637	31	100.0	145	2	Q6SE40	YERPS	Q6SE40	yersinia pe
565	31	100.0	139	2	Q6CKI8	KLUDA	Q6CKI8	kluyveromyc	638	31	100.0	145	2	Q7NQ61	CHRYO	Q7NQ61	chryso
566	31	100.0	139	2	Q6ENV3	HUMAN	Q6ENV3	homo sapien	639	31	100.0	145	2	Q5P2H5	AZOSE	Q5P2H5	azarcus sp
567	31	100.0	139	2	Q5TSB2	ANOGA	Q5TSB2	anopheles g	640	31	100.0	146	2	Q5N844	ORYSA	Q5N844	oryza sativ
568	31	100.0	139	2	Q9VUG9	DROME	Q9VUG9	drosohilla	641	31	100.0	146	2	Q82EK3	STRAM	Q82EK3	streptomyce
569	31	100.0	139	2	Q7YRL0	PIC	Q7YRL0	sus scrofa	642	31	100.0	146	2	Q8Q2D6	MELUD	Q8Q2D6	melopsittac
570	31	100.0	139	2	Q57I52	SALCH	Q57I52	salmonella	643	31	100.0	147	2	Q5BHK3	SCMA	Q5BHK3	schistosoma
571	31	100.0	139	2	Q5LBI1	BACFN	Q5LBI1	bacterioides	644	31	100.0	147	2	Q89164	BRJJA	Q89164	bradyrhizob
572	31	100.0	139	2	Q73AT5	BACCI	Q73AT5	baclillus ce	645	31	100.0	148	2	Q5MIS6	AEDAL	Q5MIS6	aedes albop
573	31	100.0	139	2	Q8Z4J6	SALTI	Q8Z4J6	salmonella	646	31	100.0	148	2	Q9CASI	ARATH	Q9CASI	arabidopsis
574	31	100.0	139	2	Q8ZMX4	SALTY	Q8ZMX4	salmonella	647	31	100.0	148	2	Q4US63	XANCP	Q4US63	xanthomonas
575	31	100.0	139	2	Q5PUD7	SALPA	Q5PUD7	salmonella	648	31	100.0	148	2	Q5Z2A0	NOCFA	Q5Z2A0	nocardia fa
576	31	100.0	139	2	Q6DID1	ERNCT	Q6DID1	erwinia car	649	31	100.0	148	2	Q8PMZ8	XANCP	Q8PMZ8	xanthomonas
577	31	100.0	139	2	Q67747	AQUAE	Q67747	aquifex aeo	650	31	100.0	148	2	Q8PB82	XANCP	Q8PB82	xanthomonas
578	31	100.0	139	2	Q7NZ16	CHRYO	Q7NZ16	chromobacte	651	31	100.0	149	2	Q5JTP9	HUMAN	Q5JTP9	homo sapien
579	31	100.0	139	2	Q743D8	MYCPA	Q743D8	mycobacteri	652	31	100.0	149	2	Q8N1G6	CORGL	Q8N1G6	corynebace
580	31	100.0	139	2	Q605Y8	METCA	Q605Y8	methylococc	653	31	100.0	149	2	Q988U5	RHIZO	Q988U5	rhizobium l
581	31	100.0	139	2	Q62778	RAT	Q62778	rattus norv	654	31	100.0	150	2	Q5DPA0	SCHJA	Q5DPA0	schistosoma
582	31	100.0	140	1	TRKM	CHIRE	TRKM	chlamydomon	655	31	100.0	150	2	Q84XS0	CHIRE	Q84XS0	chlamydomon
583	31	100.0	140	2	Q9C9Y6	ARATH	Q9C9Y6	arabidopsis	656	31	100.0	151	2	Q9SRD7	ARATH	Q9SRD7	arabidopsis
584	31	100.0	140	2	Q81SR5	BACAN	Q81SR5	baclillus an	657	31	100.0	151	2	Q826F1	STRAM	Q826F1	streptomyce
585	31	100.0	140	2	Q9C8C8	MYCLE	Q9C8C8	mycobacteri	658	31	100.0	152	2	Q6ER81	ORYSA	Q6ER81	oryza sativ
586	31	100.0	140	2	Q8BFI1	SHRON	Q8BFI1	shewanella	659	31	100.0	152	2	Q4UOW0	NICAL	Q4UOW0	nicotiana a
587	31	100.0	140	2	Q72IL5	THERT2	Q72IL5	thermus the	660	31	100.0	152	2	Q84XS2	CHIRE	Q84XS2	chlamydomon
588	31	100.0	140	2	Q5S193	THERT	Q5S193	thermus the	661	31	100.0	152	2	Q8H6X3	TOBAC	Q8H6X3	nicotiana t
589	31	100.0	140	2	Q5Z0Y6	CHICK	Q5Z0Y6	gallus gall	662	31	100.0	152	2	Q4SKX5	TETNG	Q4SKX5	tetrarodon n
590	31	100.0	141	1	LSHB	BOVIN	LSHB	bos taurus	663	31	100.0	153	2	Q7XY47	GRJJA	Q7XY47	griffithsia
591	31	100.0	141	1	LSHB	CERSI	LSHB	ceratoheri	664	31	100.0	153	2	Q9FYJ3	ARATH	Q9FYJ3	arabidopsis
592	31	100.0	141	1	LSHB	HUMAN	LSHB	homo sapien	665	31	100.0	153	2	Q4UNK3	RICFE	Q4UNK3	ricicetia
593	31	100.0	141	1	LSHB	MACFA	LSHB	macaca fasc	666	31	100.0	154	1	KRSC	CHICK	KRSC	chick
594	31	100.0	141	1	LSHB	MOUSE	LSHB	mus musculu	667	31	100.0	154	2	Q4K890	PSEF5	Q4K890	pseudomonas
595	31	100.0	141	1	LSHB	PYG	LSHB	sus scrofa	668	31	100.0	154	2	Q8BMC7	PSEBK	Q8BMC7	pseudomonas
596	31	100.0	141	1	LSHB	RAT	LSHB	rattus norv	669	31	100.0	154	2	Q8AB92	BACAN	Q8AB92	bacterioides
597	31	100.0	141	1	LSHB	SHEEP	LSHB	ovis aries	670	31	100.0	155	2	Q4ZQ39	PSEBY	Q4ZQ39	pseudomonas
598	31	100.0	141	2	Q4JBR7	SUIAC	Q4JBR7	sulfolobus	671	31	100.0	155	2	Q8BFE6	SHRON	Q8BFE6	shewanella
599	31	100.0	141	2	Q6FVN1	CANGA	Q6FVN1	candida gla	672	31	100.0	155	2	Q8B5Z3	PSESM	Q8B5Z3	pseudomonas
600	31	100.0	141	2	Q61Y74	RABIT	Q61Y74	oryctolagus	673	31	100.0	155	2	Q64R60	BACFR	Q64R60	bacterioides
601	31	100.0	141	2	Q8H2R9	AILFU	Q8H2R9	ailurus ful	674	31	100.0	156	1	DYLS	CHIRE	DYLS	chlamydomon
602	31	100.0	141	2	Q8WN18	AILME	Q8WN18	ailuropoda	675	31	100.0	156	2	Q622F8	CABER	Q622F8	caenorhabdi
603	31	100.0	141	2	Q4H6T8	9DEIO	Q4H6T8	delinococcus	676	31	100.0	156	2	Q5FBE9	9ORTO	Q5FBE9	influenza c
604	31	100.0	141	2	Q6H100	BACCH	Q6H100	baclillus th	677	31	100.0	156	2	Q8QZG1	9ORTO	Q8QZG1	influenza c
605	31	100.0	141	2	Q63DH7	BACCH	Q63DH7	baclillus ce	678	31	100.0	156	2	Q8QZL6	9ORTO	Q8QZL6	influenza c
606	31	100.0	141	2	Q5LW40	SILPO	Q5LW40	silicibacte	679	31	100.0	156	2	Q8QZL9	9ORTO	Q8QZL9	influenza c
607	31	100.0	141	2	Q9RVS8	DEIRA	Q9RVS8	delinococcus	680	31	100.0	156	2	Q8QZM1	9ORTO	Q8QZM1	influenza c
608	31	100.0	141	2	Q7MH77	BORBA	Q7MH77	bordelella	681	31	100.0	156	2	Q8QZM2	9ORTO	Q8QZM2	influenza c
609	31	100.0	141	2	Q7W990	BORBA	Q7W990	bordelella	682	31	100.0	156	2	Q8QZM3	9ORTO	Q8QZM3	influenza c
610	31	100.0	141	2	Q7VYP8	BORPE	Q7VYP8	bordelella	683	31	100.0	156	2	Q8QZM4	9ORTO	Q8QZM4	influenza c
611	31	100.0	141	2	Q6F7Y4	ACTAD	Q6F7Y4	acinetobact	684	31	100.0	156	2	Q8QZM5	9ORTO	Q8QZM5	influenza c
612	31	100.0	141	2	Q6UUC1	MERON	Q6UUC1	merionas un	685	31	100.0	156	2	Q8BCC2	9ORTO	Q8BCC2	influenza c
613	31	100.0	141	2	Q6V3B5	MESAU	Q6V3B5	mesocricetu	686	31	100.0	156	2	Q8BCC3	9ORTO	Q8BCC3	influenza c
614	31	100.0	141	2	Q6V3B6	MASCO	Q6V3B6	mascomys co	687	31	100.0	156	2	Q6BCC4	9ORTO	Q6BCC4	influenza c
615	31	100.0	142	2	Q61985	CAEBL	Q61985	caenorhabdi	688	31	100.0	156	2	Q6BCC4	9ORTO	Q6BCC4	influenza c

689	31	100.0	156	2	068CC5_9ORTO	068cc5_influenza c	762	31	100.0	158	2	Q7RU85_NEUCR	Q7ru85_neutropora
690	31	100.0	156	2	068CC6_9ORTO	068cc6_influenza c	763	31	100.0	158	2	Q94282_CABEL	Q94282_caenorhabdi
691	31	100.0	156	2	068CC7_9ORTO	068cc7_influenza c	764	31	100.0	159	2	Q93V09_ARATH	Q93v09_arabidopsi
692	31	100.0	156	2	068CC8_9ORTO	068cc8_influenza c	765	31	100.0	160	2	Q64CW9_GARCH	Q64cw9_uncultured
693	31	100.0	156	2	068CC9_9ORTO	068cc9_influenza c	766	31	100.0	160	2	Q8PUY7_METMA	Q8puv7_methanosarc
694	31	100.0	156	2	068CD0_9ORTO	068cd0_influenza c	767	31	100.0	160	2	Q4P051_USTMA	Q4p051_ustiliago ma
695	31	100.0	156	2	068CD1_9ORTO	068cd1_influenza c	768	31	100.0	160	2	Q854C9_9CAUD	Q854c9_mycoabacteri
696	31	100.0	156	2	068CD2_9ORTO	068cd2_influenza c	769	31	100.0	160	2	Q7XDQ6_ORYSA	Q7xdq6_oryza sativ
697	31	100.0	156	2	068CD3_9ORTO	068cd3_influenza c	770	31	100.0	160	2	P95355_NEIGO	P95355_neisseria g
698	31	100.0	156	2	068CD4_9ORTO	068cd4_influenza c	771	31	100.0	160	2	Q5F5K1_NEIG1	Q5f5k1_neisseria g
699	31	100.0	156	2	068CD5_9ORTO	068cd5_influenza c	772	31	100.0	160	2	Q604X8_MERCA	Q604x8_methylcoccc
700	31	100.0	156	2	068CD6_9ORTO	068cd6_influenza c	773	31	100.0	160	2	Q9UWT2_NEIMA	Q9uwt2_neisseria m
701	31	100.0	156	2	068CD7_9ORTO	068cd7_influenza c	774	31	100.0	160	2	Q9K1R4_NEIMB	Q9k1r4_neisseria m
702	31	100.0	156	2	068CD8_9ORTO	068cd8_influenza c	775	31	100.0	160	2	Q63QP3_BURPS	Q63qp3_burkholderi
703	31	100.0	156	2	068CD9_9ORTO	068cd9_influenza c	776	31	100.0	161	2	Q8T1A1_METAC	Q8t1a1_methanosarc
704	31	100.0	156	2	068CE0_9ORTO	068ce0_influenza c	777	31	100.0	161	2	Q8TG10_PODAN	Q8tg10_podospora a
705	31	100.0	156	2	068CE1_9ORTO	068ce1_influenza c	778	31	100.0	161	2	Q856T3_9CAUD	Q856t3_mycoabacteri
706	31	100.0	156	2	068CE2_9ORTO	068ce2_influenza c	779	31	100.0	161	2	Q51LBX8_BACFN	Q51lbx8_bacterioides
707	31	100.0	156	2	068CE3_9ORTO	068ce3_influenza c	780	31	100.0	161	2	Q64SV7_BACFR	Q64sv7_bacterioides
708	31	100.0	156	2	068CE4_9ORTO	068ce4_influenza c	781	31	100.0	163	2	Q6ZSV7_HUMAN	Q6zsv7_homo sapien
709	31	100.0	156	2	068CE5_9ORTO	068ce5_influenza c	782	31	100.0	163	2	Q59J06_9BACT	Q59j06_uncultured
710	31	100.0	156	2	068CE6_9ORTO	068ce6_influenza c	783	31	100.0	163	2	Q8D6F4_VIBVU	Q8d6f4_vibrio vuln
711	31	100.0	156	2	068CE6_9ORTO	068ce6_influenza c	784	31	100.0	163	2	Q7MDA8_VIBVY	Q7mda8_vibrio vuln
712	31	100.0	156	2	Q91Q61_9ORTO	Q91q61_influenza c	785	31	100.0	164	2	VEGPA_CAVPO	V26617 cavia porce
713	31	100.0	156	2	Q9Q221_9ORTO	Q9q221_influenza c	786	31	100.0	164	2	Q7PSP7_ANOGA	Q7psp7_anopheles g
714	31	100.0	156	2	Q9Q224_9ORTO	Q9q224_influenza c	787	31	100.0	165	2	Q8PY73_METMA	Q8py73_methanosarc
715	31	100.0	156	2	Q9Q227_9ORTO	Q9q227_influenza c	788	31	100.0	165	1	THIOM_BOVIN	Q95108 bos taurus
716	31	100.0	156	2	Q9Q232_9ORTO	Q9q232_influenza c	789	31	100.0	166	1	THIOM_HUMAN	Q97957 homo sapien
717	31	100.0	156	2	Q9Q235_9ORTO	Q9q235_influenza c	790	31	100.0	166	1	THIOM_MOUSE	Q97493 mus musculu
718	31	100.0	156	2	Q9Q238_INCNB	Q9q238_influenza c	791	31	100.0	166	1	THIOM_RAT	P97615 rattus norv
719	31	100.0	156	2	Q9Q241_9ORTO	Q9q241_influenza c	792	31	100.0	166	2	Q6FH60_HUMAN	Q6fh60_homo sapien
720	31	100.0	156	2	Q9Q244_9ORTO	Q9q244_influenza c	793	31	100.0	166	2	Q5K553_9BACT	Q5k553_uncultured
721	31	100.0	156	2	Q9Q247_9ORTO	Q9q247_influenza c	794	31	100.0	166	2	Q6N4H2_RHOPA	Q6n4h2_rhodopseu
722	31	100.0	156	2	Q9Q250_9ORTO	Q9q250_influenza c	795	31	100.0	166	2	Q545D5_MOUSE	Q545d5_mus musculu
723	31	100.0	156	2	Q9Q253_9ORTO	Q9q253_influenza c	796	31	100.0	166	2	Q6P131_BRARB	Q6p131_brachydanio
724	31	100.0	156	2	Q8B040_9ORTO	Q8b040_influenza c	797	31	100.0	167	1	TRKM_MAIIZE	Q41664 zea mays (m
725	31	100.0	156	2	Q8B041_9ORTO	Q8b041_influenza c	798	31	100.0	167	2	Q6H5W8_ORYSA	Q6h5w8_oryza sativ
726	31	100.0	156	2	Q8B042_9ORTO	Q8b042_influenza c	799	31	100.0	167	2	Q8L7S9_ARATH	Q8l7s9_arabidopsi
727	31	100.0	156	2	Q8B043_9ORTO	Q8b043_influenza c	800	31	100.0	167	2	Q5UR27_MIMIV	Q5ur27_mimivirus.
728	31	100.0	156	2	Q8B044_9ORTO	Q8b044_influenza c	801	31	100.0	169	1	LSHB_EGUS	P19794 equus asinu
729	31	100.0	156	2	Q8B045_9ORTO	Q8b045_influenza c	802	31	100.0	169	1	LSHB_EGUBU	Q46641 equus burch
730	31	100.0	156	2	Q8B046_9ORTO	Q8b046_influenza c	803	31	100.0	169	1	LSHB_HORSE	P08751 equus caball
731	31	100.0	156	2	Q8B047_9ORTO	Q8b047_influenza c	804	31	100.0	169	2	Q6P6C5_RHITR	Q6p6c5_thizobium t
732	31	100.0	156	2	Q8B048_9ORTO	Q8b048_influenza c	805	31	100.0	169	2	Q7MXC8_PORGI	Q7mxc8_porphyromon
733	31	100.0	156	2	Q8B049_9ORTO	Q8b049_influenza c	806	31	100.0	169	2	Q6MLM7_BDESA	Q6mlm7_bdellovibri
734	31	100.0	156	2	Q8B050_9ORTO	Q8b050_influenza c	807	31	100.0	170	2	Q8KDH8_CHLRE	Q8kdh8_chlorobium
735	31	100.0	156	2	Q8B051_9ORTO	Q8b051_influenza c	808	31	100.0	170	2	Q7ZYG6_XENIA	Q7zyg6_xenopus lae
736	31	100.0	156	2	Q8B052_9ORTO	Q8b052_influenza c	809	31	100.0	170	2	Q641J6_XENTR	Q641j6_xenopus tto
737	31	100.0	156	2	Q8B053_9ORTO	Q8b053_influenza c	810	31	100.0	172	1	TRXM_ORYSA	Q92920_oryza sativ
738	31	100.0	156	2	Q8B054_9ORTO	Q8b054_influenza c	811	31	100.0	172	1	Q6NPF9_ARATH	P48384 pisum sativ
739	31	100.0	156	2	Q8B055_9ORTO	Q8b055_influenza c	812	31	100.0	172	2	Q50039_MYCLE	Q50039_mycoabacteri
740	31	100.0	156	2	Q8B056_9ORTO	Q8b056_influenza c	813	31	100.0	172	1	TRXM3_ARATH	Q99697 arabidopsi
741	31	100.0	156	2	Q8B057_9ORTO	Q8b057_influenza c	814	31	100.0	173	2	Q9VM81_DROME	Q9vm81_drosophila
742	31	100.0	156	2	Q8B058_9ORTO	Q8b058_influenza c	815	31	100.0	173	2	Q84XR8_CHLRE	Q84xr8_chlamydomon
743	31	100.0	156	2	Q8B059_9ORTO	Q8b059_influenza c	816	31	100.0	173	2	Q6H7E4_ORYSA	Q6h7e4_oryza sativ
744	31	100.0	156	2	Q8B060_9ORTO	Q8b060_influenza c	817	31	100.0	173	2	Q681Y9_ARATH	Q681y9_arabidopsi
745	31	100.0	156	2	Q8B061_9ORTO	Q8b061_influenza c	818	31	100.0	173	2	Q67ZHT7_ARATH	Q67zht7_arabidopsi
746	31	100.0	156	2	Q8B062_9ORTO	Q8b062_influenza c	819	31	100.0	173	2	Q67XN4_ARATH	Q67xn4_arabidopsi
747	31	100.0	156	2	Q8B063_9ORTO	Q8b063_influenza c	820	31	100.0	173	2	Q4NX02_9DELT	Q4nx02_aeaeromyxob
748	31	100.0	156	2	Q8B064_9ORTO	Q8b064_influenza c	821	31	100.0	174	2	Q8NDY2_HUMAN	Q8ndy2_homo sapien
749	31	100.0	156	2	Q8B065_9ORTO	Q8b065_influenza c	822	31	100.0	174	2	Q4V449_HUMAN	Q4v449_homo sapien
750	31	100.0	156	2	Q8B066_9ORTO	Q8b066_influenza c	823	31	100.0	174	2	Q623W5_CAEBR	Q623w5_caenorhabdi
751	31	100.0	156	2	Q8B067_9ORTO	Q8b067_influenza c	824	31	100.0	174	2	Q8XVP6_RALISO	Q8xvp6_ralstonia s
752	31	100.0	156	2	Q8B068_9ORTO	Q8b068_influenza c	825	31	100.0	175	1	TRXM_WHEAT	Q92p21_triticum ae
753	31	100.0	156	2	Q4U6Y3_9ORTO	Q4u6y3_influenza c	826	31	100.0	175	1	Q9AV49_CUCME	Q9av49_cucumis mel
754	31	100.0	156	2	Q4U6Y4_9ORTO	Q4u6y4_influenza c	827	31	100.0	175	2	Q91KWO_LYCPS	Q91kwo_lycopersico
755	31	100.0	156	2	Q4U6Y5_9ORTO	Q4u6y5_influenza c	828	31	100.0	175	2	Q91V12_ARATH	Q91v12_arabidopsi
756	31	100.0	156	2	Q4U6Y6_9ORTO	Q4u6y6_influenza c	829	31	100.0	175	2	Q5ND46_TRITRU	Q5nd46_triticum tu
757	31	100.0	157	1	THIOR_DROME	Thior_drosophila	830	31	100.0	175	2	Q7P629_FUSNV	Q7p629_fusobacteri
758	31	100.0	157	1	VHCB_METVO	Vhcb_methanococc	831	31	100.0	177	1	TRXM_BRANA	Q9xg60_braesica na
759	31	100.0	157	2	Q8A7R8_BACTIN	Q8a7r8_bacterioides	832	31	100.0	177	2	Q6EPES_9RHIZ	Q6epes_mesorhizobi
760	31	100.0	157	2	VG09_ICHVI	VG09_ictaluriid h	833	31	100.0	177	2	Q7WS25_BRECH	Q7ws25_brevibacill
761	31	100.0	158	1			834	31	100.0				

835	31	100.0	178	1	TRXF1_ARATH	09xfth8	arabidopsis	908	31	100.0	192	2	066PE4_9RHIZ	066PE4	rhizobium s
836	31	100.0	178	2	083WD6_MICGR	083WD6	microcosm	909	31	100.0	192	2	04HB83_9DELTA	04HB83	delinococcus
837	31	100.0	179	1	TRXW1_ARATH	083737	arabidopsis	910	31	100.0	193	1	TRXW4_ARATH	09seu6	delinococcus
838	31	100.0	179	2	09AD7_CAUCR	09AD7	caulobacter	911	31	100.0	194	2	064764_ARATH	064764	arabidopsis
839	31	100.0	180	2	07XRD0_ORYSA	07XRD0	oryza sativ	912	31	100.0	194	2	066PC8_RHILE	066PC8	rhizobium l
840	31	100.0	180	2	095AH9_PEA	095AH9	pisum sativ	913	31	100.0	195	2	05YJ05_9ASPA	05YJ05	hyacinthus
841	31	100.0	180	2	07XBR5_ORYSA	07XBR5	oryza sativ	914	31	100.0	196	2	04NY01_9DELTA	04NY01	anaeromyxob
842	31	100.0	180	2	066PD0_RHILE	066PD0	rhizobium l	915	31	100.0	197	2	06ZN00_HUMAN	06ZN00	anaeromyxob
843	31	100.0	180	2	066PE8_RHIME	066PE8	rhizobium m	916	31	100.0	197	2	06M318_BDERA	06M318	bdellovibri
844	31	100.0	181	1	TRXM_SPTOL	07551	spinacia ol	917	31	100.0	197	2	073SQ1_MYCPA	073SQ1	mycobacteri
845	31	100.0	181	1	06QAT5_DROWA	06QAT5	drosofila	918	31	100.0	198	2	072H15_THRET2	072H15	thermus the
846	31	100.0	181	2	06QAT6_DROSI	06QAT6	drosofila	919	31	100.0	198	2	083368_9GARM	083368	murine leuk
847	31	100.0	181	2	06QAT7_DROSI	06QAT7	drosofila	920	31	100.0	199	2	06C4U8_YARLI	06C4U8	yarowia li
848	31	100.0	181	2	06JES7_NICBE	06JES7	nicotiana b	921	31	100.0	201	1	SYA_RHILV	SYA	rhiliv
849	31	100.0	181	2	06JES8_NICBE	06JES8	nicotiana b	922	31	100.0	202	2	09NFW2_HUMAN	09NFW2	homo sapien
850	31	100.0	181	2	04SS63_TETNG	04SS63	tetracodon n	923	31	100.0	202	2	04USY3_CORKJ	04USY3	corynebacte
851	31	100.0	182	1	TRXF_BRANA	048897	braessica na	924	31	100.0	202	2	073K50_TRADE	073K50	treponema d
852	31	100.0	182	1	TRXF_PEA	029450	pisum sativ	925	31	100.0	203	2	06AQD6_DESPS	06AQD6	desulfotale
853	31	100.0	182	1	TRXX_ARATH	081449	arabidopsis	926	31	100.0	204	2	086XZ5_HUMAN	086XZ5	homo sapien
854	31	100.0	182	2	0724P9_HUMAN	0724P9	homo sapien	927	31	100.0	205	2	075PA3_ASHGO	075PA3	ashbya gos
855	31	100.0	183	2	08LFA3_ARATH	08LFA3	arabidopsis	928	31	100.0	205	2	06ZRD4_HUMAN	06ZRD4	homo sapien
856	31	100.0	183	2	09W7X9_ARATH	09W7X9	arabidopsis	929	31	100.0	205	2	07F449_ORYSA	07F449	oryza sativ
857	31	100.0	183	2	066PE1_RHIME	066PE1	rhizobium m	930	31	100.0	205	2	084634_CHLTR	084634	chlamydia t
858	31	100.0	183	2	066PE6_9BRAD	066PE6	bradyrhizob	931	31	100.0	206	2	06QPD9_9ADEN	06QPD9	simian aden
859	31	100.0	184	2	08HY70_MUSVI	08HY70	muscula vis	932	31	100.0	207	2	05JRY5_HUMAN	05JRY5	homo sapien
860	31	100.0	184	2	04NOC9_9DELT	04NOC9	anaeromyxob	933	31	100.0	207	2	04LLZ3_9BURK	04LLZ3	trypanosoma
861	31	100.0	184	2	04MUT0_BACE	04MUT0	bacillus ce	934	31	100.0	208	2	0582P3_9TRYR	0582P3	trypanosoma
862	31	100.0	184	2	073AC8_BACCI	073AC8	bacillus ce	935	31	100.0	208	2	05QGR1_MASBA	05QGR1	maetigamoeb
863	31	100.0	184	2	081F76_BACCR	081F76	bacillus an	936	31	100.0	208	2	070K47_9ACTO	070K47	gordonia we
864	31	100.0	184	2	081S90_BACAN	081S90	bacillus an	937	31	100.0	208	2	07UV64_RHOBA	07UV64	rhodospirill
865	31	100.0	184	2	06HKG7_BACHK	06HKG7	bacillus th	938	31	100.0	208	2	06QPA3_9ADEN	06QPA3	simian aden
866	31	100.0	184	2	063D26_BACGZ	063D26	bacillus ce	939	31	100.0	209	2	05Z300_NOCFA	05Z300	nocardia fa
867	31	100.0	184	2	08RYO6_CORRF	08RYO6	corynebacte	940	31	100.0	211	2	04HX91_GIBZE	04HX91	gibberella
868	31	100.0	185	1	TFZLY_HUMAN	081UE0	homo sapien	941	31	100.0	211	2	09VW14_DROME	09VW14	dreophilla
869	31	100.0	185	1	TRXF2_ARATH	09XTH9	arabidopsis	942	31	100.0	211	2	0671A9_SYWTH	0671A9	syndyobacte
870	31	100.0	185	2	09WZJ6_MACMU	09WZJ6	macaca mula	943	31	100.0	212	2	06XN29_RHOER	06XN29	rhodococcus
871	31	100.0	185	2	097R36_STEPN	097R36	streptococc	944	31	100.0	212	2	05VP81_NOCFA	05VP81	nocardia fa
872	31	100.0	185	2	09RXW6_DEIRA	09RXW6	delinococcus	945	31	100.0	213	2	04X9X7_PLACH	04X9X7	plasmodium
873	31	100.0	186	1	TRXW2_ARATH	09seu8	arabidopsis	946	31	100.0	214	1	VEGFA_CANPA	VEGFA	canis faml
874	31	100.0	186	2	08LG26_ARATH	08LG26	arabidopsis	947	31	100.0	214	2	09GLF5_PIG	09GLF5	sus scrofa
875	31	100.0	186	2	056YG4_ARATH	056YG4	arabidopsis	948	31	100.0	214	2	066PD1_9RHIZ	066PD1	uncultured
876	31	100.0	186	2	066PC4_RHILE	066PC4	rhizobium l	949	31	100.0	214	2	066PD2_9RHIZ	066PD2	uncultured
877	31	100.0	186	2	066PC7_RHILE	066PC7	rhizobium l	950	31	100.0	214	2	066PD3_9RHIZ	066PD3	uncultured
878	31	100.0	186	2	050189_MYCHY	050189	mycoplasma	951	31	100.0	214	2	066PD5_9RHIZ	066PD5	uncultured
879	31	100.0	186	2	06ZGX6_BURMA	06ZGX6	burkholderi	952	31	100.0	214	2	066PD6_9RHIZ	066PD6	uncultured
880	31	100.0	187	2	06ZVA2_HUMAN	06ZVA2	homo sapien	953	31	100.0	214	2	066PD7_9RHIZ	066PD7	uncultured
881	31	100.0	187	2	08S091_ORYSA	08S091	oryza sativ	954	31	100.0	214	2	066PE0_9RHIZ	066PE0	uncultured
882	31	100.0	187	2	08DTZ1_STEPM	08DTZ1	streptococc	955	31	100.0	214	2	066PE2_9RHIZ	066PE2	uncultured
883	31	100.0	188	2	066PC9_RHILE	066PC9	rhizobium l	956	31	100.0	214	2	066PE3_9RHIZ	066PE3	uncultured
884	31	100.0	188	2	08RZV7_MOUSE	08RZV7	mus musculu	957	31	100.0	215	1	NRG2D_RAT	NRG2D	rattus norv
885	31	100.0	189	2	096MK4_HUMAN	096MK4	homo sapien	958	31	100.0	216	1	NRG2D_HUMAN	NRG2D	homo sapien
886	31	100.0	189	2	0951Q4_FELCA	0951Q4	felis silve	959	31	100.0	216	1	NRG2D_MACPA	NRG2D	macaca falc
887	31	100.0	189	2	0655X0_ORYSA	0655X0	oryza sativ	960	31	100.0	216	1	NRG2D_MACMU	NRG2D	macaca mula
888	31	100.0	189	2	08H2V6_ORYSA	08H2V6	oryza sativ	961	31	100.0	216	1	NRG2D_PANTR	NRG2D	pan troglod
889	31	100.0	189	2	066PE7_9BRAD	066PE7	bradyrhizob	962	31	100.0	216	2	08MTH1_PONPY	08MTH1	pongo pygma
890	31	100.0	190	1	TRXF_SPTOL	099856	spinacia ol	963	31	100.0	216	2	08MTH1_PONPY	08MTH1	pongo pygma
891	31	100.0	190	1	VEGFA_BOVIN	015591	bos taurus	964	31	100.0	216	2	07ORD4_MACMU	07ORD4	macaca mula
892	31	100.0	190	1	VEGFA_HORSE	099RTO	equus caball	965	31	100.0	216	2	08W2X9_ORYSA	08W2X9	oryza sativ
893	31	100.0	190	1	VEGFA_PIG	049151	sus scrofa	966	31	100.0	216	2	049816_MYCLE	049816	mycobacteri
894	31	100.0	190	2	077643_SHEEP	077643	ovis aries	967	31	100.0	216	2	07U1U8_MYCBO	07U1U8	mycobacteri
895	31	100.0	191	1	TRXF_MESCR	081332	mesembryant	968	31	100.0	216	2	066392_MYCCTU	066392	mycobacteri
896	31	100.0	191	2	09NBS0_RIFPA	09NBS0	rificia pach	969	31	100.0	217	2	05AT09_EMENT	05AT09	aspergillus
897	31	100.0	191	2	095MNS_MACPA	095MNS	macaca falc	970	31	100.0	217	2	0658N4_HUMAN	0658N4	homo sapien
898	31	100.0	191	2	04NMH0_BACE	04NMH0	bacillus ce	971	31	100.0	217	2	0726Q0_DESVH	0726Q0	desulfovibr
899	31	100.0	191	2	08DQ10_STRK6	08DQ10	streptococc	972	31	100.0	218	2	07PPY7_ANOGA	07PPY7	anopheles g
900	31	100.0	191	2	0733M6_BACCI	0733M6	bacillus ce	973	31	100.0	218	2	09PJ34_CHLAMU	09PJ34	chlamydia m
901	31	100.0	191	2	081AF9_BACCR	081AF9	bacillus an	974	31	100.0	219	2	08N4W2_HUMAN	08N4W2	homo sapien
902	31	100.0	191	2	081Y83_BACAN	081Y83	bacillus an	975	31	100.0	220	2	096BVS_HUMAN	096BVS	homo sapien
903	31	100.0	191	2	06HF17_BACHK	06HF17	bacillus th	976	31	100.0	220	2	09ZVT3_ARATH	09ZVT3	arabidopsis
904	31	100.0	191	2	0637L5_BACGZ	0637L5	bacillus ce	977	31	100.0	220	2	05TMM0_NOCFA	05TMM0	nocardia fa
905	31	100.0	192	2	09YEH7_AERPE	09YEH7	aeropyrum p	978	31	100.0	220	2	098253_MCV1	098253	molluscum c
906	31	100.0	192	2	06VQ14_HYDMA	06VQ14	hydra magni	979	31	100.0	220	2	04TGF7_TETNG	04TGF7	tetracodon n
907	31	100.0	192	2	066NW9_RHILE	066NW9	rhizobium l	980	31	100.0	222	2	07S153_NEUCR	07S153	neurospora

```

881 31 100.0 222 2 Q6SN38_CERMO Q6sn38_cercopthec
882 31 100.0 222 2 Q6SN76_9PRIM Q6sn76_cercocebus
983 31 100.0 222 2 Q6SNH6_COLGU Q6snh6_colobus_gue
984 31 100.0 222 2 Q6SNP3_PAPPA Q6snp3_papio_papio
985 31 100.0 222 2 Q6LD11_ARATH Q6ld11_arabidopsis
986 31 100.0 222 2 Q6ASV5_PROAC Q6asv5_propionibac
987 31 100.0 222 2 Q6RG01_FUSNN Q6rg01_fusobacteri
988 31 100.0 222 2 Q6CB61_MYCLE Q6cb61_mycobacteri
989 31 100.0 223 2 Q6Z5M4_ORYSA Q6z5m4_oryza_sativ
990 31 100.0 223 2 Q6GMH2_STRGL Q6gmh2_streptomyce
991 31 100.0 223 2 Q6JNF4_ARTNI Q6jnf4_arthrobacte
992 31 100.0 223 2 Q6Z234_RAT Q6z234_rattus_norv
993 31 100.0 224 2 Q6NAB0_HUMAN Q6nab0_homo_sapien
994 31 100.0 224 2 Q6UMD8_HUMAN Q6umd8_homo_sapien
995 31 100.0 224 2 Q7K4P2_DROME Q7k4p2_drosophila
996 31 100.0 225 2 Q6C708_MOUSE Q6c708_mus_musculu
997 31 100.0 225 2 Q5BK39_RAT Q5bk39_rattus_norv
998 31 100.0 225 2 Q6P346_MOUSE Q6p346_mus_musculu
999 31 100.0 225 2 Q4REX3_TETNG Q4rex3_tetradon_n
1000 31 100.0 226 2 Q7UL27_RHOBA Q7ul27_rhodoptrell

```

ALIGNMENTS

RESULT 1

SCXP_ANDMA STANDARD; PRT; 35 AA.

```

AC P01496;
DT 21-JUL-1986 (Rel. 01, Created)
DT 05-JUL-1986 (Rel. 01, Last sequence update)
DE Neurotoxin P2.
OS Androctonus mauretanicus mauretanicus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butridae; Butchioidea; Butridae; Androctonus.
OX NCBI_TaxID=6860;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=5193276; PubMed=3992595; DOI=10.1016/0041-0101(85)90114-X;
RA Robso J.-P., Rochat H.;
RT "Characterization of ten proteins from the venom of the Moroccan
RT scorpion Androctonus mauretanicus mauretanicus, six of which are toxic
RT to the mouse."
RL Toxicon 23:113-125(1985).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family.

```

```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR: A01758; NTSRPM.
CC HSSP: P15222; 1S1S.
DR InterPro: IPR007958; toxin_5.
DR Pfam: PF05294; Toxin_5; 1.
KM Direct protein sequencing; Neurotoxin; Toxin.
FT DISULFID 1 18 By similarity.
FT DISULFID 4 25 By similarity.
FT DISULFID 15 30 By similarity.
FT DISULFID 19 32 By similarity.
SQ SEQUENCE 35 AA; 3673 MW; 21365926289EB5A CRC64;

```

Query March 100.0%; Score 31; DB 1; Length 35;

Best local Similarity 100.0%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

||||

Db 1 CGPC 4

RESULT 2

BS14_BUTSI STANDARD; PRT; 36 AA.

```

AC P59887;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Chlorotoxin-like peptide Bs 14 (Bs14).
OS Butyrus sindicus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butridae; Butchioidea; Butridae; Mesobuthus.
OX NCBI_TaxID=42519;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=99157745; PubMed=10048185; DOI=10.1016/S1095-6433(98)10140-X;
RA Ali S.A., Stoeva S., Schuetz J., Kaye R., Abbasi A., Zaidi Z.H.,
RA Voelter W.;
RT "Purification and primary structure of low molecular mass peptides
RT from scorpion (Butyrus sindicus) venom."
RL Comp. Biochem. Physiol. 121A:323-332(1998).
CC -1- FUNCTION: Probable chloride channel ligand, which blocks small-
CC conductance chloride channels (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=3648.3; METHOD=MALDI; RANGE=1-36;
CC NOT=Ref.1.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Chloride
CC channel inhibitor subfamily.

```

```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC DR InterPro: IPR007958; toxin_5.
CC Pfam: PF05294; Toxin_5; 1.
KM Chloride channel inhibitor; Direct protein sequencing;
KM Ionic channel inhibitor; Neurotoxin; Toxin.
FT DISULFID 1 18 By similarity.
FT DISULFID 4 25 By similarity.
FT DISULFID 15 30 By similarity.
FT DISULFID 19 32 By similarity.
SQ SEQUENCE 36 AA; 3847 MW; 536117F8E5015A0 CRC64;

```

Query March 100.0%; Score 31; DB 1; Length 36;

Best local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

||||

Db 1 CGPC 4

RESULT 3

046621_TAPIN PRELIMINARY; PRT; 38 AA.

```

AC 046621;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Luteinizing hormone beta-subunit (Fragment).
GN Name=LH-beta;
OS Tapirus indicus (Asiatic tapir) (Malayan tapir).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Tapiridae;
OC Tapirus.
OX NCBI_TaxID=9802;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
 RA Fischer S., Velts J., Meyer H.H.D.;
 RL Submitted (PEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047606; AAC04364.1; -, Genomic_DNA.
 DR HSSP; P01233; IHCN.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR006208; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 FT NON_TER
 SQ SEQUENCE 38 AA; 3928 MW; 5DBB7A21170C60A0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 38;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 7 CGPC 10

RESULT 4
 ID 046620 EQUAS PRELIMINARY; PRT; 42 AA.
 AC 046620;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fb; Synonyms=Dhtc2;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Fischer S., Velts J., Meyer H.H.D.;
 RL Submitted (PEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF047605; AAC04363.1; -, Genomic_DNA.
 DR HSSP; P01233; IHCN.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR InterPro; IPR006208; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 FT NON_TER
 SQ SEQUENCE 42 AA; 4332 MW; 7D4A6C35B138589D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 42;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 6 CGPC 9

RESULT 5
 ID 023947 DROHY PRELIMINARY; PRT; 49 AA.
 AC 023947;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fa; Synonyms=Dhtc3;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41117.1; -, Genomic_DNA.
 DR FlyBase; FBgn0015096; Dhyd\Mst87Fa.
 SQ SEQUENCE 49 AA; 4610 MW; BE158FEC51369F01 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 3 CGPC 6

RESULT 6
 ID 023948 DROHY PRELIMINARY; PRT; 49 AA.
 AC 023948;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Testis-specific RNA.
 GN Name=Mst87Fb; Synonyms=Dhtc2;
 OS Drosophila hydei (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7224;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Kuech A., Buenemann H.;
 RL Submitted (DEC-1990) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X58114; CAA41118.1; -, Genomic_DNA.
 DR FlyBase; FBgn0015097; Dhyd\Mst87Fb.
 SQ SEQUENCE 49 AA; 4550 MW; 24758FEC51369F1D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 49;
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 DB 3 CGPC 6

RESULT 7
 ID 08MUN5 DROME PRELIMINARY; PRT; 51 AA.
 AC 08MUN5;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE CG30430-PA (IP04475D).
 GN Name=CG30430; ORFNames=CG30430;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Bottler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettecourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.,
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.,
 RT "Protophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP NUCLEOTIDE SEQUENCE.

RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Celniker S.,
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003466; AAM68330.1; -; Genomic_DNA.
 DR EMBL; BT023672; AAY85072.1; -; mRNA.
 DR EMBL; CG30430; *Drosophila melanogaster*.
 DR FlyBase; FBgn0050430; CG30430.
 SQ SEQUENCE 51 AA; 5077 MW; 0C26A637E5D2949B CRC64;
 QY Query Match 100.0%; Score 31; DB 2; Length 51;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 3 CGPC 6
 QY 2 CGPC 5
 Db 3 CGPC 6
 RESULT 8
 Q6QAU0 DROMA PRELIMINARY; PRT; 52 AA.
 ID Q6QAU0 DROMA PRELIMINARY; PRT; 52 AA.
 AC Q6QAU0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE M8T84DC.
 GN Name=M8T84DC; ORFName=CG17945;
 OS *Drosophila mauritiana* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 NCBI_TaxID=7226;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=952;
 RX PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michalak P., Noor M.A.F.,
 RT "Association of misexpression with sterility in hybrids of *Drosophila*
 RT *simulans* and *D. mauritiana*.";
 RL J. Mol. Evol. 59:277-282(2004).
 DR EMBL; AY549556; AAS55565.1; -; Genomic DNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0042742; P:defense response to bacteria; IEA.
 DR GO; GO:0009613; P:response to pest, pathogen or parasite; IEA.
 DR InterPro; IPR001450; 4Fe4S_Ferredoxin.
 DR InterPro; IPR006081; Defensin_alpha.
 DR InterPro; IPR001007; VWF_C.
 DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
 DR PROSITE; PS00269; DEFENSIN_1.
 DR PROSITE; PS01208; VWF_C_1.
 SQ SEQUENCE 52 AA; 4908 MW; DE0F3DE43F66EE3A CRC64;
 QY Query Match 100.0%; Score 31; DB 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 3 CGPC 6
 QY 2 CGPC 5
 Db 3 CGPC 6
 RESULT 9
 MS84C DROME STANDARD; PRT; 55 AA.
 ID MS84C DROME STANDARD; PRT; 55 AA.
 AC Q01644; Q9VIA0;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Male specific sperm protein Mst84C.


```

DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE MST84DC.
GN Name=Mst84Dc; ORFNames=CG17945;
OS Drosophila mauritiana (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7226;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MS11.
RC PubMed=15486701; DOI=10.1007/s00239-004-2622-y;
RA Michalak P., Noor M.A.F.;
RT "Association of misexpression with sterility in hybrids of Drosophila
RT simulans and D. mauritiana.";
RL J. Mol. Evol. 59:277-282(2004).
DR EMBL; AY549955; AAS55564.1; -; Genomic_DNA.
DR InterPro; IPR001450; 4Fe4s_Ferredoxin.
DR InterPro; IPR005634; MSSP.
DR InterPro; IPR001007; VWF_C.
DR Pfam; PF03940; MSSP.1.
DR PROSITE; PS00198; 4Fe4s_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS01208; VWF_C.1.
SQ SEQUENCE 55 AA; 5165 MW; 95A12F27D07B6F6C CRC64;

Query Match 100.0%; Score 31; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 12
MS87F_DROME STANDARD; PRT; 56 AA.
ID MS87F_DROME
AC P08175; Q9VFO6;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
GN Male specific sperm protein Mst87F.
DN Name=Mst87F; Synonyms=mst(3)g1-9; ORFNames=CG17956;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Canton-S;
RC MEDLINE=8621157; PubMed=2835228;
RA Kuhn R., Schaefer U., Schaefer M.;
RT "cis-acting regions sufficient for spermatocyte-specific
RT transcripional and spermatid-specific translational control of the
RT Drosophila melanogaster gene mst(3)g1-9.";
RL EMBO J. 7:447-454(1988).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkelley;
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolonchak S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

```

```

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Honck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mikhlin N.V., Modyarty C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Maasman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RN Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitefield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
CC motifs.
CC -1- SIMILARITY: Belongs to the MST(3)CGP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; Y00831; CA66761.1; -; Genomic DNA.
CC EMBL; AB003702; AAF54994.1; -; Genomic DNA.
CC F01R; S00340; WTFP.
CC DR HSSP; P01180; JUK6.
CC DR Ensemble; CG17956; Drosophila melanogaster.
CC DR FlyBase; FBgn0002862; Mst87F.
CC Developmental protein. Differentiation; Multigene family; Repeat;
CC Spermatogenesis.
SQ SEQUENCE 56 AA; 5233 MW; 830CD13212C34A47 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 56;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 13
Q595V9_NEITIA

```

ID Q595V9 NEI1A PRELIMINARY; PRT; 56 AA.
 AC Q595V9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DR Rebreddoxin.
 OS Neisseria lactamica.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_Taxid=486;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA van Passel M.W.J., Bart A., Luyf A.C.M., van Kampen A.H.C.,
 RT "Identification of anomalous sequences in Neisseria lactamica expands
 the neisserial gene pool."; Genomic DNA.
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY532628; AAM21818.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 KW Electron transport; Iron; Metal-binding; Rubredoxin.
 SQ SEQUENCE 56 AA; 6345 MW; 17DACA86E7DB8CF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 6 CGPC 9

RESULT 14
 Q5F8A3_NEIG1 PRELIMINARY; PRT; 56 AA.
 ID Q5F8A3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Putative rubredoxin.
 GN OrderedLocusNames=NGC00885;
 OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_Taxid=242231;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [Large Scale Genomic DNA].
 RA Lewis L.A., Gillaepy A.F., McLaughlin R.E., Gibson M., Ducey T.F.,
 RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
 RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
 RA Kenyon S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
 RT "The complete sequence of Neisseria gonorrhoeae.";
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE004969; AAM89584.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR004039; Rubredox.
 DR InterPro; IPR001052; Rubredoxin.
 DR Pfam; PF00301; Rubredoxin; 1.
 DR PRINTS; PR00163; RUBREDOXIN.
 DR PRODOM; PD001610; Rubredoxin.
 DR PROSITE; PS00202; RUBREDOXIN; 1.
 DR PROSITE; PS0903; RUBREDOXIN LIKE; 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6345 MW; 17DACA86E7DB8CF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 6 CGPC 9

RESULT 15
 Q7DDJ1_NEIMB PRELIMINARY; PRT; 56 AA.
 ID Q7DDJ1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Rubredoxin.
 GN OrderedLocusNames=MNB0993;
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_Taxid=491;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=MC58 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
 RA Dodson R.J., Nelson W.C., Gwin M.L., Deboy R.T., Peterson J.D.,
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
 RA Clifton H., Clark B.B., Cotton M.D., Ueberback T.R., Khouri H.M.,
 RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzi M.,
 RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
 RA Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58.";
 RT Science 287:1809-1815 (2000).
 RL EMBL; AE002098; AAF41396.1; -; Genomic DNA.
 DR HSP; P24297; 1105.
 DR TIGR; NMB0993; -;
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR004039; Rubredox.
 DR InterPro; IPR001052; Rubredoxin.
 DR Pfam; PF00301; Rubredoxin; 1.
 DR PRINTS; PR00163; RUBREDOXIN.
 DR PRODOM; PD001610; Rubredoxin.
 DR PROSITE; PS00202; RUBREDOXIN; 1.
 DR PROSITE; PS0903; RUBREDOXIN LIKE; 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6369 MW; F2CE9BA86E7DB8C9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 6 CGPC 9

RESULT 16
 Q9JON3_NEIMA PRELIMINARY; PRT; 56 AA.
 ID Q9JON3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative rubredoxin.
 GN OrderedLocusNames=MMA1201;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 NCBI_Taxid=65659;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parikh I.J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.,
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria*
 RT meningitidis 22491."
 RL Nature 404:502-506 (2000).
 DR EMBL, AL162755; CAB84462.1; -; Genomic_DNA.
 DR PIR, H81133; H81133.
 DR HSSP, P24297; IRWD.
 DR GO, GO:0005489; F:electron transporter activity; IEA.
 DR GO, GO:0046872; F:metal ion binding; IEA.
 DR GO, GO:0006118; P:electron transport; IEA.
 DR InterPro, IPR004039; Rubredox.
 DR InterPro, IPR001052; Rubredoxin.
 DR Pfam, PF00301; Rubredoxin.1.
 DR PRINTS, PR00163; RUBREDOXIN.
 DR ProDom, PD001610; Rubredox; 1.
 DR PROSITE, PS00202; RUBREDOXIN, 1.
 DR PROSITE, PS50903; RUBREDOXIN LIKE, 1.
 KW Complete proteome; Electron transport; Iron; Metal-binding;
 KW Rubredoxin.
 SQ SEQUENCE 56 AA; 6369 MW; F2CE9EA86E7DB8C9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 6 CGPC 9

RESULT 17
 Q6GAT8 DROSI
 ID Q6GAT8_DROSI PRELIMINARY; PRT; 58 AA.
 AC Q6GAT8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE M8184DC.
 GN Name=M8184DC; ORFNames=CG17945;
 OS Drosophila simulans (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCB1_TaxId=7240;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Valparaiso.
 RX PubMed=15486701; DOI=10.1007/s00239-004-2622-Y;
 RA Michalak P., Noor M.A.F.,
 RT "Association of misexpression with sterility in hybrids of *Drosophila*
 RT simulans

Query Match 100.0%; Score 31; DB 2; Length 58;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db ||||
 3 CGPC 6

RESULT 18
 SCCT MESMA
 ID SCCT MESMA STANDARD; PRT; 59 AA.
 AC Q9UAD0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Neurotoxin BmKCT precursor (Cl-channel toxin) (CT neurotoxin) (Short-
 DE chain toxin KCT) (BmKCL1) (TXCL1).
 OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butrida; Butiroidea; Butiridae; Mesobuthus.
 OC NCB1_TaxId=34649;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RX MEDLINE=20175769; PubMed=10708793; DOI=10.1016/S0041-0101(99)00212-3;
 RA Zeng X.-C., Li W.-X., Zhu S.-Y., Peng F., Zhu Z.-H., Wu K.-L.,
 RA Yang F.-H.,
 RT "Cloning and characterization of a cDNA sequence encoding the
 RT precursor of a chlorotoxin-like peptide from the Chinese scorpion
 RT Buthus martensii Karach."
 RL Toxicon 38:1009-1014 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Wu J.-J., Dai L., Chi C.-W.,
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RA Shunyi Z., Wenxin L.,
 RT "cDNA encoding a putative insect toxin from BmK."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Shunyi Z., Wenxin L.,
 RT "Genomic DNA of a scorpion Cl-channel toxin."
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Chloride channel ligand. Blocks small-conductance
 CC chloride channels (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Chloride
 CC channel inhibitor subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF135821; AAG01185.1; -; mRNA.
 CC EMBL, AF079059; AAD47373.1; -; Genomic_DNA.
 CC EMBL, AF159976; AAK61823.1; -; mRNA.
 CC EMBL, AF419252; AAN32699.1; -; Genomic_DNA.
 CC HSSP, P15222; 1S1S.
 DR InterPro, IPR007958; toxin_5.
 DR Pfam, PF05294; Toxin_5; 1.
 KW Chloride channel inhibitor; Ionic channel inhibitor; Neurotoxin;
 KW Signal; Toxin.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 59 Neurotoxin BmKCT.
 FT DISULFID 25 42 By similarity.
 FT DISULFID 28 49 By similarity.
 FT DISULFID 39 54 By similarity.
 FT DISULFID 43 56 By similarity.
 SQ SEQUENCE 59 AA; 6467 MW; C9FAABAFB8B82EA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 59;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||

DB 25 CGPC 28

RESULT 19

SCCX MESMA STANDARD; PRT; 59 AA.

AC Q9BJW4; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Neurotoxin Bm12-b precursor.

OS Mesobuthus martensii (Manchurian scorpion) (Butus martensii);

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Scorpiones;

OX Butidae; Butioidae; Butidae; Mesobuthus.

NCBI_Taxid=34649;

RP NUCLEOTIDE SEQUENCE.

XU C.-Q., Chi C.-W.;

RT "A novel neurotoxin from scorpion BmK.";

Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

CC -1 FUNCTION: Chloride channel ligand. Blocks small-conductance

chloride channels (By similarity).

CC -1 SUBCELLULAR LOCATION: Secreted.

CC -1 TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1 SIMILARITY: Belongs to the short scorpion toxin family. Chloride

channel inhibitor subfamily.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation-

the European Bioinformatics Institute. There are no restrictions on its

use as long as its content is in no way modified and this statement is not

removed.

CC EMBL: AF327643; AAK16444.1; -; mRNA.

DR HSP: P15222; IIS.

DR InterPro: IPR007958; Toxin_5.

DR Pfam: PF05294; Toxin_5; 1.

KW Chloride channel inhibitor; Ionic channel inhibitor; Neurotoxin;

KW Signal; Toxin.

FT SIGNAL 1 24 Potential.

FT CHAIN 25 59 Neurotoxin Bm12-b.

FT DISULFID 25 42 By similarity.

FT DISULFID 28 49 By similarity.

FT DISULFID 39 54 By similarity.

FT DISULFID 43 56 By similarity.

SQ SEQUENCE 59 AA; 6484 MW; C2BABAFCB8BD9EA CRC64;

Query Match 100.0%; Score 31; DB 1; Length 59;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||

DB 25 CGPC 28

RESULT 20

Q71DAO DROVA PRELIMINARY; PRT; 60 AA.

AC Q71DAO; 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TReMBLrel. 27, Last annotation update)

OS Drosophila yakuba (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_Taxid=7245;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;

RA Domazet-Loso T., Tautz D.;

RT "An evolutionary analysis of orphan genes in Drosophila."

genome Res. 13:2213-2219(2003).

DR EMBL: AF531969; AAQ09868.1; -; mRNA.

FT NON_TER 1 1

FT NON_TER 60 60

SQ SEQUENCE 60 AA; 6105 MW; BF1072E1DA7C14AA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||

DB 41 CGPC 44

RESULT 21

Q8MSH6 DROME PRELIMINARY; PRT; 60 AA.

AC Q8MSH6; 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

GN ORFNames=CG4959;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_Taxid=7227;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Berkley.

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA Champagne M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guatin H., Kronmiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nuno J., Pacled J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;

RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY118808; AAM50668.1; -; mRNA.

DR FlyBase: FBgn0028883; CG4959.

SQ SEQUENCE 60 AA; 6117 MW; BEFF72E1C0CC14BC CRC64;

Query Match 100.0%; Score 31; DB 2; Length 60;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||

DB 41 CGPC 44

RESULT 22

Q8T403 DROME PRELIMINARY; PRT; 61 AA.

AC Q8T403; 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)

DE 10-MAY-2005 (TReMBLrel. 30, Last annotation update)

GN ORFNames=CG31740;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_Taxid=7227;

RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,
 RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo K., Pacle J., Paragas V., Park S.,
 RA Patel S., Phouneavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Buam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fostel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwu C.,
 RA Jellai M., Kalush H., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshneff A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skipski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams J.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [4]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [5]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield R.J., Bayraktaroglu L., Bernan B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [6]
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY089413; AAL90151.1; -; mRNA.
 DR EMBL; AE003657; AAN1177.1; -; Genomic DNA.
 DR Ensembl; CG31740; *Drosophila melanogaster*.
 DR FlyBase; FBgn0051740; CG31740.
 SQ SQUENCE 61 AA; 5965 MW; 94390FEB1D844D4 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 61;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Gaps 0;
 Matches 4; Conservative 0; Indels 0; Gaps 0;
 Db 34 CGPC 37
 Qy 2 CGPC 5
 Db 34 CGPC 37
 RESULT 23
 SCIT_MESRA
 ID SCIT_MESRA STANDARD; PRT; 62 AA.
 AC P81761; O8TOX4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Lepidopteran-selective toxin precursor (Butatr) (BrCh12).
 OS Mesobuthus tamulus (Eastern Indian scorpion) (Butus tamulus).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Butrida; Buthoidea; Butridae; Mesobuthus.
 OX NCBI_TaxID=34647;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Venom gland;
 RA Newton K.A., Armugam A., Strong P.N., Jeyaseelan K.;
 RT "Insect toxin from *Mesobuthus tamulus*.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN PROTEIN SEQUENCE OF 25-61, FUNCTION, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX PubMed=11782289; DOI=10.1186/1472-2091-2-16;
 RA Widyasagiri R., Inceoglu B., Herrmann R., Derbel M., Choudary P.V.,
 RA Hammock B.D.;
 RT "Isolation and characterization of a novel lepidopteran-selective
 RT toxin from the venom of South Indian red scorpion, *Mesobuthus*
 RT *tamulus*.";
 RL BMC Biochem. 2:16-16(2001).
 CC -1- FUNCTION: Induces flaccid paralysis in *H. virescens* larvae. Is not
 CC toxic to *S. falculata* larvae or mice.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=3856.77; METHOD=Electropray; RANGE=25-61;
 CC NOTE=Ref.2.
 CC -1- SIMILARITY: Belongs to the short scorpion toxin family.

```

CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AF481881; AAL87237.1; -; mRNA.
DR HSSP; P15222; 1S1S.
DR GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0019870; F:potassium channel inhibitor activity; NMS.
DR GO; GO:0009405; P:pachogenesis; IDA.
DR InterPro; IPR007958; toxin_5.
DR Pfam; PF05294; Toxin_5; 1.
KW Direct protein sequencing; Neurotoxin; Signal; Toxin.
FT SIGNAL 1 24
FT CHAIN 25 61
FT PROPEP 62 62
FT DISULFID 26 43
FT DISULFID 29 51
FT DISULFID 40 56
FT DISULFID 44 58
SQ SEQUENCE 62 AA; 6656 MW; 32E0B3AF238597E CRC64;

Query Match 100.0%; Score 31; DB 1; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 26 CGPC 29

RESULT 24
MS84A_DROME STANDARD; PRT; 63 AA.
ID MS84A_DROME
AC Q01642; Q9VIA3;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Male specific sperm protein Msc84Da.
GN Name=Msc84Da; ORFNames=CG17946;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
CC Ephydroidea; Drosophilidae; Drosophila.
CC NCBI_taxid=7227;
OK [1]
RP NUCLEOTIDE SEQUENCE.
RN STRAIN=Oregon-R;
RC MEDLINE=92102953; PubMed=1684716; DOI=10.1016/0925-4773(91)90064-D;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U., Schaefer M.,
RT "A cluster of four genes selectively expressed in the male germ line
RT of Drosophila melanogaster.";
RL Mech. Dev. 35:143-151 (1991).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abiri J.F., Adganyi A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
RA Beeson K.Y., Bencs P.V., Bertan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Borkan M.R., Bouck J., Brockstein P., Brottier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

```

```

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glöckel A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosten D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Modarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiert K.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong K., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Mira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktoglu L., Berman B.P.,
RA Bertencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-C-P
CC motifs.
CC -1- SIMILARITY: Belongs to the MST(3)CGP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X67703; CAA47937.1; -; Genomic DNA.
DR EMBL; AE003672; AAF54022.1; -; Genomic DNA.
DR PIR; S25772; S25772.
DR Ensemble; CG17946; Drosophila melanogaster.
DR FlyBase; FBgn0004172; Msc84Da.
DR InterPro; IPR005634; MSSP.
DR Pfam; PF03940; MSSP; 1.
KW Developmental protein; Differentiation; Multigene family; Repeat;
KW Spermatogenesis.
SQ SEQUENCE 63 AA; 5806 MW; BF84CD74CBEFDF3 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 17 CGPC 20

RESULT 25
Q8MI19_SHEEP
ID Q8MI19_SHEEP PRELIMINARY; PRT; 64 AA.
AC Q8MI19;

```

```

DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Vascular endothelial growth factor 188 isoform (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RC TRISSE=Placental artery endothelium;
RA Chung J.-Y., Teol S.C.M., Wen Y.-X., Magness R.R., Zheng J.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF534638; AAN04109.1; -, mRNA.
DR SMR: Q8M119; 15-64.
DR InterPro: IPR001212; Somatomedin_B.
DR PRINTS: PR00022; SOMATOMEDINB.
FT NON TER 1
SQ SEQUENCE 64 AA; 7674 MW; 8BF719596DDEF6B6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 3,4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 16 CGPC 19

RESULT 26
Q6IWK3 PIG PRELIMINARY; PRT; 66 AA.
ID Q6IWK3_PIG PRELIMINARY;
AC 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Vascular endothelial growth factor (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
NCBI_TaxID=9823;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RA Tuzade C., Black G.P., Croy A.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY161676; AAT3876.1; -, mRNA.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0008083; F:growth factor activity; IEA.
DR GO: GO:0008283; P:cell proliferation; IEA.
DR GO: GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro: IPR00072; PD_growth_factor.
DR Pfam: PF00341; PDGF_1.
DR ProDom: PD001629; PD_growth_factor; 1.
DR PROSITE: PS50278; PDGF_2; 1.
KW Growth factor; Mitogen.
FT NON TER 1
SQ SEQUENCE 66 AA; 7796 MW; 2D3E1DD07BB63620 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 66;
Best Local Similarity 100.0%; Pred. No. 3,5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 56 CGPC 59

RESULT 27
Q9VM83_DROME PRELIMINARY; PRT; 67 AA.
ID Q9VM83_DROME PRELIMINARY;

```

```

AC Q9VM83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE CG17376-PB, isoform B (GH22658p).
GN CG17376-PB;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
AD Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sultion G.G., Wortman J.R., Yandel M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Ashby A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.B., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Iasko P., Lei Y., Levitsky A.A., Li U.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverdy T., Munz D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodegren R.J.,
RA Svirskas R., Taber P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers S.E., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).

```


[4]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Sylvestras R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RP [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Berkeley.
 RA Stapleton M., Carlson J., Chavez C., Friese E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celinker S.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003615; AAF52440.1; -; Genomic_DNA.
 DR EMBL; BF011549; AAS15685.1; -; mRNA.
 DR Ensembl; CG17376; Drosophila melanogaster.
 DR Flybase; FBgn0042189; CG17376.
 SQ SEQUENCE 67 AA; 6871 MW; B9442P2C7B567C76 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 8 CGPC 11

RESULT 28
 ID O6EPUB ORYSA PRELIMINARY; PRT; 69 AA.
 AC O6EPUB;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DE Hypothetical protein OSJNBa0016D04.29.
 GN Name=OSJNBa0016D04.29;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nippondare(GAS) genomic DNA, chromosome 2, BAC
 RT clone:OSJNBa0016D04.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005800; BAD2328.1; -; Genomic_DNA.
 DR Gramene; O6EPUB; -;
 KW Hypothetical protein.
 SQ SEQUENCE 69 AA; 7109 MW; 9FBA6730BE5730A6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 69;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 31 CGPC 34

RESULT 29
 ID O7PK85 ANOGA PRELIMINARY; PRT; 71 AA.
 AC O7PK85;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DE ENSANGP0000023827 (Fragment).
 GN ORFNames=ENSANGG0000020560;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT "Anopheles gambiae re-annotation.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008980; EAA3469.2; -; Genomic_DNA.
 DR InterPro; IPR005634; MSSP.
 DR Pfam; PF03940; MSSP; 1.
 FT NON_TER 1 71
 FT NON_TER 71 71
 SQ SEQUENCE 71 AA; 6483 MW; 192B4F10C5613BE CRC64;

Query Match 100.0%; Score 31; DB 2; Length 71;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 2 CGPC 5

RESULT 30
 ID MS84D DROME STANDARD; PRT; 72 AA.
 AC 001645; OSV199;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Male specific sperm protein Mst84d.
 GN Name=Mst84d; ORFNames=CG17935;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND
 RP DEVELOPMENTAL STAGE.
 RC STRAIN=Oregon-R;
 RA MEDLINE=92102953; PubMed=1684716; DOI=10.1016/0925-4773(91)90064-D;
 RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U., Schaefer M.;
 RT "A cluster of four genes selectively expressed in the male germ line
 RT of Drosophila melanogaster.";

RL Mech. Dev. 35:143-151 (1991).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Adair J.F., Agbayani A., An H.-J., Andrews-Pianko C., Baldwin D.,
 RA Bailly R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borchen M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lai Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195 (2000).
 [3]
 RN GENOME REANNOTATION.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review."
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
 CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
 motifs.
 CC -1- SIMILARITY: Belongs to the MST(3)CGP family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: X67703; CAA47940.1; -; Genomic DNA.
 DR EMBL: AB003672; AAF54026.1; -; Genomic DNA.
 DR PIR: S25775; S25775.
 DR Ensemble: CG17935; Drosophila melanogaster.
 DR FlyBase: FBgn004175; Mst84Dd.

DR InterPro: IPR005634; MSSP.
 DR Pfam: PF03940; MSSP; 1.
 KW Developmental protein; Differentiation; Multigene family; Repeat;
 KW Spermatogenesis.
 FT CONFLICT 13
 SQ SEQUENCE 72 AA; 6840 MW; 8CE374495F88ABA CRC64;
 Query Match 100.0%; Score 31; DB 1; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 10 CGPC 13
 RESULT 31
 QSTU4 ANOGA
 ID QSTU4 ANOGA PRELIMINARY; PRT; 72 AA.
 AC QSTU4;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DE ENSANGP0000029185 (Fragment).
 GN ORFNames=ENSANG0000023294;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
 OC Anophelinae; Anopheles.
 OC NCBI_Taxid=180454;
 RX NUCLEOTIDE SEQUENCE.
 RP STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC -----
 DR EMBL: AAB01008900; BAI40455.1; -; Genomic DNA.
 DR GO: GO:0005576; C:extracellular region; IEA.
 DR GO: GO:0005179; F:hormone activity; IEA.
 DR InterPro: IPR000381; Inhibin_betaab.
 DR PRINTS: PR00671; INHIBINB.
 FT NON TER 1
 FT NON TER 72
 SQ SEQUENCE 72 AA; 6596 MW; DA63390CA9DF3A01 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 38 CGPC 41
 RESULT 32
 Q4V3L2 DROME
 ID Q4V3L2 DROME PRELIMINARY; PRT; 72 AA.
 AC Q4V3L2;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE I002161P.
 GN Name=Mst84Dd;
 OS Drosophila melanogaster (Fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Celniker S.;
 RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BT023344; AAY55760.1; -; mRNA.
 SQ SEQUENCE 72 AA; 6840 MW; 8CE374495F88ABA CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 10 CGPC 13
 RESULT 33
 ID Q74DK8_GEOSL PRELIMINARY; PRT; 72 AA.
 AC Q74DK8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN OrderedLocustNames=GSU1308;
 OS Geobacter sulfurreducens.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
 OC Geobacteraceae; Geobacter.
 OK NCBI_TaxID=35554;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PCA / ATCC 51573;
 RX PubMed=14671304; DOI=10.1126/science.1088727;
 RA Melte B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C.,
 RA Heidelberg J.F., Wu D., Wu M., Ward N.L., Benan M.J., Dodson R.J.,
 RA Madupu R., Brinkac L.M., Daugherty S.C., Deboy R.T., Durkin A.S.,
 RA Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
 RA Daviden T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,
 RA Weidman J.F., Khouir H.M., Feldblyum T.V., Uterback T.R.,
 RA Van Aken S.E., Loyley D.R., Fraser C.M.;
 RA "Genome of Geobacter sulfurreducens: metal reduction in subsurface
 RT environments.";
 RT Science 302:1967-1969(2003).
 RL EMBL; AE017180; AAR34684.1; -; Genomic_DNA.
 DR TIGR; GSU1308; -;
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 72 AA; 8191 MW; F25B550B9D43BB9 CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 38 CGPC 41
 RESULT 34
 ID Q4KRY5_MOUSE PRELIMINARY; PRT; 72 AA.
 AC Q4KRY5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN Name=Pkd1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oaw and Lamb;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Roak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Oaw and Lamb;
 RG NIH MGC Project;
 RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC099589; AAH9589.1; -; mRNA.
 DR MGI; MGI:97603; Pkd1.
 KW Hypothetical protein.
 SQ SEQUENCE 72 AA; 7108 MW; 37F5B94C6918C0FD CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 72;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGPC 5
 DB 30 CGPC 33
 RESULT 35
 ID Q6EPJ3_ORYSA PRELIMINARY; PRT; 73 AA.
 AC Q6EPJ3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE Hypothetical protein OSJNBa0016D04.34.
 GN Name=OSJNBa0016D04.34;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaristidae; Oryzaceae; Oryza.
 OK NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sasaki T., Matsunoto T., Katayose Y.;
 RT "Oryza sativa nipponbare(GAS) genomic DNA, chromosome 2, BAC
 RT clone:OSJNBa0016D04.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005800; BAD29333.1; -; Genomic_DNA.
 DR Gramene; Q6EPJ3; -;
 KW Hypothetical protein.
 SQ SEQUENCE 73 AA; 7746 MW; 3EF220FB4F36D10A CRC64;
 Query Match 100.0%; Score 31; DB 2; Length 73;
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      2 CGPC 5
      ||||
Db      37 CGPC 40

RESULT 36
QYH54 CHICK PRELIMINARY; PRT; 73 AA.
ID QYH54 CHICK
AC QYH54
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Keratin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX
RN
RP NCLECTIDE SEQUENCE.
RX MEDLINE=85122780; PubMed=2578818; DOI=10.1016/0167-4781(85)90049-1;
RL "Isolation and characterization of keratin mRNA from the scale
RT epidermis of the embryonic chick."
RL Biochim. Biophys. Acta 824:201-208(1985).
DR EMBL; M25641; AAA48932.1; -; mRNA.
DR PIR; A60136; A60136.
DR Ensembl; ENSGALG00000009189; Gallus gallus.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR InterPro; IPR003461; Keratin.
DR Pfam; PF02422; Keratin; 1.
KW Keratin.
FT NON_TER 1 1
SQ SEQUENCE 73 AA; 7468 MW; B108CEBA52106B5F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      70 CGPC 73

RESULT 37
MS84B_DROME STANDARD; PRT; 74 AA.
ID MS84B_DROME
AC Q01643; Q8MZE2; Q9V1A1;
DT 01-JUL-1993 (Rel. 26, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Male specific sperm protein Mst84b.
GN Name=Mst84b; ORFNames=CG17934;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
OX
RN
RP NCLECTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND
RP DEVELOPMENTAL STAGE.
RC STRAIN=Oregon-R;
RX MEDLINE=92102953; PubMed=1684716; DOI=10.1016/0925-4773(91)90064-D;
RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U., Schaefer M.;
RT "A cluster of four genes selectively expressed in the male germ line
RL of Drosophila melanogaster."
RL Mech. Dev. 35:143-151(1991).
RN
RP NCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

```

```

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benoe P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busan D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostrel A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Waasman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN
RP
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.U., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Belencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN
RP
RP NCLECTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=Berkely; TISSUE=Testis;
RX MEDLINE=22426066; PubMed=12537569;
RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA George R.A., Garin H., Krommiller B., Pacle J.M., Park S., Wan K.H.,
RA Rubin G.M., Celinker S.E.;
RT "A Drosophila full-length cDNA resource."
RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.6(2002).
RN
RP
CC -1- TISSUE SPECIFICITY: Testis.
CC -1- DEVELOPMENTAL STAGE: Primary spermatocytes.
CC -1- DOMAIN: This protein is mostly composed of repetitive C-G-P
CC motifs.
CC -1- SIMILARITY: Belongs to the MST(3)GSP family.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to wrong
CC choice of frame.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

```

```

CC -----
DR EMBL: X67703; CAA47938.1; -; Genomic DNA.
DR EMBL: AF003672; AAF54024.1; -; Genomic DNA.
DR EMBL: AY113221; AAM29226.1; ALT_SEQ; mRNA.
DR PIR: S25773; S25773.
DR HSSP: Q957B3; IEH.
DR Ensembl: CG17934; Drosophila melanogaster.
DR FlyBase: FBgn0004173; MsrB4Db.
DR InterPro: IPR005634; MSSP.
DR Pfam: PF03940; MSSP; 1.
KW Developmental protein; Differentiation; Multigene family; Repeat;
KW Spermatogenesis.
FT COMPBIAS 2 74 Cys/Gly/Pro-rich.
FT CONFLICT 42 42 C -> W (in Ref. 1).
FT CONFLICT 60 60 P -> L (in Ref. 1).
SQ SEQUENCE 74 AA; 6725 MW; CC6FF07A7B7CABC CRC64;

Query Match 100.0%; Score 31; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 38
Q5TW29_NOCFA PRELIMINARY; PRT; 75 AA.
ID 05YW29;
AC Q5YW29;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative ferredoxin.
GN OrderedLocustNames=hf24450;
OS Nocardia fasciata.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Nocardia.
OX NCBI_TaxID=37329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=IFM 10152;
RX PubMed=15466710; DOI=10.1073/pnas.0406410101;
RA Ishikawa J., Yamashita A., Mikami Y., Hoshino Y., Kurita H., Hotta K.,
RA Shiba T., Hattori M.,
RT "The complete genomic sequence of Nocardia fasciata IFM 10152."
RT Proc. Natl. Acad. Sci. U.S.A. 101:14925-14930(2004).
DR EMBL: AP006618; BAD57292.1; -; Genomic DNA.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam: PF00037; Fer4; 2.
DR PRINTS: PR00353; 4FE4SFRDOXIN.
DR PROSITE: PS00198; 4FE4S_FERRDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Transport.
SQ SEQUENCE 75 AA; 8193 MW; F6994795E7B2D209 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 54 CGPC 57

RESULT 39
Q82DW2_STRAW PRELIMINARY; PRT; 75 AA.
ID 082DW2;
AC Q82DW2;

```

```

DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative ferredoxin.
GN Name=fdx; OrderedLocustNames=SAV4856;
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis."
RT Nat. Biotechnol. 21:526-531(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osomoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites."
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [3]
RC EMBL: BA000030; BAC72568.1; -; Genomic DNA.
DR HSSP: P00214; IPRM.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0005506; F:iron ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR001450; 4Fe4S_Fe_S_bd.
DR Pfam: PF00037; Fer4; 2.
DR PRINTS: PR00353; 4FE4SFRDOXIN.
DR PROSITE: PS00198; 4FE4S_FERRDOXIN; 1.
KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
KW Metal-binding; Transport.
SQ SEQUENCE 75 AA; 8139 MW; 8070930081708437 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 54 CGPC 57

RESULT 40
Q4RP51_TETNG PRELIMINARY; PRT; 75 AA.
ID 04RP51;
AC 04RP51;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome 1 SCAFL5008, whole genome shotgun sequence.
GN ORFNames=GSTENG00031275001;
OS Tetradon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Uallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Coetz C., Benoit A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Davila C., Salanoubat M., Levy M., Boudet N., Castellano S.,

```

RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
 RA Bismont C., Skalli Z., Cattolico L., Poulain J., De Bernardis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volf J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Lander P., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissbach J., Roest Crollius H.,
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype.",
 RL Nature 431:946-957(2004).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAB0105008; CAG09831.1; -; Genomic DNA.
 SQ SEQUENCE 75 AA; 7913 MW; 4918F75E5D548359 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 75;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 17 CGPC 20

RESULT 41
 O6UYH8_9CAUD
 ID O6UYH8_9CAUD PRELIMINARY; PRT; 76 AA.
 AC O6UYH8;

DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Putative head-tail joining protein.
 OS Burkholderia cepacia phage BcepHagZu1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
 OK NCBI_TaxID=242861;

RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Sumner E.J., Peek M.L., Halburton J.R., Hall E., Heusinkveld K.,
 RA Simser J., No E.G., Gonzalez C.F., Young R.F.,
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A3535782; AA063363.1; -; Genomic DNA.
 DR GO; GO:0019067; P:Viral assembly, maturation, egress, and rel. .; IEA.
 DR InterPro; IPR004174; gpW.
 DR ProDom; PD019366; gpW; 1.
 SQ SEQUENCE 76 AA; 8345 MW; 9DBFDD73E5A96799 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 60 CGPC 63

RESULT 42
 Q7A114_MYCPA
 ID Q7A114_MYCPA PRELIMINARY; PRT; 76 AA.
 AC Q7A114;

DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=WAP1106;
 OS Mycobacterium paratuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;

OC Mycobacterium avium complex (MAC).
 OK NCBI_TaxID=1770;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=k10;
 RA Li U., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.,
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017230; AAS03423.1; -; Genomic DNA.
 DR HSSP; P00214; 1B0T.

DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0005506; F:iron ion binding; IEA.
 DR GO; GO:0046872; F:metal ion binding; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR001450; 4Fe4S_Fe_s_bd.
 DR Pfam; PF00037; Fer4; 2.
 DR PRINTS; PR00353; 4FE4SFRDOXIN.
 DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 KW 4Fe-4S; Complete proteome; Electron transport; Iron; Iron-sulfur;
 KW Metal-binding; Transport.
 SQ SEQUENCE 76 AA; 8289 MW; 8CF5D7803DB838F6 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 76;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 55 CGPC 58

RESULT 43
 O8XHP3_CLOPE
 ID O8XHP3_CLOPE PRELIMINARY; PRT; 77 AA.
 AC O8XHP3;

DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Probable glutaredoxin.
 GN OrderedLocusNames=CPE2439;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OK NCBI_TaxID=1502;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=13 / Type A;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hatcori M., Kohara S., Hayashi H.,
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL; BA000016; BAB82145.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR011911; G1rx_Yrnb.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR TRIFPAMS; TIGR02196; G1rx_Yrnb; 1.
 KW Complete proteome.
 SQ SEQUENCE 77 AA; 8641 MW; 3337E0EB2A301508 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 DB 10 CGPC 13

RESULT 44
 Q4S047_TETNG
 ID Q4S047_TETNG PRELIMINARY; PRT; 77 AA.
 AC Q4S047;

AC Q4S47;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAR14576, whole genome shotgun sequence.
 GN ORFNames=GSTEN00017363001;
 OS Tetradonca nigrovittata (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetradontiformes;
 OC Tetradontidae; Tetradontidae; Tetradont.
 NC NCB1_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lucifalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Blemont C., Skalli Z., Catellico L., Poulain J., De Berardinis V.,
 RA Crnaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volt J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RA "Genome duplication in the teleost fish Tetradonca nigrovittata reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAEB01014576; CAF99335.1; -; Genomic DNA.
 SQ SEQUENCE 77 AA; 9043 MW; 25F48C1751A7D3A3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 ||||
 Db 25 CGPC 28

RESULT 45
 OSYUM5_DROME PRELIMINARY; PRT; 80 AA.
 ID OSYUM5_DROME PRELIMINARY; PRT; 80 AA.
 AC OSYUM5;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE CG13245-PA.
 GN Name=CG13245; ORFNames=CG13245;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidae; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20196006; PubMed=10731132, DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 RA Abiri J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balow R.M., Baxendale J., Bayraktoglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.A., Bouck J., Brokstein P., Broctier P.,
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RA "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celinker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktoglu L., Berman B.P.,
 RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celinker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]

```

RP NUCLEOTIDE SEQUENCE.
RG Flybase:
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
CC -i- INTERACTION:
CC Q9X7N4:bx; NDExp=1; IntAct=EBI-85165, EBI-159245;
CC CC Q9VVA1:CG9706; NDExp=1; IntAct=EBI-85165, EBI-177365;
DR EMBL; A8003649; AAF53497.1; -; Genomic_DNA.
DR Intact; Q9VJMS; -.
DR Ensemble; CG13245; Drosophila melanogaster.
DR Flybase; FBgn0045827; CG13245.
SQ SEQUENCE 80 AA; 8815 MW; EB813234878838A0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 46
Q95JG5_BOVIN PRELIMINARY; PRT; 80 AA.
AC Q95JG5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Natural killer cell receptor group D variant 2 (Fragment).
GN Name=KLR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2131526; Pubmed=11457486; DOI=10.1016/S0165-2427(01)00295-1;
RA Govaerts M.M., Goddeeris B.M.; cell receptors NKG2-D and NKR-P1
RT "Homologues of natural killer cell receptors NKG2-D and NKR-P1
RT expressed in cattle.";
RL Vet. Immunol. Immunopathol. 80:339-344(2001).
DR EMBL; AF322885; AAK73810.1; -; mRNA.
DR HSSP; O54709; 1H08.
DR SMR; Q95JG5; 1-80.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreezeit.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEIT.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
DR KEGG; K00007; Gly_knot.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9401 MW; 87A0D11CB3CB5FA0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 47
Q95JG6_BOVIN PRELIMINARY; PRT; 80 AA.
AC Q95JG6;
DT 01-DEC-2001 (Tremblrel. 19, Created)

```

```

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Natural killer cell receptor group D variant 1 (Fragment).
GN Name=KLR;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=2131526; Pubmed=11457486; DOI=10.1016/S0165-2427(01)00295-1;
RA Govaerts M.M., Goddeeris B.M.;
RT "Homologues of natural killer cell receptors NKG2-D and NKR-P1
RT expressed in cattle.";
RL Vet. Immunol. Immunopathol. 80:339-344(2001).
DR EMBL; AF322884; AAK73809.1; -; mRNA.
DR HSSP; O54709; 1H08.
DR SMR; Q95JG6; 1-80.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR002353; Antifreezeit.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin_C; 1.
DR PRINTS; PR00356; ANTIFREEZEIT.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PSS0041; C_TYPE_LLECTIN_2; 1.
DR KEGG; K00007; Gly_knot.
FT NON_TER 1
FT NON_TER 80
SQ SEQUENCE 80 AA; 9429 MW; 87A0D11CA1405FA0 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 48
Q63013_RAT PRELIMINARY; PRT; 80 AA.
AC Q63013;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Testicular luteinizing hormone beta subunit.
GN Name=TLHB3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
OC Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague Dawley;
RX MEDLINE=95283549; Pubmed=7763258;
RA Zhang F.P., Rannikko A., Huttanen L.;
RT "Isolation and characterization of testis-specific cDNAs for
RT luteinizing hormone beta-subunit in the rat.";
RL Biochem. Biophys. Res. Commun. 210:858-865(1995).
DR EMBL; U25803; AAC52251.1; -; mRNA.
DR PIR; I65235; 165235.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.

```


DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
SQ SEQUENCE 80 AA; 8515 MW; F9EA66C2FD6FC97D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 49
Q4T7B7 TETNG PRELIMINARY; PRT; 80 AA.
ID Q4T7B7 TETNG PRELIMINARY; PRT; 80 AA.
AC Q4T7B7 TETNG PRELIMINARY; PRT; 80 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DE Chromosome undetermined SCAR8161, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GFENNG0005813001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicand S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
Dasilva C., Salanoubat M., Levy M., Boude N., Castellano S.,
Antouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
Biemont C., Skali Z., Catolico L., Poulin J., De Bernardis V.,
Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Parra G., Lardier G., Chapelle C., McKernan K.J., McMan P., Bosak S.,
Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
Lauder V., Schacher V., Quattler F., Saurin W., Scapellato C.,
Wincker P., Schachter V., Weissenbach J., Roest Crollins H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAAB01008161; CAF91215.1; -; Genomic_DNA.
FT NON TER 1 1
FT NON TER 80 80
SQ SEQUENCE 80 AA; 8611 MW; 64705ABEA4A5620E CRC64;

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 50
O46622 CERSI PRELIMINARY; PRT; 82 AA.
ID O46622 CERSI PRELIMINARY; PRT; 82 AA.
AC O46622 CERSI PRELIMINARY; PRT; 82 AA.
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Luteinizing hormone beta-subunit (Fragment).

GN Name=LH-beta;
OS Ceratotherium simum simum.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Rhinocerotidae;
OC Ceratotherium.
OX NCBI_TaxID=73337;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047607; AAC04365.1; -; Genomic_DNA.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHF; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
FT NON TER 1 1
SQ SEQUENCE 82 AA; 8643 MW; 270411BA19B78A37 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 51 CGPC 54

RESULT 51
Q4ZC47 9VIRU PRELIMINARY; PRT; 83 AA.
ID Q4ZC47 9VIRU PRELIMINARY; PRT; 83 AA.
AC Q4ZC47 9VIRU PRELIMINARY; PRT; 83 AA.
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE ORF063.
OS Bacteriophage EW.
OC Viruses.
OX NCBI_TaxID=320841;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15788529; DOI=10.1073/pnas.0501140102;
RA Kwan T., Liu J., Dubow M., Gros P., Pelletier J.;
RT "The complete genomes and proteomes of 27 *Staphylococcus aureus*
bacteriophages";
RL Proc. Natl. Acad. Sci. U.S.A. 102:5174-5179 (2005).
DR EMBL; AY954959; AAX91390.1; -; Genomic_DNA.
SQ SEQUENCE 83 AA; 8546 MW; 710C2C35BBA2C31 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 51 CGPC 54

RESULT 52
O60744 HUMAN PRELIMINARY; PRT; 84 AA.
ID O60744 HUMAN PRELIMINARY; PRT; 84 AA.
AC O60744 HUMAN PRELIMINARY; PRT; 84 AA.
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Thiorodoxin delta 3 (Fragment).
GN Name=TXN delta 3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=liver;
RA Wang Y., Wang Y.G., Zhang Y., Yuan Y., Ma D.;
RT "An alternative splice variant of human thioredoxin.";
RL Chin. Sci. Bull. 43:292-295(1998).
DR EMBL: AF65241; AAC17430.1; --; mRNA.
DR HSSP: P10599; IERT.
DR SMK: O60744; 1-84.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR InterPro: IPR006662; Thiredox.
DR InterPro: IPR006663; Thiredox_dom2.
DR InterPro: IPR012336; Thiredoxin-like.
DR InterPro: IPR012335; Thiredoxin_fold.
DR Pfam: PF00085; Thiredoxin_1.
DR PRINTS: PR00421; THIOREDOXIN.
DR PROSITE: PS00194; THIOREDOXIN, 1.
KM Redox-active center. 1
FT NON_TER
SQ SEQUENCE 84 AA; 9321 MW; 818FB84BA86E5721 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 31 CGPC 34

RESULT 53
Q6J821_9VIRU
ID Q6J821_9VIRU PRELIMINARY; PRT; 84 AA.
AC Q6J821;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Pas10.
GN Name=Pas10;
OS Actinoplanes phage phiAsp2.
OC Viruses.
OX NCBI_TaxID=279303;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15215690; DOI=10.1023/B:VIRU.0000032795.17713.6c;
RA Jarling M., Bartkowiak K., Pape H., Meinhardt F.;
RT "The genome of phiAsp2, an Actinoplanes infecting phage.";
RL Virus Genes 29:117-129(2004).
DR EMBL: AY576796; AY136758.1; --; Genomic DNA.
DR SQUEL: 84 AA; 8995 MW; C1ECF12181EB7C72 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 54
Q6MWB8_ORYSA
ID Q6MWB8_ORYSA PRELIMINARY; PRT; 84 AA.
AC Q6MWB8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE B1358B12.4 protein.
GN Name=B1358B12.4;

```

```

OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=59947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=12447439; DOI=10.1038/nature01183;
RA Fang Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
RA Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
RA Weng Q., Zhang L., Lu Y., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
RA Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
RA Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
RA Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
RA Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
RA Yan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
RA Han B.;
RT "Sequence and analysis of rice chromosome 4.";
RL Nature 420:316-320(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Han B., Peng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Liu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX842605; CAE75995.1; --; Genomic DNA.
DR Gramene; Q6MWB8; --;
DR InterPro: IPR006461; DUF_A_thal_Cys.
DR Pfam: PF04749; PLAC8; 1.
SQ SEQUENCE 84 AA; 9417 MW; F0B45C9C390BC7C9 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 37 CGPC 40

RESULT 55
Q16275_HUMAN
ID Q16275_HUMAN PRELIMINARY; PRT; 85 AA.
AC Q16275;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Type I hair keratin (fragments).
GN Name=Type I hair keratin (fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95092656; PubMed=7528047;
RA Bowden P.E., Hainey S., Parker G., Hodgins M.B.;
RT "Sequence and expression of human hair keratin genes.";
RL J. Dermatol. Sci. 7:0-0(0).
CC -1- SIMILARITY: Belongs to the intermediate filament family.
DR EMBL: S75797; AAB32812.1; --; Genomic DNA.
DR GO: GO:0005882; C:intermediate filament; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001664; IF.
DR Pfam: PF00038; Filament; 1.

```

DR PROSITE; PS00226; IF; 1.
 KW Intermediate filament; Keratin.
 FT NON TER 85
 SQ SEQUENCE 85 AA; 9314 MW; 4041BBDFOCC18414 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 77 CGPC 80

RESULT 56
 O5T936 HUMAN PRELIMINARY; PRT; 85 AA.
 ID O5T936;
 AC O5T936;
 DT 01-FEB-2005 (TRENBLREL. 29, Created)
 DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
 DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
 DE Thioresdoxin.
 GN Name=TXN; ORFNames=RP11-427L11.1-002;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Williams S.;
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A1158158; CAL14067.1; -; Genomic_DNA.
 DR SRR; O5T936.1-85
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiores.
 DR InterPro; IPR006663; Thioresdoxin-dom2.
 DR InterPro; IPR012336; Thioresdoxin-like.
 DR Pfam; PF00085; Thioresdoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Redox-active center.
 SQ SEQUENCE 85 AA; 9452 MW; 3CC6254BD6A1D66F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 32 CGPC 35

RESULT 57
 O8W710 9CAUD PRELIMINARY; PRT; 87 AA.
 ID O8W710;
 AC O8W710;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Thioresdoxin C3.
 OS Cyanophage P60.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
 OX NCBI_TaxID=151528;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21972319; PubMed=11976141;
 RX DOI=10.1128/AEM.68.5.2589-2594.2002;
 RA Chen F., Lu J.;
 RT "Genomic sequence and evolution of marine cyanophage P60: a new
 insight on lytic and lysogenic phages.";
 Appl. Environ. Microbiol. 68:2589-2594 (2002).
 RL

DR EMBL; AF38467; AAL73267.1; -; Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiores.
 DR PRINTS; PR00421; THIOREDOXIN.
 SQ SEQUENCE 87 AA; 9991 MW; FFBCC315381DD7FBI CRC64;

Query Match 100.0%; Score 31; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 14 CGPC 17

RESULT 58
 O9C922 ARATH PRELIMINARY; PRT; 87 AA.
 ID O9C922;
 AC O9C922;
 DT 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Putative thioresdoxin; 109829-109566.
 GN Name=FLG24.26;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Romming C.M., Koo H., Fujii C.Y., Uteback T.R.,
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Town C.D., Kaul S.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC019018; AAG52290.1; -; Genomic_DNA.
 DR HSSP; P23400; 1DBY.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiores.
 DR InterPro; IPR006663; Thioresdoxin-dom2.
 DR InterPro; IPR012336; Thioresdoxin-like.
 DR InterPro; IPR012335; Thioresdoxin_fold.
 DR Pfam; PF00085; Thioresdoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 87 AA; 10318 MW; 5ABBB56E7A44189 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 13 CGPC 16

RESULT 59
 TH102 DICDI STANDARD; PRT; 88 AA.
 ID TH102 DICDI;
 AC P29446;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Thioresdoxin 2 (Fragment).
 GN Name=trxB; Synonyms=trxB;
 OS Dictyostelium discoideum (slime mold).
 OC Eukaryota; Metazoa; Dictyostelida; Dictyostelium.

```

OX NCBI_TaxID=44689;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92250653; PubMed=1577820;
RA Wettreiner B., Jacquot J.-P., Veron M.;
RT "Thioredoxins from Dictyostelium discoideum are a developmentally
regulated multigene family."
RL J. Biol. Chem. 267:9895-9904(1992).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M91382; AAA33259.1; -; mRNA.
DR FTR; B46264; B46264.
DR HSSP; P10599; IERV.
DR DictyBase; DDB0001983; TRX2.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredoxin-dom2.
DR InterPro; IPR012335; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin-fold.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN_1.
DR Electron transport; Multigene family; Redox-active center; Transport.
KM ELECTRON_TRANSPORT; Multigene family; Redox-active center; Transport.
FT ACT_SITE 31 31 Nucleophile (By similarity).
FT ACT_SITE 34 34 Nucleophile (By similarity).
FT SITE 25 25 Deprotonates C-terminal active site Cys
FT SITE 32 32 (By similarity).
FT SITE 32 32 Contributes to redox potential value (By
FT SITE 32 32 similarity).
FT SITE 33 33 Contributes to redox potential value (By
FT SITE 33 33 similarity).
FT DISULFID 31 34 Redox-active (By similarity).
FT NON_TER 88 88
SQ SEQUENCE 88 AA; 10103 MW; CEC73BCEFA3B607C CRC64;

Query Match 100.0%; Score 31; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 31 CGPC 34

RESULT 60
Q5V0J2 HALMA PRELIMINARY; PRT; 88 AA.
ID Q5V0J2 HALMA PRELIMINARY; PRT; 88 AA.
AC Q5V0J2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Thioredoxin.
GN Name=trx3; OrderedLocustNames=trAC2110;
OS Haloarcula marismortui (Haloacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RX PubMed=15520287; DOI=10.1101/gr.2700304;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;

```

```

RT "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea."
RL Genome Res. 14:2221-2234(2004).
DR EMBL; AY596297; AAV45961.1; -; Genomic DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR006663; Thioredoxin-dom2.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioredoxin; 1.
DR TIGRFAMs; TIGR01068; thioredoxin; 1.
KW Complete proteome.
SQ SEQUENCE 88 AA; 10011 MW; CFE9B8FAC1F69857 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 13 CGPC 16

RESULT 61
Q8PZ06 METMA PRELIMINARY; PRT; 88 AA.
ID Q8PZ06 METMA PRELIMINARY; PRT; 88 AA.
AC Q8PZ06;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioredoxin.
GN OrderedLocustNames=MM0436;
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Gael / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=2210827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wietzer A., Baumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Seckel S.,
RA Bhattacharya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea."
RT J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
DR EMBL; AE013269; AAM30132.1; -; Genomic DNA.
DR HSSP; P80579; INW2.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thioredoxin-dom2.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR012335; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin-fold.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioredoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN_1.
KW Complete proteome.
SQ SEQUENCE 88 AA; 9914 MW; D448923BF5845FA5 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGPC 5
Db 13 CGPC 16

```

```

RESULT 62
Q71UV5 HORSE
ID Q71UV5_HORSE PRELIMINARY; PRT; 88 AA.
AC Q71UV5;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE luteinizing hormone/chorionic gonadotropin beta-subunit
  (Fragment).
GN Name=lH/CG-beta;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OC NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (PEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047604; AAC04362.1; -; Genomic DNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .); IEA.
DR InterPro; IPR006208; Cys knot.
DR Pfam; PF00007; Cys knot; 1.
DR SMART; SM00068; GHF; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Chorion.
FT NON TER 1 1
FT NON TER 88 88
SQ SEQUENCE 88 AA; 9153 MW; 32E7DB6CF7B1C9CF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 43 CGPC 46

RESULT 63
Q62H93 BURMA PRELIMINARY; PRT; 88 AA.
ID Q62H93_BURMA PRELIMINARY; PRT; 88 AA.
AC Q62H93;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Hypothetical protein
  OrderedLocNames=BMA2369;
GN Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 23344;
RC PubMed=15377793; DOI=10.1073/pnas.040306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidson T.D., DeBoy R.T., Dmitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolony J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarría S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
DR EMBL; CP000010; AAU50201.1; -; Genomic DNA.
DR TIGR; BMA2369; -;
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 88 AA; 9445 MW; 7AD511CDB7B2BCD6 CRC64;

```

```

Query Match 100.0%; Score 31; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 72 CGPC 75

RESULT 64
Q9HMD0 HALSA PRELIMINARY; PRT; 89 AA.
ID Q9HMD0;
AC Q9HMD0;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE Thioredoxin.
GN Name=trxA2; OrderedLocNames=VNG2600G;
OS Halobacterium salinarum (Halobacterium halobium).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
RA Ng W.V., Kennedy S.P., Mahaisra G.G., Bergquist B., Pan M.,
RA Shukla H.D., Laszky S.R., Baliga N.S., Thorsson V., Shrogha J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Geo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocke D.G., Jablonski P.E., Krebs M.P., Angewine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Edhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005133; AAG20641.1; -; Genomic DNA.
DR PIR; B84409; B84409.
DR HSSP; P10599; IERY.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR006663; Thioredox_dom2.
DR Pfam; PF00085; Thioredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioredoxin; 1.
KW Complete proteome.
SQ SEQUENCE 89 AA; 10019 MW; BDF97B3496F70BFF CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 13 CGPC 16

RESULT 65
Q46618 EQUZE PRELIMINARY; PRT; 89 AA.
ID Q46618_EQUZE PRELIMINARY; PRT; 89 AA.
AC Q46618;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE luteinizing hormone/chorionic gonadotropin beta-subunit
  (Fragment).
GN Name=lH/CG-beta;
OS Equus zebra hartmannae.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

```

```

OX NCBI_TaxID=73335;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047602; AAC04360.1; -; Genomic_DNA.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:structural constituent of chorion (sensu In. . .; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormonB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Chorton.
FT NON_TER
FT TER
SQ SEQUENCE 89 AA; 9325 MW; 2AD973AECTEAC5C8 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 66
046619 EQUHM PRELIMINARY; PRT; 89 AA.
ID 046619 EQUHM PRELIMINARY;
AC 046619;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Lutealizing hormone/chorionic gonadotrophin beta-subunit
DE (Fragment).
GN Name=LH/CG-beta;
OS Equus hemionus (Kulan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9794;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Fischer S., Velts J., Meyer H.H.D.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF047603; AAC04361.1; -; Genomic_DNA.
DR HSSP; P01233; 1HCN.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0005213; F:structural constituent of chorion (sensu In. . .; IEA.
DR InterPro; IPR006208; Cys_knot.
DR InterPro; IPR001545; Gly_hormonB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KM Chorton.
FT NON_TER
FT TER
SQ SEQUENCE 89 AA; 9369 MW; E0EEF73778C5566 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 50 CGPC 53

RESULT 67
04HCJ2_9DEIO

```

```

ID 04HCJ2_9DEIO PRELIMINARY; PRT; 89 AA.
AC 04HCJ2;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=DgeODRAFT_2284;
OS Deinococcus geothermophilus DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=DSM 11300;
RC US DOE Joint Genome Institute (JGI-PGF);
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Deter C., Glavina T.,
RA Hammon N., Istrati S., Peticola S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermophilus
RT DSM 11300."
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermophilus
RT DSM 11300."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHE0100001; EAL84178.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 89 AA; 9776 MW; 1ABEA48510AB827A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 65 CGPC 68

RESULT 68
04LEN8 PAROL PRELIMINARY; PRT; 89 AA.
ID 04LEN8 PAROL PRELIMINARY;
AC 04LEN8;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hepcidin 2;
GN Name=JF-hep 2;
OS Paralichthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hirono I., Nozaki R., Ono Y., Kurobe T., Ohira T., Aoki T.;
RT "Two different types of hepcidins from Japanese flounder Paralichthys
RT olivaceus."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB198063; BAB06235.1; -; Genomic_DNA.
SQ SEQUENCE 89 AA; 9729 MW; 04CBB16152953F00 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

```

Db 83 CGPC 86

RESULT 69

Q4LEPO_PAROL PRELIMINARY; PRT; 89 AA.
 AC Q4LEPO;
 DT 13-SRP-2005 (TREMBlrel. 31, Created)
 DT 13-SRP-2005 (TREMBlrel. 31, last sequence update)
 DT 13-SRP-2005 (TREMBlrel. 31, last annotation update)
 DE Hepcidin 2.
 GN Name=JF-hep 2;
 OS Paralicthys olivaceus (Japanese flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
 OC Pleuronectoidae; Paralicthyidae; Paralicthys.
 OX NCBI_TaxID=8255;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hirono I., Nozaki R., Ono Y., Kurobe T., Ohira T., Aoki T.;
 RT "Two different types of hepcidins from Japanese Flounder Paralicthys
 RT olivaceus.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB198061; BAE06233.1; -; mRNA.
 SQ SEQUENCE 89 AA; 9771 MW; D9AE7173C29CB412 CRC64;

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 89;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 83 CGPC 86

RESULT 70

Q7RS22_GIALA PRELIMINARY; PRT; 90 AA.
 AC Q7RS22;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
 DE GIP 81 67830 68102.
 OS Giardia lamblia ATCC 50803.
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
 OX NCBI_TaxID=184922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=WB C6;
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
 RA Olsen G.J., Sogin M.L.;
 RT "Draft sequence of the Giardia lamblia genome."
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AACB0100003; EAA42709.1; -; Genomic DNA.
 SQ SEQUENCE 90 AA; 10714 MW; D84C3117BA31834 CRC64;

Query Match

Best Local Similarity 100.0%; Score 31; DB 2; Length 90;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
 Db 74 CGPC 77

Search completed: February 23, 2006, 00:41:45
 Job time : 177.5 secs

This Page Blank (133010)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:19 ; Search time 34.5 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-10-660-118a-2

Perfect score: 31
Sequence: 1 XCGPCX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/iaa/5 COMB.pep:*
2: /cgn2_6/prodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/prodata/1/iaa/H-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/PCTUS-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/RE-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	4	1	US-07-820-688A-5 Sequence 5, Appl1
2	31	100.0	4	1	US-08-274-043B-5 Sequence 5, Appl1
3	31	100.0	4	1	US-08-386-729A-5 Sequence 5, Appl1
4	31	100.0	4	1	US-08-687-276-3 Sequence 2, Appl1
5	31	100.0	4	1	US-08-883-804-2 Sequence 21, Appl1
6	31	100.0	4	2	US-08-504-538A-21 Sequence 1, Appl1
7	31	100.0	4	2	US-09-579-883A-1 Sequence 2, Appl1
8	31	100.0	4	2	US-09-679-705-2 Sequence 4, Appl1
9	31	100.0	6	1	US-08-883-804-4 Sequence 5, Appl1
10	31	100.0	6	1	US-08-883-804-5 Sequence 6, Appl1
11	31	100.0	6	2	US-08-627-907A-6 Sequence 3, Appl1
12	31	100.0	6	2	US-07-801-713A-3 Sequence 27, Appl1
13	31	100.0	8	1	US-08-571-985-27 Sequence 27, Appl1
14	31	100.0	8	1	US-09-116-766-27 Sequence 34, Appl1
15	31	100.0	8	2	US-08-836-480-34 Sequence 34, Appl1
16	31	100.0	8	2	US-09-562-897-34 Sequence 34, Appl1
17	31	100.0	12	2	US-08-750-142B-54 Sequence 217, Appl1
18	31	100.0	16	2	US-09-160-513-217 Sequence 217, Appl1
19	31	100.0	28	2	US-09-230-041-31 Sequence 31, Appl1
20	31	100.0	29	2	US-09-881-572A-25 Sequence 25, Appl1
21	31	100.0	30	2	US-09-881-572A-25 Sequence 5, Appl1
22	31	100.0	35	2	US-10-044-359-26 Sequence 26, Appl1
23	31	100.0	38	1	US-08-239-256-16 Sequence 16, Appl1
24	31	100.0	43	2	US-09-244-583-20 Sequence 20, Appl1
25	31	100.0	44	2	US-09-583-638-11 Sequence 11, Appl1
26	31	100.0	45	2	US-09-579-420B-11 Sequence 1, Appl1
27	31	100.0	50	2	US-09-579-420B-19 Sequence 19, Appl1

28	31	100.0	51	2	US-09-513-999C-7252 Sequence 7252, Ap
29	31	100.0	53	2	US-09-513-999C-5904 Sequence 5904, Ap
30	31	100.0	67	2	US-09-513-999C-5905 Sequence 5905, Ap
31	31	100.0	77	2	US-09-902-540-11828 Sequence 11828, A
32	31	100.0	89	2	US-09-630-273-2 Sequence 2, Appl1
33	31	100.0	80	2	US-09-621-976-6168 Sequence 6168, Ap
34	31	100.0	102	2	US-09-198-452A-697 Sequence 697, App
35	31	100.0	102	2	US-09-621-976-5629 Sequence 5629, Ap
36	31	100.0	103	1	US-08-241-853-27 Sequence 27, Appl1
37	31	100.0	103	1	US-08-850-917-27 Sequence 27, Appl1
38	31	100.0	104	2	US-09-583-110-3078 Sequence 3078, Ap
39	31	100.0	104	6	5210073-1 Patent No. 5210073
40	31	100.0	105	1	US-08-826-910-3 Sequence 3, Appl1
41	31	100.0	105	2	US-08-826-910-4 Sequence 4, Appl1
42	31	100.0	105	2	US-09-601-144-68 Sequence 68, Appl1
43	31	100.0	105	2	US-09-513-999C-8037 Sequence 8037, Ap
44	31	100.0	106	1	US-08-386-729A-10 Sequence 10, Appl1
45	31	100.0	106	2	US-09-383-586-13 Sequence 13, Appl1
46	31	100.0	106	2	US-09-823-038A-22 Sequence 22, Appl1
47	31	100.0	109	1	US-07-745-382-22 Sequence 22, Appl1
48	31	100.0	109	1	US-07-921-848-22 Sequence 22, Appl1
49	31	100.0	109	1	US-08-165-301A-22 Sequence 22, Appl1
50	31	100.0	109	1	US-08-165-301A-26 Sequence 26, Appl1
51	31	100.0	109	1	US-08-165-301A-28 Sequence 28, Appl1
52	31	100.0	109	2	US-08-810-436-22 Sequence 22, Appl1
53	31	100.0	109	2	US-08-810-436-26 Sequence 26, Appl1
54	31	100.0	109	2	US-08-810-436-28 Sequence 28, Appl1
55	31	100.0	109	2	US-09-485-885-17 Sequence 17, Appl1
56	31	100.0	109	2	US-09-166-966E-10 Sequence 10, Appl1
57	31	100.0	109	2	US-09-248-796A-19911 Sequence 19911, A
58	31	100.0	109	4	PCT-US94-14179-26 Sequence 22, Appl1
59	31	100.0	109	4	PCT-US94-14179-26 Sequence 26, Appl1
60	31	100.0	109	4	PCT-US94-14179-28 Sequence 28, Appl1
61	31	100.0	110	2	US-09-621-976-4028 Sequence 4028, Ap
62	31	100.0	111	2	US-09-264-416C-6 Sequence 6, Appl1
63	31	100.0	111	2	US-09-134-001C-3859 Sequence 3859, Ap
64	31	100.0	112	2	US-09-107-532A-6739 Sequence 6739, Ap
65	31	100.0	113	2	US-10-104-047-3199 Sequence 3199, Ap
66	31	100.0	114	2	US-08-918-288-71 Sequence 71, Appl1
67	31	100.0	114	2	US-09-282-357-71 Sequence 71, Appl1
68	31	100.0	114	2	US-09-897-425-41 Sequence 41, Appl1
69	31	100.0	114	2	US-09-107-433-2930 Sequence 2930, Ap
70	31	100.0	114	2	US-09-786-715-11 Sequence 11, Appl1
71	31	100.0	116	2	US-09-882-835-5 Sequence 5, Appl1
72	31	100.0	118	2	US-09-786-715-4 Sequence 4, Appl1
73	31	100.0	118	2	US-09-786-715-10 Sequence 10, Appl1
74	31	100.0	118	2	US-09-786-715-13 Sequence 13, Appl1
75	31	100.0	120	2	US-09-438-185A-661 Sequence 661, App
76	31	100.0	120	2	US-09-786-715-6 Sequence 6, Appl1
77	31	100.0	121	2	US-10-360-101-251 Sequence 251, App
78	31	100.0	122	2	US-09-540-014-2 Sequence 2, Appl1
79	31	100.0	122	2	US-09-630-273-1 Sequence 1, Appl1
80	31	100.0	122	2	US-09-543-681A-4397 Sequence 4397, Ap
81	31	100.0	122	2	US-09-513-999C-7856 Sequence 7856, Ap
82	31	100.0	122	2	US-09-538-864-25 Sequence 25, Appl1
83	31	100.0	122	2	US-10-091-841A-2 Sequence 2, Appl1
84	31	100.0	122	2	US-09-786-715-8 Sequence 8, Appl1
85	31	100.0	123	2	US-09-489-039A-8017 Sequence 8017, Ap
86	31	100.0	124	2	US-09-603-208A-70 Sequence 70, Appl1
87	31	100.0	124	2	US-09-949-016-9663 Sequence 9663, Ap
88	31	100.0	125	2	US-09-902-540-12427 Sequence 12427, A
89	31	100.0	125	2	US-09-786-715-12 Sequence 12, Appl1
90	31	100.0	126	2	US-09-540-014-4 Sequence 4, Appl1
91	31	100.0	127	2	US-09-621-976-6292 Sequence 6292, Ap
92	31	100.0	127	2	US-10-091-841A-4 Sequence 4, Appl1
93	31	100.0	129	2	US-10-104-047-2145 Sequence 2145, Ap
94	31	100.0	130	1	US-08-826-910-1 Sequence 1, Appl1
95	31	100.0	130	2	US-09-540-014-6 Sequence 6, Appl1
96	31	100.0	130	2	US-10-091-841A-6 Sequence 6, Appl1
97	31	100.0	134	2	US-08-543-246B-20 Sequence 20, Appl1
98	31	100.0	134	2	US-09-272-342B-5 Sequence 5, Appl1
99	31	100.0	137	2	US-08-961-083-40 Sequence 40, Appl1
100	31	100.0			

101	31	100.0	137	2	US-09-536-784-40	Sequence 40, Appl	174	31	100.0	215	2	US-09-468-647A-105	Sequence 105, App
102	31	100.0	137	2	US-09-765-271-40	Sequence 40, Appl	175	31	100.0	215	6	5219739-22	Patent No. 5219739
103	31	100.0	137	2	US-09-328-272A-40	Sequence 40, Appl	176	31	100.0	215	6	5240848-7	Patent No. 5240848
104	31	100.0	145	2	US-09-328-352-5360	Sequence 5360, Ap	177	31	100.0	216	2	US-08-543-248B-9	Sequence 9, Appl1
105	31	100.0	145	2	US-09-523-323-59	Sequence 59, Appl	178	31	100.0	216	2	US-08-543-248B-24	Sequence 24, Appl
106	31	100.0	146	2	US-08-469-260A-520	Sequence 520, App	179	31	100.0	223	2	US-09-949-002-508	Sequence 508, App
107	31	100.0	147	2	US-08-488-446-520	Sequence 520, App	180	31	100.0	224	2	US-10-104-047-3343	Sequence 3343, Ap
108	31	100.0	147	2	US-08-467-344A-520	Sequence 520, App	181	31	100.0	231	4	PCT-US96-09001-10	Sequence 10, Appl
109	31	100.0	147	2	US-08-424-550B-520	Sequence 520, App	182	31	100.0	232	1	US-08-824-966-9	Sequence 9, Appl1
110	31	100.0	149	1	US-08-425-673-5	Sequence 5, Appl1	183	31	100.0	232	1	US-08-824-966-9	Sequence 9, Appl1
111	31	100.0	152	2	US-09-270-767-62449	Sequence 62449, A	184	31	100.0	232	2	US-08-807-992B-4	Sequence 4, Appl1
112	31	100.0	159	2	US-09-166-966E-8	Sequence 8, Appl1	185	31	100.0	232	2	US-09-042-105-7	Sequence 7, Appl1
113	31	100.0	160	2	US-09-489-039A-11628	Sequence 11628, A	186	31	100.0	232	2	US-09-574-708A-10	Sequence 10, Appl
114	31	100.0	163	2	US-09-949-016-10680	Sequence 10680, A	187	31	100.0	232	2	US-09-532-310B-4	Sequence 4, Appl1
115	31	100.0	164	6	5194596-17	Patent No. 5194596	188	31	100.0	232	2	US-08-465-968-5	Sequence 5, Appl1
116	31	100.0	164	6	5219739-17	Patent No. 5219739	189	31	100.0	232	2	US-10-084-488-7	Sequence 7, Appl1
117	31	100.0	164	6	5219739-18	Patent No. 5219739	190	31	100.0	232	2	US-09-897-425-46	Sequence 46, Appl
118	31	100.0	165	2	US-08-882-816-3	Sequence 3, Appl1	191	31	100.0	232	2	US-09-814-982-33	Sequence 33, Appl
119	31	100.0	165	2	US-08-802-052B-3	Sequence 3, Appl1	192	31	100.0	232	2	US-10-268-447-10	Sequence 10, Appl
120	31	100.0	165	2	US-09-706-722A-3	Sequence 3, Appl1	193	31	100.0	234	2	US-08-918-288-9	Sequence 9, Appl1
121	31	100.0	165	6	5194596-19	Patent No. 5194596	194	31	100.0	234	2	US-09-282-357-9	Sequence 9, Appl1
122	31	100.0	165	6	5219739-19	Patent No. 5219739	195	31	100.0	259	2	US-09-270-767-48758	Sequence 48758, A
123	31	100.0	166	1	US-08-775-978-1	Sequence 1, Appl1	196	31	100.0	261	2	US-09-461-325-413	Sequence 413, App
124	31	100.0	166	1	US-08-775-978-3	Sequence 3, Appl1	197	31	100.0	261	2	US-10-012-542-413	Sequence 413, App
125	31	100.0	167	2	US-09-741-243C-4	Sequence 4, Appl1	198	31	100.0	261	2	US-10-115-123-413	Sequence 413, App
126	31	100.0	169	2	US-09-897-425-44	Sequence 44, Appl	199	31	100.0	264	2	US-09-949-016-11555	Sequence 11555, A
127	31	100.0	169	2	US-09-902-540-10496	Sequence 10496, A	200	31	100.0	265	2	US-08-778-717-17	Sequence 17, Appl
128	31	100.0	170	2	US-09-270-767-32473	Sequence 32473, A	201	31	100.0	268	2	US-09-270-767-42351	Sequence 42351, A
129	31	100.0	170	2	US-09-270-767-47690	Sequence 47690, A	202	31	100.0	271	2	US-09-936-019-1	Sequence 1, Appl1
130	31	100.0	173	2	US-09-270-767-32359	Sequence 32359, A	203	31	100.0	282	2	US-09-461-912A-38	Sequence 38, Appl
131	31	100.0	173	2	US-09-270-767-47576	Sequence 47576, A	204	31	100.0	291	2	US-09-949-016-11416	Sequence 11416, A
132	31	100.0	174	2	US-08-311-731A-261	Sequence 261, App	205	31	100.0	296	1	US-07-745-382-14	Sequence 14, Appl
133	31	100.0	177	2	US-09-272-342B-6	Sequence 6, Appl1	206	31	100.0	296	1	US-07-921-848-14	Sequence 14, Appl
134	31	100.0	178	2	US-08-748-506-17	Sequence 17, Appl	207	31	100.0	296	1	US-08-115-680-4	Sequence 4, Appl1
135	31	100.0	183	2	US-09-902-540-11982	Sequence 14982, A	208	31	100.0	296	1	US-07-941-372-4	Sequence 4, Appl1
136	31	100.0	185	2	US-09-583-110-5222	Sequence 5222, Ap	209	31	100.0	296	1	US-08-165-301A-14	Sequence 14, Appl
137	31	100.0	188	2	US-09-252-991A-32934	Sequence 32934, A	210	31	100.0	296	2	US-08-810-436-14	Sequence 14, Appl
138	31	100.0	188	2	US-09-893-737-16	Sequence 16, Appl	211	31	100.0	296	4	PCT-US94-14179-14	Sequence 14, Appl1
139	31	100.0	190	6	5332671-3	Patent No. 5332671	212	31	100.0	296	4	PCT-US94-14179-14	Sequence 14, Appl
140	31	100.0	191	2	US-08-567-200A-2	Sequence 2, Appl1	213	31	100.0	299	2	US-09-286-529-17	Sequence 17, Appl
141	31	100.0	191	2	US-08-807-992B-2	Sequence 2, Appl1	214	31	100.0	300	1	US-08-794-796-2	Sequence 2, Appl1
142	31	100.0	191	2	US-08-691-79A-2	Sequence 2, Appl1	215	31	100.0	300	2	US-09-632-277A-2	Sequence 2, Appl1
143	31	100.0	191	2	US-08-795-430-56	Sequence 56, Appl	216	31	100.0	300	2	US-09-523-323-52	Sequence 52, Appl
144	31	100.0	191	2	US-09-392-932-3	Sequence 3, Appl1	217	31	100.0	300	2	US-09-896-096A-1	Sequence 1, Appl1
145	31	100.0	191	2	US-09-355-700-56	Sequence 56, Appl	218	31	100.0	301	2	US-09-936-019-3	Sequence 3, Appl1
146	31	100.0	191	2	US-08-882-816-2	Sequence 2, Appl1	219	31	100.0	301	2	US-09-252-991A-26483	Sequence 26483, A
147	31	100.0	191	2	US-09-574-708A-6	Sequence 6, Appl1	220	31	100.0	304	2	US-09-397-550-16	Sequence 16, Appl
148	31	100.0	191	2	US-08-802-052B-2	Sequence 2, Appl1	221	31	100.0	310	2	US-09-949-016-7763	Sequence 7763, Ap
149	31	100.0	191	2	US-09-431-888-4	Sequence 4, Appl1	222	31	100.0	321	2	US-08-748-506-10	Sequence 10, Appl
150	31	100.0	191	2	US-09-532-110B-2	Sequence 2, Appl1	223	31	100.0	321	2	US-08-748-506-11	Sequence 11, Appl
151	31	100.0	191	2	US-08-671-573B-55	Sequence 55, Appl	224	31	100.0	321	2	US-08-748-506-12	Sequence 12, Appl
152	31	100.0	191	2	US-09-392-931-6	Sequence 6, Appl1	225	31	100.0	321	2	US-08-748-506-13	Sequence 13, Appl
153	31	100.0	191	2	US-09-631-092B-55	Sequence 55, Appl	226	31	100.0	321	2	US-08-748-506-18	Sequence 18, Appl
154	31	100.0	191	2	US-08-734-443-14	Sequence 14, Appl	227	31	100.0	321	2	US-08-748-506-19	Sequence 19, Appl
155	31	100.0	191	2	US-09-534-376A-56	Sequence 56, Appl	228	31	100.0	321	2	US-08-748-506-20	Sequence 20, Appl
156	31	100.0	191	2	US-10-268-447-6	Sequence 6, Appl1	229	31	100.0	323	2	US-09-397-550-17	Sequence 17, Appl
157	31	100.0	191	6	5332671-4	Patent No. 5332671	230	31	100.0	325	2	US-09-599-360B-74	Sequence 74, Appl
158	31	100.0	192	2	US-09-438-046-10	Sequence 10, Appl	231	31	100.0	329	2	US-09-248-796A-19909	Sequence 19909, A
159	31	100.0	194	2	US-09-107-433-5104	Sequence 5104, Ap	232	31	100.0	330	2	US-09-252-991A-24637	Sequence 24637, A
160	31	100.0	195	2	US-09-902-540-15448	Sequence 15448, A	233	31	100.0	333	2	US-09-949-016-7678	Sequence 7678, Ap
161	31	100.0	196	2	US-09-949-016-7039	Sequence 7039, Ap	234	31	100.0	350	2	US-09-397-550-18	Sequence 18, Appl
162	31	100.0	208	2	US-09-244-583-26	Sequence 26, Appl	235	31	100.0	355	2	US-10-012-896-1011	Sequence 1011, Ap
163	31	100.0	209	2	US-09-166-966E-11	Sequence 11, Appl	236	31	100.0	374	2	US-09-732-615-10	Sequence 10, Appl
164	31	100.0	210	2	US-08-180-371-6	Sequence 6, Appl1	237	31	100.0	374	2	US-10-373-051-10	Sequence 10, Appl
165	31	100.0	210	4	PCT-US92-05707-6	Sequence 6, Appl1	238	31	100.0	380	2	US-08-468-846-2	Sequence 2, Appl1
166	31	100.0	211	4	US-09-286-529-20	Sequence 20, Appl	239	31	100.0	380	2	US-08-915-096A-2	Sequence 2, Appl1
167	31	100.0	214	2	US-09-963-156A-1	Sequence 1, Appl1	240	31	100.0	383	2	US-09-489-039A-11768	Sequence 11768, A
168	31	100.0	214	6	5240848-11	Patent No. 5240848	241	31	100.0	388	2	US-09-949-016-9661	Sequence 9661, Ap
169	31	100.0	215	2	US-08-867-992B-3	Sequence 3, Appl1	242	31	100.0	388	2	US-09-248-796A-17265	Sequence 17265, A
170	31	100.0	215	2	US-08-586-039B-49	Sequence 49, Appl	243	31	100.0	392	2	US-09-764-325A-23	Sequence 23, Appl
171	31	100.0	215	2	US-09-699-769-49	Sequence 49, Appl	244	31	100.0	392	2	US-09-764-325A-23	Sequence 23, Appl
172	31	100.0	215	2	US-09-532-310B-3	Sequence 3, Appl1	245	31	100.0	392	2	US-09-912-935-23	Sequence 23, Appl
173	31	100.0	215	2	US-09-392-931-8	Sequence 8, Appl1	246	31	100.0	392	2	US-09-912-935-25	Sequence 25, Appl

247	31	100.0	404	2	US-09-949-016-6202	Sequence 6202, Ap	320	31	100.0	747	2	US-09-999-833A-459	Sequence 459, App
248	31	100.0	406	2	US-09-543-681A-5458	Sequence 5458, Ap	321	31	100.0	747	2	US-10-020-445A-459	Sequence 459, App
249	31	100.0	408	1	US-08-683-007A-2	Sequence 2, App1	322	31	100.0	765	2	US-09-949-016-10117	Sequence 10117, A
250	31	100.0	416	2	US-09-949-016-6201	Sequence 6201, Ap	323	31	100.0	780	1	US-08-887-799-2	Sequence 2, App1
251	31	100.0	425	2	US-09-252-991A-29556	Sequence 29556, A	324	31	100.0	786	2	US-09-949-016-10898	Sequence 10898, A
252	31	100.0	425	2	US-09-912-935-35	Sequence 35, App1	325	31	100.0	816	2	US-09-949-016-10664	Sequence 10664, A
253	31	100.0	426	2	US-08-675-499A-6	Sequence 6, App1	326	31	100.0	824	2	US-09-626-589-3	Sequence 3, App1
254	31	100.0	426	2	US-08-812-008-6	Sequence 6, App1	327	31	100.0	832	2	US-08-677-734A-12	Sequence 12, App1
255	31	100.0	428	2	US-09-423-340-2	Sequence 2, App1	328	31	100.0	832	2	US-09-097-055-12	Sequence 12, App1
256	31	100.0	428	2	US-09-423-340-2	Sequence 2, App1	329	31	100.0	850	2	US-10-029-180-96	Sequence 96, App1
257	31	100.0	428	2	US-09-820-155-2	Sequence 2, App1	330	31	100.0	858	2	US-10-237-551-92	Sequence 92, App1
258	31	100.0	428	2	US-09-820-155-4	Sequence 4, App1	331	31	100.0	859	2	US-10-029-180-108	Sequence 108, App
259	31	100.0	430	2	US-10-104-047-2204	Sequence 2204, Ap	332	31	100.0	881	2	US-09-489-030A-10137	Sequence 10137, A
260	31	100.0	433	2	US-09-252-991A-20376	Sequence 20376, A	333	31	100.0	886	2	US-09-543-681A-5627	Sequence 5627, Ap
261	31	100.0	433	2	US-09-949-016-10900	Sequence 10900, A	334	31	100.0	889	4	PCT-US93-11725-2	Sequence 2, App1
262	31	100.0	436	2	US-09-949-016-6983	Sequence 6983, Ap	335	31	100.0	893	2	US-09-328-352-6626	Sequence 6626, Ap
263	31	100.0	448	2	US-09-342-681C-17	Sequence 17, App1	336	31	100.0	898	2	US-09-902-540-11561	Sequence 11561, A
264	31	100.0	448	2	US-09-342-681C-19	Sequence 19, App1	337	31	100.0	905	2	US-10-104-047-2728	Sequence 2728, Ap
265	31	100.0	449	2	US-09-912-935-34	Sequence 34, App1	338	31	100.0	915	2	US-09-540-236-3026	Sequence 3026, Ap
266	31	100.0	454	1	US-08-166-316-2	Sequence 2, App1	339	31	100.0	956	2	US-09-949-016-11332	Sequence 11332, A
267	31	100.0	457	2	US-09-949-016-7165	Sequence 7165, Ap	340	31	100.0	958	1	US-08-426-236-4	Sequence 4, App1
268	31	100.0	467	2	US-09-513-442-2	Sequence 2, App1	341	31	100.0	961	2	US-09-657-472-4	Sequence 4, App1
269	31	100.0	468	2	US-09-949-016-10793	Sequence 10793, A	342	31	100.0	961	4	PCT-US93-11725-4	Sequence 4, App1
270	31	100.0	473	2	US-09-902-540-13895	Sequence 13895, A	343	31	100.0	965	2	US-09-538-092-650	Sequence 650, App
271	31	100.0	484	2	US-09-248-796A-18223	Sequence 18223, A	344	31	100.0	968	1	US-08-426-236-2	Sequence 2, App1
272	31	100.0	484	2	US-09-949-016-9440	Sequence 9440, Ap	345	31	100.0	970	2	US-09-949-016-10131	Sequence 10131, A
273	31	100.0	499	2	US-09-912-935-31	Sequence 31, App1	346	31	100.0	976	1	US-08-449-645A-18	Sequence 18, App1
274	31	100.0	500	1	US-08-260-582-77	Sequence 77, App1	347	31	100.0	976	1	US-08-702-367A-18	Sequence 18, App1
275	31	100.0	500	4	PCT-US95-05471-77	Sequence 77, App1	348	31	100.0	976	4	US-09-949-016-6499	Sequence 6499, Ap
276	31	100.0	511	1	US-08-821-355A-9	Sequence 9, App1	349	31	100.0	976	4	PCT-US95-04661-18	Sequence 18, App1
277	31	100.0	511	1	US-09-003-687A-9	Sequence 9, App1	350	31	100.0	977	1	US-08-673-789-8	Sequence 8, App1
278	31	100.0	511	2	US-09-136-605-9	Sequence 9, App1	351	31	100.0	1003	2	US-08-851-843A-217	Sequence 217, App
279	31	100.0	525	2	US-10-101-464A-613	Sequence 613, App	352	31	100.0	1003	2	US-08-974-549A-336	Sequence 336, App
280	31	100.0	529	2	US-09-912-935-28	Sequence 28, App1	353	31	100.0	1003	2	US-08-854-050-217	Sequence 217, App
281	31	100.0	529	2	US-09-912-935-40	Sequence 40, App1	354	31	100.0	1003	2	US-09-430-323-217	Sequence 217, App
282	31	100.0	530	2	US-09-912-935-38	Sequence 38, App1	355	31	100.0	1003	2	US-09-402-181B-336	Sequence 336, App
283	31	100.0	546	2	US-10-057-531A-1	Sequence 1, App1	356	31	100.0	1003	2	US-09-721-456-336	Sequence 336, App
284	31	100.0	551	2	US-09-741-243C-2	Sequence 2, App1	357	31	100.0	1003	2	US-10-054-295-217	Sequence 217, App
285	31	100.0	553	2	US-09-447-497-14	Sequence 14, App1	358	31	100.0	1003	2	US-09-438-486A-217	Sequence 217, App
286	31	100.0	566	2	US-09-252-991A-18531	Sequence 18531, A	359	31	100.0	1004	2	US-09-949-016-9925	Sequence 9925, Ap
287	31	100.0	580	2	US-09-452-991A-22943	Sequence 22943, A	360	31	100.0	1013	2	US-09-949-016-7991	Sequence 7991, Ap
288	31	100.0	584	1	US-08-313-288B-17	Sequence 17, App1	361	31	100.0	1073	2	US-09-949-016-9771	Sequence 9771, Ap
289	31	100.0	585	2	US-09-370-807-4	Sequence 4, App1	362	31	100.0	1196	2	US-10-237-551-200	Sequence 200, App
290	31	100.0	585	2	US-09-921-259-4	Sequence 4, App1	363	31	100.0	1196	2	US-10-237-551-232	Sequence 232, App
291	31	100.0	596	1	US-08-821-355A-6	Sequence 6, App1	364	31	100.0	1208	2	US-09-463-702A-2	Sequence 2, App1
292	31	100.0	596	1	US-09-003-687A-6	Sequence 6, App1	365	31	100.0	1208	2	US-09-699-135-2	Sequence 2, App1
293	31	100.0	596	2	US-09-136-605-6	Sequence 6, App1	366	31	100.0	1285	2	US-08-974-549A-600	Sequence 600, App
294	31	100.0	615	2	US-09-345-473E-49	Sequence 49, App1	367	31	100.0	1285	2	US-08-912-951-314	Sequence 314, App
295	31	100.0	615	2	US-08-862-027-49	Sequence 49, App1	368	31	100.0	1285	2	US-09-402-181B-600	Sequence 600, App
296	31	100.0	622	2	US-09-252-991A-30739	Sequence 30739, A	369	31	100.0	1285	2	US-09-721-445-600	Sequence 600, App
297	31	100.0	643	2	US-09-252-991A-23842	Sequence 23842, A	370	31	100.0	1441	2	US-09-949-016-10397	Sequence 10397, A
298	31	100.0	645	2	US-09-915-127-8	Sequence 8, App1	371	31	100.0	1452	2	US-09-127-227-2	Sequence 2, App1
299	31	100.0	645	2	US-09-915-127-9	Sequence 9, App1	372	31	100.0	1725	2	US-09-562-702A-20	Sequence 20, App1
300	31	100.0	654	2	US-09-315-127-11	Sequence 11, App1	373	31	100.0	1725	2	US-09-561-818A-20	Sequence 20, App1
301	31	100.0	654	2	US-09-315-127-12	Sequence 12, App1	374	31	100.0	1725	2	US-10-037-182-12	Sequence 12, App1
302	31	100.0	658	2	US-09-248-796A-17674	Sequence 17674, A	375	31	100.0	1786	2	US-09-562-702A-18	Sequence 18, App1
303	31	100.0	671	2	US-09-248-796A-18563	Sequence 18563, A	376	31	100.0	1786	2	US-09-561-818A-18	Sequence 18, App1
304	31	100.0	687	1	US-08-164-839-31	Sequence 31, App1	377	31	100.0	1786	2	US-10-037-182-12	Sequence 12, App1
305	31	100.0	687	1	US-08-164-839-33	Sequence 33, App1	378	31	100.0	2813	2	US-08-896-449A-2	Sequence 2, App1
306	31	100.0	687	1	US-08-583-799-31	Sequence 31, App1	379	31	100.0	2813	2	US-09-132-652-2	Sequence 2, App1
307	31	100.0	687	1	US-08-583-799-33	Sequence 33, App1	380	31	100.0	2813	2	US-09-886-900A-2	Sequence 2, App1
308	31	100.0	688	1	US-08-164-839-70	Sequence 70, App1	381	31	100.0	2813	2	US-09-652-478C-2	Sequence 2, App1
309	31	100.0	688	1	US-08-164-839-72	Sequence 72, App1	382	31	100.0	4302	2	US-08-658-136-5	Sequence 5, App1
310	31	100.0	688	1	US-08-583-799-70	Sequence 70, App1	383	31	100.0	4302	2	US-09-052-465-8	Sequence 8, App1
311	31	100.0	694	1	US-08-583-799-72	Sequence 72, App1	384	31	100.0	4302	2	US-08-422-582-8	Sequence 8, App1
312	31	100.0	694	1	US-08-164-839-4	Sequence 4, App1	385	31	100.0	4302	2	US-09-052-262-8	Sequence 2, App1
313	31	100.0	694	1	US-08-583-799-4	Sequence 4, App1	386	31	100.0	4303	1	US-08-460-751-2	Sequence 2, App1
314	31	100.0	695	1	US-08-164-839-6	Sequence 6, App1	387	31	100.0	4303	2	US-09-479-647A-2	Sequence 2, App1
315	31	100.0	695	1	US-08-164-839-8	Sequence 8, App1	388	31	100.0	4303	2	US-09-655-160-2	Sequence 2, App1
316	31	100.0	695	1	US-08-583-799-6	Sequence 6, App1	389	31	80.6	7	US-08-335-833-19	Sequence 19, App1	
317	31	100.0	695	1	US-08-583-799-8	Sequence 8, App1	390	31	80.6	9	US-08-482-880-8	Sequence 8, App1	
318	31	100.0	696	1	US-08-164-839-10	Sequence 10, App1	391	31	80.6	9	US-08-273-274-8	Sequence 8, App1	
319	31	100.0	696	1	US-08-583-799-10	Sequence 10, App1	392	31	80.6	9	US-08-475-041-8	Sequence 8, App1	

393	25	80.6	9	1	US-08-484-773-8	Sequence 8, App1	466	25	80.6	97	2	US-10-100-785-53	Sequence 53, App1
394	25	80.6	10	1	US-08-335-832-8	Sequence 8, App1	467	25	80.6	97	2	US-10-101-279-53	Sequence 53, App1
395	25	80.6	11	1	US-08-335-832-40	Sequence 40, App1	468	25	80.6	97	2	US-09-709-201B-53	Sequence 53, App1
396	25	80.6	11	2	US-09-623-548A-1374	Sequence 1374, Ap	469	25	80.6	97	2	US-10-100-759-53	Sequence 53, App1
397	25	80.6	11	2	US-09-657-276-1374	Sequence 1374, Ap	470	25	80.6	99	2	US-09-252-991A-21529	Sequence 21529, A
398	25	80.6	12	2	US-09-910-009A-463	Sequence 463, App	471	25	80.6	99	2	US-09-252-991A-24967	Sequence 24967, A
399	25	80.6	13	2	US-09-910-009A-452	Sequence 452, App	472	25	80.6	99	2	US-09-248-796A-27022	Sequence 27022, A
400	25	80.6	16	2	US-09-910-009A-462	Sequence 462, App	473	25	80.6	104	2	US-09-252-991A-23064	Sequence 23064, A
401	25	80.6	16	2	US-09-954-987B-199	Sequence 199, App	474	25	80.6	105	1	US-08-103-170-12	Sequence 12, App1
402	25	80.6	17	2	US-09-910-009A-414	Sequence 414, App	475	25	80.6	106	2	US-10-232-858-78	Sequence 78, App1
403	25	80.6	32	2	US-08-632-511A-6	Sequence 6, App1	476	25	80.6	106	2	US-09-338-062A-75	Sequence 78, App1
404	25	80.6	32	2	US-09-091-590A-12	Sequence 12, App1	477	25	80.6	106	2	US-10-104-047-2975	Sequence 2975, Ap
405	25	80.6	32	2	US-09-488-200-6	Sequence 6, App1	478	25	80.6	110	2	US-09-902-540-11228	Sequence 11228, A
406	25	80.6	38	2	US-09-270-767-60645	Sequence 60645, A	479	25	80.6	111	1	US-08-543-238-8	Sequence 8, App1
407	25	80.6	40	2	US-09-270-767-61997	Sequence 61997, A	480	25	80.6	111	1	US-08-420-526-8	Sequence 8, App1
408	25	80.6	45	2	US-08-803-954B-10	Sequence 10, App1	481	25	80.6	114	2	US-09-774-639-156	Sequence 156, App
409	25	80.6	46	2	US-09-270-767-58428	Sequence 58428, A	482	25	80.6	116	2	US-09-540-236-3774	Sequence 3774, Ap
410	25	80.6	49	2	US-09-461-325-425	Sequence 425, App	483	25	80.6	120	2	US-09-252-991A-22272	Sequence 22272, A
411	25	80.6	49	2	US-10-012-542-425	Sequence 425, App	484	25	80.6	120	2	US-09-710-279-2214	Sequence 2214, Ap
412	25	80.6	49	2	US-10-115-123-425	Sequence 425, App	485	25	80.6	123	2	US-09-489-039A-12685	Sequence 12685, A
413	25	80.6	50	2	US-09-896-720-22	Sequence 22, App1	486	25	80.6	123	2	US-09-855-266A-13	Sequence 13, App1
414	25	80.6	53	1	US-08-238-821B-53	Sequence 53, App1	487	25	80.6	124	2	US-09-270-767-48315	Sequence 48315, A
415	25	80.6	53	1	US-09-621-976-6711	Sequence 6711, Ap	488	25	80.6	125	2	US-09-134-001C-5464	Sequence 5464, Ap
416	25	80.6	53	4	PCT-US95-05744-53	Sequence 53, App1	489	25	80.6	126	2	US-09-328-352-7886	Sequence 7886, Ap
417	25	80.6	57	2	US-09-621-976-7258	Sequence 7258, Ap	490	25	80.6	126	2	US-09-270-767-43094	Sequence 43094, A
418	25	80.6	61	2	US-09-580-201A-14	Sequence 14, App1	491	25	80.6	127	2	US-08-467-023-190	Sequence 190, App
419	25	80.6	62	2	US-09-252-991A-25973	Sequence 25973, A	492	25	80.6	131	2	US-09-489-039A-13310	Sequence 13310, A
420	25	80.6	63	2	US-09-910-009A-333	Sequence 333, App	493	25	80.6	131	2	US-09-270-767-40391	Sequence 40391, A
421	25	80.6	65	2	US-09-461-325-457	Sequence 457, App	494	25	80.6	132	2	US-09-270-767-56207	Sequence 56207, A
422	25	80.6	65	2	US-10-012-542-457	Sequence 457, App	495	25	80.6	132	2	US-09-523-323-55	Sequence 55, App1
423	25	80.6	66	2	US-10-115-123-457	Sequence 457, App	496	25	80.6	132	2	US-10-104-047-1315	Sequence 3315, Ap
424	25	80.6	66	2	US-09-543-681A-4836	Sequence 4836, Ap	497	25	80.6	135	2	US-09-252-991A-11226	Sequence 17226, A
425	25	80.6	67	2	US-09-910-009A-168	Sequence 168, App	498	25	80.6	136	2	US-09-252-991A-26088	Sequence 26088, A
426	25	80.6	67	2	US-09-910-009A-327	Sequence 327, App	499	25	80.6	137	2	US-09-252-991A-20915	Sequence 20915, A
427	25	80.6	68	1	US-08-117-952-768	Sequence 768, App	500	25	80.6	138	2	US-08-828-682A-20	Sequence 20, App1
428	25	80.6	68	1	US-08-117-952-769	Sequence 769, App	501	25	80.6	139	2	US-08-706-9450-130	Sequence 130, App
429	25	80.6	69	2	US-08-866-545-11	Sequence 11, App1	502	25	80.6	140	2	US-09-252-991A-30585	Sequence 30585, A
430	25	80.6	69	2	US-09-627-775-11	Sequence 11, App1	503	25	80.6	143	2	US-10-232-858-77	Sequence 77, App1
431	25	80.6	69	2	US-09-583-110-3686	Sequence 3686, Ap	504	25	80.6	143	2	US-09-338-062A-77	Sequence 77, App1
432	25	80.6	69	2	US-09-910-009A-108	Sequence 108, App	505	25	80.6	145	2	US-10-232-858-15	Sequence 15, App1
433	25	80.6	69	2	US-09-910-009A-342	Sequence 342, App	506	25	80.6	145	2	US-09-338-062A-15	Sequence 15, App1
434	25	80.6	74	2	US-09-107-433-4683	Sequence 4683, Ap	507	25	80.6	146	2	US-09-523-323-58	Sequence 58, App1
435	25	80.6	76	2	US-09-621-976-5646	Sequence 5646, Ap	508	25	80.6	147	2	US-09-527-236A-20	Sequence 20, App1
436	25	80.6	77	1	US-07-881-075-8	Sequence 8, App1	509	25	80.6	147	2	US-09-756-854-20	Sequence 20, App1
437	25	80.6	77	1	US-08-120-827-8	Sequence 8, App1	510	25	80.6	147	2	US-10-041-574-20	Sequence 20, App1
438	25	80.6	77	1	US-08-478-675-8	Sequence 8, App1	511	25	80.6	147	2	US-09-095-094-20	Sequence 20, App1
439	25	80.6	77	1	US-08-311-731A-239	Sequence 239, App	512	25	80.6	150	2	US-09-252-991A-22199	Sequence 22199, A
440	25	80.6	79	2	US-09-520-268A-3	Sequence 3, App1	513	25	80.6	150	2	US-09-252-991A-24700	Sequence 24700, A
441	25	80.6	79	2	US-09-902-540-9889	Sequence 9889, Ap	514	25	80.6	151	2	US-09-270-767-32572	Sequence 32572, A
442	25	80.6	80	2	US-09-107-433-4240	Sequence 4240, Ap	515	25	80.6	151	2	US-09-270-767-47789	Sequence 47789, A
443	25	80.6	80	2	US-09-902-540-15658	Sequence 15658, A	516	25	80.6	152	2	US-09-621-976-4169	Sequence 4169, Ap
444	25	80.6	81	2	US-09-252-991A-28421	Sequence 28421, A	517	25	80.6	154	2	US-10-232-858-13	Sequence 13, App1
445	25	80.6	83	2	US-09-198-452A-1191	Sequence 1191, Ap	518	25	80.6	154	2	US-09-338-062A-13	Sequence 13, App1
446	25	80.6	84	2	US-09-248-796A-23070	Sequence 23070, A	519	25	80.6	157	2	US-09-270-767-37143	Sequence 37143, A
447	25	80.6	84	2	US-10-232-858-82	Sequence 82, App1	520	25	80.6	157	2	US-09-270-767-47789	Sequence 47789, A
448	25	80.6	84	2	US-09-338-063A-82	Sequence 82, App1	521	25	80.6	158	2	US-09-422-680A-24	Sequence 24, App1
449	25	80.6	87	2	US-09-253-991A-20264	Sequence 20264, A	522	25	80.6	159	2	US-09-461-697-48	Sequence 48, App1
450	25	80.6	90	2	US-09-198-452A-597	Sequence 597, App	523	25	80.6	159	2	US-09-252-991A-30696	Sequence 30696, A
451	25	80.6	92	2	US-09-270-767-51823	Sequence 51823, A	524	25	80.6	161	2	US-09-632-277A-3	Sequence 3, App1
452	25	80.6	92	2	US-09-270-767-47040	Sequence 47040, A	525	25	80.6	163	2	US-09-252-991A-23129	Sequence 29128, A
453	25	80.6	92	2	US-09-438-185A-560	Sequence 560, App	526	25	80.6	163	2	US-09-270-767-34568	Sequence 34568, A
454	25	80.6	93	2	US-09-270-767-40817	Sequence 40817, A	527	25	80.6	166	2	US-09-270-767-49785	Sequence 49785, A
455	25	80.6	93	2	US-09-270-767-56033	Sequence 56033, A	528	25	80.6	167	2	US-09-248-796A-28011	Sequence 28011, A
456	25	80.6	94	2	US-08-851-843A-215	Sequence 215, App	529	25	80.6	167	2	US-10-104-047-32930	Sequence 32930, Ap
457	25	80.6	94	2	US-08-974-549A-334	Sequence 334, App	530	25	80.6	168	2	US-09-252-991A-30752	Sequence 30752, A
458	25	80.6	94	2	US-08-854-050-215	Sequence 215, App	531	25	80.6	170	2	US-09-252-991A-22362	Sequence 22362, A
459	25	80.6	94	2	US-09-430-333-215	Sequence 333, App	532	25	80.6	172	2	US-09-673-395A-581	Sequence 581, App
460	25	80.6	94	2	US-09-402-181B-334	Sequence 334, App	533	25	80.6	174	2	US-09-489-039A-10526	Sequence 10526, A
461	25	80.6	94	2	US-09-721-456-334	Sequence 334, App	534	25	80.6	175	2	US-09-252-991A-16749	Sequence 16749, A
462	25	80.6	94	2	US-10-054-295-215	Sequence 215, App	535	25	80.6	177	2	US-09-252-991A-25407	Sequence 25407, A
463	25	80.6	94	2	US-09-438-486A-215	Sequence 215, App	536	25	80.6	184	2	US-09-252-991A-26087	Sequence 26087, A
464	25	80.6	97	2	US-09-025-596-53	Sequence 53, App1	537	25	80.6	187	2	US-09-199-637A-287	Sequence 287, App
465	25	80.6	97	2	US-09-073-661-53	Sequence 53, App1	538	25	80.6	187	2	US-09-252-991A-21454	Sequence 21454, A

539	25	80.6	187	2	US-10-232-858-81	Sequence 81, Appl	612	25	80.6	249	2	US-09-252-991A-30320	Sequence 30320, A
540	25	80.6	187	2	US-09-338-063A-81	Sequence 81, Appl	613	25	80.6	250	2	US-09-540-236-3224	Sequence 3224, Ap
541	25	80.6	188	2	US-09-252-991A-30309	Sequence 30309, A	614	25	80.6	250	2	US-09-949-016-8090	Sequence 8090, Ap
542	25	80.6	191	2	US-09-252-991A-25365	Sequence 25365, A	615	25	80.6	253	2	US-09-252-991A-32747	Sequence 32747, A
543	25	80.6	193	2	US-09-489-039A-7517	Sequence 7517, Ap	616	25	80.6	254	2	US-10-126-279-27	Sequence 27, Appl
544	25	80.6	194	2	US-09-252-991A-22032	Sequence 22032, A	617	25	80.6	254	2	US-10-126-279-30	Sequence 30, Appl
545	25	80.6	194	2	US-09-252-991A-24154	Sequence 24154, A	618	25	80.6	254	2	US-10-286-606-27	Sequence 27, Appl
546	25	80.6	195	2	US-09-252-991A-22042	Sequence 22042, A	619	25	80.6	254	2	US-10-286-606-30	Sequence 30, Appl
547	25	80.6	196	2	US-09-513-999C-4249	Sequence 4249, Ap	620	25	80.6	255	1	US-08-236-912A-8	Sequence 8, Appl1
548	25	80.6	197	2	US-09-252-991A-28579	Sequence 28579, A	621	25	80.6	255	1	US-08-816-605-9	Sequence 9, Appl1
549	25	80.6	197	2	US-10-232-858-76	Sequence 76, Appl	622	25	80.6	255	2	US-09-006-353A-11	Sequence 11, Appl1
550	25	80.6	197	2	US-09-338-063A-76	Sequence 76, Appl	623	25	80.6	255	2	US-09-007-097-2	Sequence 2, Appl1
551	25	80.6	198	2	US-09-252-991A-22691	Sequence 22691, A	624	25	80.6	255	2	US-09-150-864A-8	Sequence 8, Appl1
552	25	80.6	199	1	US-08-264-53A-4	Sequence 4, Appl1	625	25	80.6	255	2	US-09-573-986-11	Sequence 11, Appl
553	25	80.6	199	1	US-08-465-500-4	Sequence 4, Appl1	626	25	80.6	255	2	US-09-578-764A-2	Sequence 2, Appl1
554	25	80.6	199	1	US-08-346-126-4	Sequence 4, Appl1	627	25	80.6	255	2	US-09-623-545A-2	Sequence 2, Appl1
555	25	80.6	199	1	US-08-346-128-4	Sequence 4, Appl1	628	25	80.6	255	2	US-09-877-338-2	Sequence 2, Appl1
556	25	80.6	199	1	US-08-893-828-4	Sequence 4, Appl1	629	25	80.6	255	4	PCT-US96-03965-8	Sequence 8, Appl1
557	25	80.6	199	2	US-09-482-273-205	Sequence 205, App	630	25	80.6	256	2	US-09-252-991A-23974	Sequence 23974, A
558	25	80.6	201	2	US-09-252-991A-24077	Sequence 24077, A	631	25	80.6	259	2	US-09-006-353A-2	Sequence 2, Appl1
559	25	80.6	201	2	US-09-252-991A-29895	Sequence 29895, A	632	25	80.6	259	2	US-09-253-316-27	Sequence 27, Appl
560	25	80.6	202	2	US-09-252-991A-17852	Sequence 17852, A	633	25	80.6	259	2	US-09-573-986-2	Sequence 2, Appl1
561	25	80.6	204	2	US-09-149-476-429	Sequence 429, App	634	25	80.6	259	2	US-09-976-594-229	Sequence 229, App
562	25	80.6	204	2	US-09-999-833A-36	Sequence 36, Appl	635	25	80.6	259	2	US-09-919-039-109	Sequence 109, App
563	25	80.6	204	2	US-10-020-445A-36	Sequence 36, Appl	636	25	80.6	259	2	US-09-949-001-17	Sequence 17, Appl
564	25	80.6	205	2	US-09-949-016-9980	Sequence 9980, Ap	637	25	80.6	259	6	5212074-3	Patent No. 5212074
565	25	80.6	205	2	US-09-949-016-9981	Sequence 9981, Ap	638	25	80.6	263	2	US-09-107-532A-6468	Sequence 6468, Ap
566	25	80.6	205	2	US-09-949-016-9982	Sequence 9982, Ap	639	25	80.6	265	2	US-09-903-455-77	Sequence 77, Appl
567	25	80.6	207	2	US-08-974-022-47	Sequence 47, Appl	640	25	80.6	267	2	US-10-000-489-80	Sequence 80, Appl
568	25	80.6	207	2	US-08-795-445A-47	Sequence 47, Appl	641	25	80.6	269	2	US-09-252-991A-29917	Sequence 29917, A
569	25	80.6	207	2	US-08-795-447A-47	Sequence 47, Appl	642	25	80.6	269	2	US-09-248-796A-15865	Sequence 15865, A
570	25	80.6	207	2	US-08-974-186-47	Sequence 47, Appl	643	25	80.6	271	2	US-09-248-796A-14877	Sequence 14877, A
571	25	80.6	207	2	US-08-795-446A-47	Sequence 47, Appl	644	25	80.6	272	2	US-09-949-016-7520	Sequence 7520, Ap
572	25	80.6	207	2	US-08-706-945D-133	Sequence 133, App	645	25	80.6	272	2	US-10-232-858-75	Sequence 75, Appl
573	25	80.6	207	2	US-08-577-788C-47	Sequence 47, Appl	646	25	80.6	272	2	US-09-338-063A-75	Sequence 75, Appl
574	25	80.6	207	2	US-09-603-703B-1726	Sequence 68, Appl	647	25	80.6	274	2	US-09-949-016-9995	Sequence 9095, Ap
575	25	80.6	207	2	US-09-605-703B-1726	Sequence 1726, Ap	648	25	80.6	276	2	US-09-270-767-45156	Sequence 45156, A
576	25	80.6	211	2	US-10-104-047-3219	Sequence 3219, Ap	649	25	80.6	277	1	US-08-195-967-2	Sequence 2, Appl1
577	25	80.6	211	2	US-09-949-016-11620	Sequence 11620, A	650	25	80.6	277	2	US-08-137-784-2	Sequence 2, Appl1
578	25	80.6	216	2	US-09-252-991A-22597	Sequence 22597, A	651	25	80.6	277	2	US-09-006-353A-12	Sequence 12, Appl
579	25	80.6	217	2	US-09-902-540-15578	Sequence 15578, A	652	25	80.6	277	2	US-08-472-940-2	Sequence 2, Appl1
580	25	80.6	219	1	US-08-152-019A-32	Sequence 32, Appl	653	25	80.6	277	2	US-09-573-986-12	Sequence 12, Appl
581	25	80.6	223	2	US-09-541-759-1	Sequence 1, Appl1	654	25	80.6	277	2	US-09-880-939-2	Sequence 2, Appl1
582	25	80.6	225	2	US-09-252-991A-24245	Sequence 24245, A	655	25	80.6	277	2	US-09-804-200-2	Sequence 2, Appl1
583	25	80.6	225	2	US-09-252-991A-29348	Sequence 29348, A	656	25	80.6	277	2	US-08-469-633A-4	Sequence 4, Appl1
584	25	80.6	225	2	US-09-252-991A-30156	Sequence 30156, A	657	25	80.6	278	2	US-10-046-433-3	Sequence 3, Appl1
585	25	80.6	225	2	US-09-352-991A-30156	Sequence 30156, A	658	25	80.6	278	2	US-09-252-991A-19433	Sequence 19433, A
586	25	80.6	228	2	US-09-270-767-44746	Sequence 44746, A	659	25	80.6	280	2	US-09-252-991A-22385	Sequence 22385, A
587	25	80.6	229	2	US-09-247-155-97	Sequence 97, Appl	660	25	80.6	280	2	US-09-991-181-319	Sequence 319, App
588	25	80.6	229	2	US-09-991-181-424	Sequence 424, App	661	25	80.6	280	2	US-09-990-444-319	Sequence 319, App
589	25	80.6	229	2	US-09-990-444-424	Sequence 424, App	662	25	80.6	280	2	US-09-997-333-319	Sequence 319, App
590	25	80.6	229	2	US-09-903-190-97	Sequence 97, Appl	663	25	80.6	280	2	US-09-992-596-319	Sequence 319, App
591	25	80.6	229	2	US-09-997-333-424	Sequence 424, App	664	25	80.6	281	2	US-08-893-654B-2	Sequence 2, Appl1
592	25	80.6	230	2	US-09-992-598-424	Sequence 424, App	665	25	80.6	284	1	US-09-055-095-1	Sequence 1, Appl1
593	25	80.6	230	2	US-09-252-991A-31737	Sequence 31737, A	666	25	80.6	293	1	US-08-264-53A-9	Sequence 9, Appl1
594	25	80.6	235	2	US-09-620-405B-487	Sequence 487, App	667	25	80.6	293	1	US-08-083-991A-4	Sequence 4, Appl1
595	25	80.6	235	2	US-09-328-352-6597	Sequence 6597, Ap	668	25	80.6	293	1	US-08-465-500-9	Sequence 9, Appl1
596	25	80.6	235	2	US-09-604-287A-487	Sequence 487, App	669	25	80.6	293	1	US-08-346-126-9	Sequence 9, Appl1
597	25	80.6	235	2	US-09-334-759-487	Sequence 487, App	670	25	80.6	293	1	US-08-346-128-9	Sequence 9, Appl1
598	25	80.6	235	2	US-10-076-622-487	Sequence 487, App	671	25	80.6	293	1	US-08-532-384-4	Sequence 4, Appl1
599	25	80.6	236	2	US-09-270-767-46803	Sequence 46803, A	672	25	80.6	293	2	US-08-893-828-9	Sequence 9, Appl1
600	25	80.6	236	2	US-10-126-279-28	Sequence 28, Appl	673	25	80.6	293	2	US-09-896-096A-18	Sequence 18, Appl
601	25	80.6	236	2	US-10-286-606-28	Sequence 28, Appl	674	25	80.6	296	2	US-09-252-991A-21951	Sequence 21951, A
602	25	80.6	239	2	US-09-252-991A-30037	Sequence 30037, A	675	25	80.6	299	2	US-09-153-927-3	Sequence 3, Appl1
603	25	80.6	240	2	US-09-902-540-15169	Sequence 15169, A	676	25	80.6	299	2	US-09-134-618-4	Sequence 4, Appl1
604	25	80.6	243	2	US-09-134-001C-4360	Sequence 4360, Ap	677	25	80.6	299	2	US-09-949-016-6422	Sequence 6422, Ap
605	25	80.6	246	2	US-10-104-047-2232	Sequence 2232, Ap	678	25	80.6	301	2	US-09-949-016-9189	Sequence 9189, Ap
606	25	80.6	246	2	US-10-104-047-2243	Sequence 2243, Ap	679	25	80.6	301	2	US-09-902-540-11985	Sequence 11985, A
607	25	80.6	247	2	US-10-126-279-29	Sequence 29, Appl	680	25	80.6	303	2	US-09-461-325-466	Sequence 426, App
608	25	80.6	247	2	US-10-286-606-29	Sequence 29, Appl	681	25	80.6	303	2	US-10-012-542-426	Sequence 426, App
609	25	80.6	247	2	US-10-104-047-2790	Sequence 2790, Ap	682	25	80.6	304	2	US-10-115-123-426	Sequence 304, App
610	25	80.6	248	2	US-09-552-991A-17358	Sequence 17358, A	683	25	80.6	304	2	US-09-893-737-304	Sequence 304, App
611	25	80.6	249	2	US-09-252-991A-28972	Sequence 28972, A	684	25	80.6	305	2	US-09-252-991A-26204	Sequence 26204, A

685	25	80.6	312	2	US-09-270-767-39065	Sequence 39065, A	758	25	80.6	391	2	US-10-232-858-106	Sequence 106, App
686	25	80.6	312	2	US-09-270-767-54282	Sequence 54282, A	759	25	80.6	391	2	US-09-338-063A-106	Sequence 106, App
687	25	80.6	314	1	US-08-460-309-19	Sequence 19, Appl	760	25	80.6	393	2	US-10-232-858-79	Sequence 79, Appl
688	25	80.6	314	1	US-08-125-077-19	Sequence 19, Appl	761	25	80.6	393	2	US-09-338-063A-79	Sequence 79, Appl
689	25	80.6	314	2	US-09-949-001-23	Sequence 23, Appl	762	25	80.6	394	2	US-10-232-858-9	Sequence 9, Appl
690	25	80.6	315	2	US-09-172-952-13	Sequence 13, Appl	763	25	80.6	394	2	US-09-338-063A-9	Sequence 9, Appl
691	25	80.6	317	1	US-08-118-770-10	Sequence 10, Appl	764	25	80.6	396	2	US-09-489-039A-10242	Sequence 10242, A
692	25	80.6	317	4	PCT-US93-08528-10	Sequence 10, Appl	765	25	80.6	396	2	US-09-489-039A-12215	Sequence 12215, A
693	25	80.6	331	2	US-10-232-858-80	Sequence 80, Appl	766	25	80.6	398	2	US-10-104-047-2769	Sequence 2769, App
694	25	80.6	331	2	US-09-338-063A-80	Sequence 80, Appl	767	25	80.6	399	2	US-10-232-858-73	Sequence 73, App
695	25	80.6	332	2	US-09-252-991A-3141	Sequence 3141, A	768	25	80.6	399	2	US-09-949-002-437	Sequence 437, App
696	25	80.6	335	1	US-08-292-549-2	Sequence 2, Appl	769	25	80.6	399	2	US-09-338-063A-73	Sequence 73, Appl
697	25	80.6	335	2	US-09-042-785A-9	Sequence 9, Appl	770	25	80.6	401	2	US-08-974-022-6	Sequence 6, Appl
698	25	80.6	335	4	PCT-US91-02207-2	Sequence 2, Appl	771	25	80.6	401	2	US-09-072-993C-1	Sequence 12, Appl
699	25	80.6	336	1	US-08-292-549-4	Sequence 4, Appl	772	25	80.6	401	2	US-08-795-445A-6	Sequence 6, Appl
700	25	80.6	336	2	US-10-232-858-71	Sequence 71, Appl	773	25	80.6	401	2	US-08-974-186-6	Sequence 6, Appl
701	25	80.6	336	2	US-09-338-063A-71	Sequence 71, Appl	774	25	80.6	401	2	US-08-974-186-6	Sequence 6, Appl
702	25	80.6	336	4	PCT-US91-02207-4	Sequence 4, Appl	775	25	80.6	401	2	US-08-795-445A-6	Sequence 6, Appl
703	25	80.6	327	2	US-09-290-640-66	Sequence 66, Appl	776	25	80.6	401	2	US-09-153-927-1	Sequence 1, Appl
704	25	80.6	327	2	US-09-665-615B-66	Sequence 66, Appl	777	25	80.6	401	2	US-09-072-993C-1	Sequence 1, Appl
705	25	80.6	327	2	US-10-232-858-72	Sequence 72, Appl	778	25	80.6	401	2	US-08-577-788C-6	Sequence 128, App
706	25	80.6	327	2	US-09-338-063A-72	Sequence 72, Appl	779	25	80.6	401	2	US-08-577-788C-6	Sequence 6, Appl
707	25	80.6	328	2	US-09-252-991A-23826	Sequence 23826, A	780	25	80.6	401	2	US-08-577-788C-6	Sequence 56, Appl
708	25	80.6	328	2	US-09-252-991A-26586	Sequence 26586, A	781	25	80.6	401	2	US-09-064-832-2	Sequence 2, Appl
709	25	80.6	329	2	US-09-336-910A-5	Sequence 5, Appl	782	25	80.6	401	2	US-10-232-858-5	Sequence 5, Appl
710	25	80.6	334	2	US-09-949-016-8549	Sequence 8549, Ap	783	25	80.6	401	2	US-10-232-858-62	Sequence 62, Appl
711	25	80.6	334	2	US-09-949-016-8571	Sequence 8571, Ap	784	25	80.6	401	2	US-10-232-858-63	Sequence 63, Appl
712	25	80.6	339	2	US-09-171-461-36	Sequence 36, Appl	785	25	80.6	401	2	US-10-232-858-65	Sequence 65, Appl
713	25	80.6	339	2	US-09-252-991A-25235	Sequence 25235, A	786	25	80.6	401	2	US-10-232-858-66	Sequence 66, Appl
714	25	80.6	339	2	US-09-970-711-36	Sequence 36, Appl	787	25	80.6	401	2	US-10-332-858-66	Sequence 66, Appl
715	25	80.6	345	2	US-09-403-768-4	Sequence 36, Appl	788	25	80.6	401	2	US-09-338-063A-5	Sequence 5, Appl
716	25	80.6	345	2	US-09-252-991A-32869	Sequence 32869, A	789	25	80.6	401	2	US-09-338-063A-62	Sequence 62, Appl
717	25	80.6	348	2	US-09-830-807-43	Sequence 43, Appl	790	25	80.6	401	2	US-09-338-063A-63	Sequence 63, Appl
718	25	80.6	348	2	US-09-006-353A-13	Sequence 13, Appl	791	25	80.6	401	2	US-09-338-063A-65	Sequence 65, Appl
719	25	80.6	349	2	US-09-573-986-13	Sequence 13, Appl	792	25	80.6	401	2	US-09-338-063A-65	Sequence 65, Appl
720	25	80.6	349	2	US-09-780-996A-7	Sequence 7, Appl	793	25	80.6	402	2	US-09-338-063A-66	Sequence 66, Appl
721	25	80.6	350	2	US-10-726-721A-7	Sequence 7, Appl	794	25	80.6	402	2	US-09-270-67-61551	Sequence 61551, A
722	25	80.6	350	2	US-10-046-433-41	Sequence 41, Appl	795	25	80.6	419	2	US-09-252-991A-21423	Sequence 21423, A
723	25	80.6	351	2	US-10-232-858-74	Sequence 74, Appl	796	25	80.6	419	2	US-09-252-991A-18123	Sequence 18123, A
724	25	80.6	351	2	US-09-338-063A-74	Sequence 74, Appl	797	25	80.6	425	2	US-09-538-092-1366	Sequence 5362, Ap
725	25	80.6	353	2	US-09-252-991A-26394	Sequence 26394, A	798	25	80.6	427	2	US-09-328-452-5312	Sequence 5312, Ap
726	25	80.6	353	2	US-10-104-047-2052	Sequence 2052, Ap	799	25	80.6	430	2	US-09-352-991A-25287	Sequence 25287, A
727	25	80.6	355	1	US-08-292-549-6	Sequence 6, Appl	800	25	80.6	434	2	US-09-452-991A-27235	Sequence 27235, A
728	25	80.6	355	2	US-09-006-353A-14	Sequence 14, Appl	801	25	80.6	435	2	US-09-252-991A-21698	Sequence 21698, A
729	25	80.6	355	2	US-09-403-768-6	Sequence 6, Appl	802	25	80.6	437	2	US-09-353-332-2	Sequence 2, Appl
730	25	80.6	356	2	US-09-573-986-14	Sequence 14, Appl	803	25	80.6	447	2	US-09-949-016-10534	Sequence 10534, A
731	25	80.6	356	2	US-09-235-103-2	Sequence 2, Appl	804	25	80.6	450	2	US-09-896-720-2	Sequence 2, Appl
732	25	80.6	356	2	US-09-235-103-4	Sequence 4, Appl	805	25	80.6	458	2	US-09-949-016-8791	Sequence 8791, Ap
733	25	80.6	356	2	US-09-235-103-13	Sequence 13, Appl	806	25	80.6	466	1	US-08-194-338-11	Sequence 11, Appl
734	25	80.6	357	2	US-09-270-767-60452	Sequence 60452, A	807	25	80.6	466	2	US-09-826-509-515	Sequence 515, App
735	25	80.6	359	2	US-10-232-858-70	Sequence 70, Appl	808	25	80.6	466	2	US-09-252-991A-31436	Sequence 31436, A
736	25	80.6	359	2	US-09-338-063A-70	Sequence 70, Appl	809	25	80.6	469	2	US-09-393-171-7	Sequence 7, Appl
737	25	80.6	362	2	US-10-232-858-11	Sequence 11, Appl	810	25	80.6	480	1	US-08-201-118-1	Sequence 1, Appl
738	25	80.6	362	2	US-09-338-063A-11	Sequence 11, Appl	811	25	80.6	480	1	US-08-201-118-7	Sequence 7, Appl
739	25	80.6	363	2	US-10-232-858-59	Sequence 59, Appl	812	25	80.6	480	1	US-08-201-118-5	Sequence 5, Appl
740	25	80.6	363	2	US-09-338-063A-69	Sequence 69, Appl	813	25	80.6	480	1	US-08-201-118-7	Sequence 7, Appl
741	25	80.6	364	2	US-08-706-945D-142	Sequence 142, App	814	25	80.6	480	1	US-08-201-118-9	Sequence 9, Appl
742	25	80.6	365	2	US-09-503-219B-8	Sequence 8, Appl	815	25	80.6	480	1	US-08-201-118-11	Sequence 11, Appl
743	25	80.6	365	2	US-10-039-659A-10	Sequence 10, Appl	816	25	80.6	480	1	US-08-201-118-13	Sequence 13, Appl
744	25	80.6	366	2	US-09-252-991A-31958	Sequence 31958, A	817	25	80.6	480	1	US-08-238-821B-1	Sequence 1, Appl
745	25	80.6	368	2	US-09-949-016-8818	Sequence 8818, Ap	818	25	80.6	480	1	US-08-238-821B-3	Sequence 3, Appl
746	25	80.6	376	2	US-09-949-016-7545	Sequence 7545, Ap	819	25	80.6	480	1	US-08-238-821B-5	Sequence 5, Appl
747	25	80.6	377	2	US-09-270-767-44972	Sequence 44972, A	820	25	80.6	480	1	US-08-238-821B-7	Sequence 7, Appl
748	25	80.6	377	2	US-09-949-016-8141	Sequence 8141, Ap	821	25	80.6	480	1	US-08-238-821B-9	Sequence 9, Appl
749	25	80.6	380	2	US-10-232-858-4	Sequence 4, Appl	822	25	80.6	480	1	US-08-238-821B-11	Sequence 11, Appl
750	25	80.6	380	2	US-09-338-063A-4	Sequence 4, Appl	823	25	80.6	480	1	US-08-238-821B-13	Sequence 13, Appl
751	25	80.6	386	2	US-09-086-483A-2	Sequence 2, Appl	824	25	80.6	480	2	US-09-949-016-5989	Sequence 5989, Ap
752	25	80.6	386	2	US-09-130-491-6	Sequence 6, Appl	825	25	80.6	480	2	US-09-949-016-5990	Sequence 5990, Ap
753	25	80.6	386	2	US-09-580-212-2	Sequence 2, Appl	826	25	80.6	480	4	PCT-US95-05744-1	Sequence 1, Appl
754	25	80.6	386	2	US-09-759-402-2	Sequence 2, Appl	827	25	80.6	480	4	PCT-US95-05744-3	Sequence 3, Appl
755	25	80.6	386	2	US-09-949-002-357	Sequence 357, App	828	25	80.6	480	4	PCT-US95-05744-5	Sequence 5, Appl
756	25	80.6	389	2	US-09-252-991A-31590	Sequence 31590, A	829	25	80.6	480	4	PCT-US95-05744-7	Sequence 7, Appl
757	25	80.6	390	2	US-09-949-016-10020	Sequence 10020, A	830	25	80.6	480	4	PCT-US95-05744-9	Sequence 9, Appl

831	25	80.6	490	4	PCT-US95-05744-11	Sequence 11, Appl	904	25	80.6	700	2	US-08-933-711B-5	Sequence 5, Appl
832	25	80.6	490	4	PCT-US95-05744-13	Sequence 13, Appl	905	25	80.6	709	2	US-08-753-247-6	Sequence 6, Appl
833	25	80.6	492	2	US-09-252-991A-18218	Sequence 18218, A	906	25	80.6	713	2	US-08-753-247-9	Sequence 9, Appl
834	25	80.6	495	2	US-09-949-016-10481	Sequence 10481, A	907	25	80.6	716	2	US-09-312-283C-183	Sequence 183, Appl
835	25	80.6	495	2	US-09-949-016-10532	Sequence 10532, A	908	25	80.6	719	2	US-08-753-247-12	Sequence 12, Appl
836	25	80.6	495	2	US-09-949-016-10533	Sequence 10533, A	909	25	80.6	721	2	US-09-134-000C-5466	Sequence 5466, Appl
837	25	80.6	498	1	US-07-688-352C-20	Sequence 20, Appl	910	25	80.6	729	2	US-09-107-532A-3970	Sequence 3970, Ap
838	25	80.6	498	1	US-08-474-379C-20	Sequence 20, Appl	911	25	80.6	744	2	US-09-252-991A-10945	Sequence 10945, A
839	25	80.6	498	1	US-09-146-249A-20	Sequence 20, Appl	912	25	80.6	762	2	US-09-489-039A-10008	Sequence 10008, A
840	25	80.6	498	2	US-08-206-188B-20	Sequence 20, Appl	913	25	80.6	771	2	US-09-188-930A-183	Sequence 183, Appl
841	25	80.6	500	1	US-08-314-601-2	Sequence 20, Appl	914	25	80.6	794	1	US-07-885-972A-2	Sequence 2, Appl
842	25	80.6	500	4	PCT-US95-13051-2	Sequence 2, Appl	915	25	80.6	794	1	US-07-885-972A-4	Sequence 4, Appl
843	25	80.6	502	2	US-09-330-970-1	Sequence 1, Appl	916	25	80.6	794	1	US-08-865-203-2	Sequence 2, Appl
844	25	80.6	505	2	US-09-620-405B-478	Sequence 478, App	917	25	80.6	794	1	US-08-745-880-2	Sequence 2, Appl
845	25	80.6	505	2	US-09-620-405B-485	Sequence 485, App	918	25	80.6	794	1	US-08-745-880-4	Sequence 4, Appl
846	25	80.6	505	2	US-09-604-287A-478	Sequence 478, App	919	25	80.6	794	1	US-08-480-382-2	Sequence 2, Appl
847	25	80.6	505	2	US-09-604-287A-485	Sequence 485, App	920	25	80.6	794	1	US-08-480-382-4	Sequence 4, Appl
848	25	80.6	505	2	US-09-834-759-478	Sequence 478, App	921	25	80.6	794	1	US-07-849-420-2	Sequence 2, Appl
849	25	80.6	505	2	US-09-834-759-485	Sequence 485, App	922	25	80.6	794	2	US-09-253-854-2	Sequence 2, Appl
850	25	80.6	505	2	US-09-590-751A-478	Sequence 478, App	923	25	80.6	794	2	US-08-955-424-2	Sequence 2, Appl
851	25	80.6	505	2	US-09-551-621A-478	Sequence 478, App	924	25	80.6	794	2	US-09-592-480-1	Sequence 2, Appl
852	25	80.6	505	2	US-09-551-621A-478	Sequence 478, App	925	25	80.6	794	2	US-10-133-910-2	Sequence 2, Appl
853	25	80.6	505	2	US-10-076-622-478	Sequence 478, App	926	25	80.6	794	2	US-09-949-016-6239	Sequence 6239, Ap
854	25	80.6	505	2	US-10-076-622-485	Sequence 485, App	927	25	80.6	820	2	US-09-949-016-9924	Sequence 9924, Ap
855	25	80.6	508	2	US-09-302-540-10562	Sequence 10562, A	928	25	80.6	863	2	US-09-619-353-14	Sequence 14, Appl
856	25	80.6	509	2	US-08-857-076-46	Sequence 46, Appl	929	25	80.6	887	1	US-07-867-106-3	Sequence 3, Appl
857	25	80.6	509	2	US-09-305-658-46	Sequence 46, Appl	930	25	80.6	934	2	US-09-949-002-289	Sequence 289, Appl
858	25	80.6	510	2	US-09-252-991A-33009	Sequence 33009, A	931	25	80.6	970	1	US-08-673-789-7	Sequence 7, Appl
859	25	80.6	514	2	US-08-67-023-134	Sequence 134, App	932	25	80.6	973	1	US-08-162-809-10	Sequence 10, Appl
860	25	80.6	516	2	US-09-949-002-547	Sequence 547, App	933	25	80.6	981	2	US-09-949-002-513	Sequence 513, Appl
861	25	80.6	519	2	US-09-270-767-41281	Sequence 41281, A	934	25	80.6	987	1	US-08-436-04-6	Sequence 6, Appl
862	25	80.6	519	2	US-09-270-767-56497	Sequence 56497, A	935	25	80.6	987	1	US-08-436-054-6	Sequence 6, Appl
863	25	80.6	524	2	US-09-549-519-27	Sequence 27, Appl	936	25	80.6	987	4	PCT-US95-08812-6	Sequence 6, Appl
864	25	80.6	524	2	US-09-549-519-28	Sequence 28, Appl	937	25	80.6	988	1	US-08-162-809-14	Sequence 14, Appl
865	25	80.6	528	2	US-09-949-016-9678	Sequence 9678, Ap	938	25	80.6	989	2	US-09-954-987B-171	Sequence 171, App
866	25	80.6	530	2	US-09-252-991A-23666	Sequence 23666, A	939	25	80.6	990	2	US-09-949-016-7235	Sequence 7235, Ap
867	25	80.6	535	2	US-09-252-991A-28236	Sequence 28236, A	940	25	80.6	991	2	US-09-949-016-7768	Sequence 7768, Ap
868	25	80.6	540	2	US-09-252-991A-33091	Sequence 33091, A	941	25	80.6	1024	2	US-09-562-737-88	Sequence 88, Appl
869	25	80.6	561	1	US-08-559-492-12	Sequence 12, Appl	942	25	80.6	1024	2	US-09-949-016-7276	Sequence 7276, Ap
870	25	80.6	563	2	US-09-352-991A-28458	Sequence 28458, A	943	25	80.6	1049	2	US-09-999-833A-496	Sequence 496, App
871	25	80.6	567	2	US-09-452-991A-28481	Sequence 28481, A	944	25	80.6	1049	2	US-09-954-987B-170	Sequence 170, App
872	25	80.6	567	2	US-09-949-016-7250	Sequence 7250, Ap	945	25	80.6	1049	2	US-09-954-987B-172	Sequence 172, App
873	25	80.6	571	2	US-09-252-991A-28549	Sequence 28549, A	946	25	80.6	1049	2	US-10-020-445A-96	Sequence 496, App
874	25	80.6	581	2	US-09-252-991A-25414	Sequence 25414, A	947	25	80.6	1074	1	US-08-470-058-2	Sequence 2, Appl
875	25	80.6	588	2	US-10-087-167-121	Sequence 121, App	948	25	80.6	1074	2	US-09-037-188-2	Sequence 2, Appl
876	25	80.6	588	2	US-10-087-167-123	Sequence 123, App	949	25	80.6	1074	2	US-09-285-310-2	Sequence 2, Appl
877	25	80.6	589	2	US-09-252-991A-33631	Sequence 33631, A	950	25	80.6	1074	2	US-09-753-385-2	Sequence 2, Appl
878	25	80.6	591	2	US-09-949-016-10026	Sequence 10026, A	951	25	80.6	1079	2	US-09-058-489-22	Sequence 22, Appl
879	25	80.6	591	2	US-10-087-167-119	Sequence 119, App	952	25	80.6	1101	2	US-09-561-709B-5	Sequence 5, Appl
880	25	80.6	593	2	US-10-087-167-125	Sequence 125, App	953	25	80.6	1149	2	US-08-560-005-5	Sequence 5, Appl
881	25	80.6	595	2	US-09-252-991A-18995	Sequence 18995, A	954	25	80.6	1149	2	US-09-418-548-5	Sequence 5, Appl
882	25	80.6	596	2	US-09-252-991A-32193	Sequence 32193, A	955	25	80.6	1149	2	US-09-969-528-5	Sequence 5, Appl
883	25	80.6	596	2	US-09-949-016-7776	Sequence 7776, App	956	25	80.6	1240	2	US-09-058-489-23	Sequence 23, Appl
884	25	80.6	599	2	US-10-087-167-127	Sequence 127, App	957	25	80.6	1253	2	US-08-506-296B-14	Sequence 14, Appl
885	25	80.6	599	2	US-10-087-167-148	Sequence 148, App	958	25	80.6	1253	1	US-09-489-039A-12097	Sequence 12097, A
886	25	80.6	602	2	US-10-087-167-143	Sequence 143, App	959	25	80.6	1257	1	US-08-340-428B-49	Sequence 49, Appl
887	25	80.6	609	2	US-09-270-767-46418	Sequence 46418, A	960	25	80.6	1260	2	US-08-506-296B-21	Sequence 21, Appl
888	25	80.6	611	1	US-08-752-307B-10	Sequence 10, Appl	961	25	80.6	1276	1	US-08-222-616-24	Sequence 24, Appl
889	25	80.6	611	2	US-09-707-802-10	Sequence 10, Appl	962	25	80.6	1276	2	US-08-446-648-24	Sequence 24, Appl
890	25	80.6	611	2	US-09-991-326-10	Sequence 10, Appl	963	25	80.6	1276	4	US-09-982-610-24	Sequence 24, Appl
891	25	80.6	615	2	US-10-087-167-135	Sequence 135, App	964	25	80.6	1276	4	PCT-US95-04228-24	Sequence 24, Appl
892	25	80.6	620	2	US-10-087-167-137	Sequence 137, App	965	25	80.6	1347	2	US-09-058-489-24	Sequence 24, Appl
893	25	80.6	627	2	US-09-902-540-15743	Sequence 15743, A	966	25	80.6	1401	2	US-09-976-598-1035	Sequence 1035, Ap
894	25	80.6	633	2	US-09-489-039A-11729	Sequence 11729, A	967	25	80.6	1404	1	US-08-400-155-2	Sequence 2, Appl
895	25	80.6	634	2	US-09-489-039A-8399	Sequence 8399, Ap	968	25	80.6	1404	2	US-08-611-752A-2	Sequence 2, Appl
896	25	80.6	635	2	US-08-857-076-101	Sequence 101, App	969	25	80.6	1404	2	US-09-195-528-2	Sequence 2, Appl
897	25	80.6	645	2	US-10-104-047-2508	Sequence 2508, Ap	970	25	80.6	1410	1	US-08-470-058-4	Sequence 4, Appl
898	25	80.6	655	2	US-10-104-047-2502	Sequence 2502, Ap	971	25	80.6	1410	2	US-09-037-188-4	Sequence 4, Appl
899	25	80.6	661	2	US-09-252-991A-18225	Sequence 18225, A	972	25	80.6	1410	2	US-09-285-310-4	Sequence 4, Appl
900	25	80.6	666	2	US-09-422-869-18	Sequence 18, Appl	973	25	80.6	1410	2	US-09-753-385-4	Sequence 4, Appl
901	25	80.6	666	6	5262177-4	Patent No. 5262177	974	25	80.6	1525	2	US-09-191-647-2	Sequence 2, Appl
902	25	80.6	698	1	US-08-175-158A-2	Sequence 2, Appl	975	25	80.6	1525	2	US-09-540-245A-2	Sequence 2, Appl
903	25	80.6	698	2	US-09-439-740-2	Sequence 2, Appl	976	25	80.6	1525	2	US-09-540-153-2	Sequence 2, Appl

```

977 25 80.6 1525 2 US-10-289-776-2 Sequence 2, Appl1
978 25 80.6 1529 2 US-09-312-283C-396 Sequence 396, App
979 25 80.6 1529 2 US-10-188-495-67 Sequence 67, Appl
980 25 80.6 1551 2 US-09-949-016-6785 Sequence 6785, Ap
981 25 80.6 1572 2 US-09-562-702A-32 Sequence 32, Appl
982 25 80.6 1572 2 US-09-561-818A-28 Sequence 28, Appl
983 25 80.6 1572 2 US-10-037-182-20 Sequence 20, Appl
984 25 80.6 1605 2 US-09-562-702A-30 Sequence 30, Appl
985 25 80.6 1605 2 US-10-037-182-18 Sequence 26, Appl
986 25 80.6 1605 2 US-10-037-182-18 Sequence 18, Appl
987 25 80.6 1656 2 US-09-949-016-7247 Sequence 7247, Ap
988 25 80.6 1681 2 US-09-920-653B-3 Sequence 3, Appl1
989 25 80.6 1720 1 US-08-477-451-12 Sequence 12, Appl
990 25 80.6 1761 2 US-09-561-709B-1 Sequence 1, Appl1
991 25 80.6 1792 2 US-09-561-818A-12 Sequence 12, Appl
992 25 80.6 1816 2 US-09-561-818A-10 Sequence 10, Appl
993 25 80.6 1821 2 US-09-949-016-5938 Sequence 5938, Ap
994 25 80.6 1833 2 US-08-479-722B-2 Sequence 2, Appl1
995 25 80.6 1833 2 US-09-592-685-2 Sequence 2, Appl1
996 25 80.6 1833 4 PCT-US95-02251-18 Sequence 18, Appl
997 25 80.6 2050 1 US-08-347-594A-2 Sequence 2, Appl1
998 25 80.6 2109 2 US-08-646-695-6 Sequence 6, Appl1
999 25 80.6 2109 4 PCT-US96-06053-6 Sequence 6, Appl1
1000 25 80.6 2813 2 US-09-381-261A-1 Sequence 1, Appl1

```

ALIGNMENTS

```

; REGISTRATION NUMBER: 32750
; REFERENCE/DOCKET NUMBER: GBRO-024/00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-7622
; TELEFAX: (415) 857-0663
; TELEEX: 380816 COOLEY PA
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: redox sequence typical for thioredoxins
; LOCATION: 1..4
US-07-820-688A-5
Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4

```

```

RESULT 1
US-07-820-688A-5
; Sequence 5, Application US/07820688A
; Patent No. 5328839
; GENERAL INFORMATION:
; APPLICANT: AHARONOWITZ, YAIR
; APPLICANT: VAN DER VOORT, LUCIA H
; APPLICANT: COHEN, GERALD
; APPLICANT: BOVENBERG, ROELOF A. L.
; APPLICANT: SCHREIBER, RACHEL
; APPLICANT: ARGAMAN, ANAT
; APPLICANT: AV-GAY, YOSEF
; APPLICANT: NAN, HELENA M.
; APPLICANT: KATTEVILDER, ALFRED
; APPLICANT: PALLISSER, HARRIET
; TITLE OF INVENTION: AN OXIDO REDUCTASE ENZYME SYSTEM
; TITLE OF INVENTION: OBTAINABLE FROM P. CHRYSOGENUM, THE SET OF GENES ENCODING
; TITLE OF INVENTION: THE SAME AND THE USE OF OXIDO REDUCTASE ENZYME SYSTEMS OR
; TITLE OF INVENTION: GENES ENCODING THE SAME FOR INCREASING ANTIBIOTIC PRODUCTION
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,688A
; FILING DATE: 19920324
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/NU91/00101
; FILING DATE: 18-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER PH.D., BARBARA

```

```

RESULT 2
US-08-274-043B-5
; Sequence 5, Application US/08274043B
; Patent No. 5652132
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yosef
; APPLICANT: Nan, Helena M.
; APPLICANT: Kattevilder, Alfred
; APPLICANT: Pallisa, Harriet
; TITLE OF INVENTION: An oxido reductase enzyme system obtainable from
; TITLE OF INVENTION: P. chrysogenum, the set of genes encoding the same and the us.
; TITLE OF INVENTION: oxido reductase enzyme systems or genes encoding the same for
; TITLE OF INVENTION: Increasing antibiotic production
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: P.O. Box 60039
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/274,043B
; FILING DATE: 12-JULY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NU91/00101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EPO 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/01US

```


TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: redox sequence typical for thioredoxins
LOCATION: 1..4
US-08-274-043B-5

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 3
US-08-386-729A-5
Sequence 5, Application US/08386729A
Patent No. 5753435

GENERAL INFORMATION:

APPLICANT: Anonowiltz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.
APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yosef
APPLICANT: Nan, Helena M.
APPLICANT: Kaltefleiter, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
TITLE OF INVENTION: production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotshall & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/NL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: redox sequence typical for thioredoxins
LOCATION: 1..4
US-08-386-729A-5

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 4
US-08-687-276-3
Sequence 3, Application US/08687276
Patent No. 5910435

GENERAL INFORMATION:

APPLICANT: Raines, Ronald T
TITLE OF INVENTION: SYNTHETIC PROTEIN FOLDING CATALYSIS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinechney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,276
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296.93952
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-687-276-3

Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 5
US-08-883-804-2
Sequence 2, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOPROXIN-LIKE MOLECULES FOR
TITLE OF INVENTION: INDUCTION OF MMSD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connel1, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-2
Query Match 100.0%; Score 31; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 6
US-08-504-538A-21
Sequence 21, Application US/08504538A
Patent No. 6004746
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: McCoy, John M.
APPLICANT: Jensen, Tim H.
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING
TITLE OF INVENTION: PROTEIN INTERACTIONS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2214
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,538A
FILING DATE: 07/20/95
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,082
FILING DATE: 07/20/94
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/259001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-504-538A-21
Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 7
US-09-579-883A-1
Sequence 1, Application US/09579883A
Patent No. 6686443
GENERAL INFORMATION:
APPLICANT: RABENSTEIN, DALLAS
APPLICANT: SHI, TIESHENG
TITLE OF INVENTION: CHEMICAL REAGENTS FOR FORMATION OF DISULFIDE BONDS IN PEPTIDES
FILE REFERENCES: 407T-891100US
CURRENT APPLICATION NUMBER: US/09/579,883A
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patent version 3.0
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-579-883A-1
Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 1 CGPC 4
RESULT 8
US-09-679-705-2
Sequence 2, Application US/09679705
Patent No. 6872563
GENERAL INFORMATION:
APPLICANT: BECKWITH, JONATHAN
APPLICANT: ASLUND, FREDRIK
APPLICANT: BRESSETTE, PAUL H.
APPLICANT: GEORGIU, GEORGE
APPLICANT: RITZ, DANIEL
APPLICANT: LIM, JACKIE EUN-AH

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
FILE REFERENCE: HMV-052.01
CURRENT APPLICATION NUMBER: US/09/679,705
CURRENT FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/157,770
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/163,939
PRIOR FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/166,044
PRIOR FILING DATE: 1999-11-17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 2
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-679-705-2

Query Match 100.0%; Score 31; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 9

US-08-883-804-4
Sequence 4, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
INDUCTION OF MMSOD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-4

Query Match 100.0%; Score 31; DB 1; Length 6;

Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 10

US-08-883-804-5
Sequence 5, Application US/08883804
Patent No. 5985261
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: Das, Kumuda C.
TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
INDUCTION OF MMSOD TO TREAT OXIDATIVE DAMAGE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Rose P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,804
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-40
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-883-804-5

Query Match 100.0%; Score 31; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 11

US-08-627-907A-6
Sequence 6, Application US/08627907A
Patent No. 6060302
GENERAL INFORMATION:
APPLICANT: HIRANO, Naoto
APPLICANT: HIRAI, Hisamaru
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
SEQUENCE ENCODING THE SAME
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,907A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-238402
FILING DATE: 24-SEP-1993
PRIOR APPLICATION DATA: PCT/JP94/01572
APPLICATION NUMBER: PCT/JP94/01572
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JR., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-627-907A-6

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 12
US-07-901-713A-3
Sequence 3, Application US/07901713A
GENERAL INFORMATION:
PATENT No. 6291205
APPLICANT: Tuttle, Michael F.
APPLICANT: Freedman, Robert B.
APPLICANT: Markus, Henry Z.
APPLICANT: Schultz, Loren D.
APPLICANT: Montgomery, Donna L.
APPLICANT: Ellis, Ronald W.
TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
FILE REFERENCE: 18469
CURRENT APPLICATION NUMBER: US/07/901,713A
CURRENT FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S. cerevisiae PDI thioredoxin active site
US-07-901-713A-3

Query Match 100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 13
US-08-571-985-27
Sequence 27, Application US/08571985
Patent No. 5783557
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rycus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
TITLE OF INVENTION: Compositions Comprising Them
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5783557thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,985
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 2163.00048
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-571-985-27

Query Match 100.0%; Score 31; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 14
US-09-116-766-27
Sequence 27, Application US/09116766
Patent No. 5968898
GENERAL INFORMATION:
APPLICANT: Burstein, Yigal
APPLICANT: Trainin, Nathan
APPLICANT: Rycus, Avigail
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical
TITLE OF INVENTION: Compositions Comprising Them
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5968898thwestern Hwy., Suite 410

CITY: Farmington Hills
STATE: Michigan
COUNTRY: USA
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,766
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 106214
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 2163.00050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-116-766-27

Query Match 100.0%; Score 31; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 3 CGPC 6

RESULT 15
US-08-836-480-34
Sequence 34, Application US/08836480
Patent No. 6103697
GENERAL INFORMATION:
APPLICANT: Bergstrand, Hakan
APPLICANT: Erickson, Tomas
APPLICANT: Karabelas, Kostas
APPLICANT: Lindvall, Magnus
APPLICANT: Sarnstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,480
FILING DATE: 14-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 95\403256-8
FILING DATE: 14-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 06275/036001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-480-34

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 3 CGPC 6

RESULT 16
US-09-562-897-34
Sequence 34, Application US/09562897
Patent No. 6228374
GENERAL INFORMATION:
APPLICANT: Bergstrand, Hakan
APPLICANT: Erickson, Tomas
APPLICANT: Karabelas, Kostas
APPLICANT: Lindvall, Magnus
APPLICANT: Sarnstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/562,897
FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,480
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34, 819
REFERENCE/DOCKET NUMBER: 06275/036001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-09-562-897-34

Query Match 100.0%; Score 31; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 3 CGPC 6

RESULT 17
US-08-750-142B-54
Sequence 54, Application US/08750142B
Patent No. 6228373
GENERAL INFORMATION:
APPLICANT: Bergstrand, Hakan
APPLICANT: Eriksson, Tomas
APPLICANT: Lindvall, Magnus
APPLICANT: Sarnstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH
TITLE OF INVENTION: IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
City: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,142B
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00365
FILING DATE: 22-MAR-1996
APPLICATION NUMBER: SE9501067-4
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06275/062001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-750-142B-54

Query Match 100.0%; Score 31; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 2 CGPC 5

RESULT 18
US-09-160-513-217
Sequence 217, Application US/09160513
Patent No. 6410775
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
APPLICANT: Marguis, David M.
APPLICANT: Jones, David S.
APPLICANT: Yu, Lin
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:

ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,513
FILING DATE: 1998-DEC-24
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-160-513-217

Query Match 100.0%; Score 31; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 4 CGPC 7

RESULT 19
US-09-230-041-31
Sequence 31, Application US/09230041A
Patent No. 6465179
GENERAL INFORMATION:
APPLICANT: THIREOS, GEORGE
APPLICANT: KARETZOPoulos, DIMITRIS
TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
CURRENT APPLICATION NUMBER: US/09/230,041A
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: EP97108240.9
EARLIER FILING DATE: 1997-05-21
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
LENGTH: 28
TYPE: PRT
ORGANISM: Rhizobium leguminosarum
US-09-230-041-31

Query Match 100.0%; Score 31; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 21 CGPC 24

RESULT 20
US-09-881-572A-25

```
; Sequence 25, Application US/09881572A
; Patent No. 6762031
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: PRF
; ORGANISM: Amphotrophic Murine Leukemia Virus
US-09-881-572A-25

Query Match          100.0%; Score 31; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 11 CGPC 14

RESULT 21
US-09-881-572A-5
; Sequence 5, Application US/09881572A
; Patent No. 6762031
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: Bupp, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRF
; ORGANISM: amphotrophic murine leukemia virus
US-09-881-572A-5

Query Match          100.0%; Score 31; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 11 CGPC 14

RESULT 22
US-10-044-359-26
; Sequence 26, Application US/10044359
; Patent No. 6740743
; GENERAL INFORMATION:
; APPLICANT: Heriman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: BBI367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
```

```
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 35
; TYPE: PRF
; ORGANISM: Androctonus mauretanicus
US-10-044-359-26

Query Match          100.0%; Score 31; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 1 CGPC 4

RESULT 23
US-08-239-256-16
; Sequence 16, Application US/08239256
; Patent No. 5585345
; GENERAL INFORMATION:
; APPLICANT: BOIME, IRVING
; APPLICANT: MATZIK, MARTIN M.
; APPLICANT: KEENE, JEFFREY L.
; TITLE OF INVENTION: CTP EXTENDED FORM OF LH
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave. N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,256
; FILING DATE: 06-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20030.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-239-256-16

Query Match          100.0%; Score 31; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 23 CGPC 26

RESULT 24
US-09-244-583-20
; Sequence 20, Application US/09244583
```

```
; Patent No. 6479654
; GENERAL INFORMATION:
; APPLICANT: BAIRD, ANDREW
; APPLICANT: ANDREASON, GRAI
; TITLE OF INVENTION: NOVEL FORMS OF THE ANGIOGENIC FACTOR
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR: VEGF
; FILE REFERENCE: 240/086
; CURRENT APPLICATION NUMBER: US/09/244,583
; CURRENT FILING DATE: 1999-02-04
; EARLIER APPLICATION NUMBER: 60/073,979
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-244-583-20
```

```
Query Match          100.0%; Score 31; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      |||||
Db      2 CGPC 5
```

```
RESULT 25
US-09-583-638-11
; Sequence 11, Application US/09583638
; Patent No. 6635421
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, MICHAEL
; APPLICANT: SOKER, SHAY
; APPLICANT: MIAO, HUA-QUNAN
; APPLICANT: TAKASHIMA, SEIJI
; TITLE OF INVENTION: NEUROFILINS AND USE THEREOF IN METHODS FOR
; TITLE OF INVENTION: DIAGNOSIS AND PROGNOSIS OF CANCER
; FILE REFERENCE: 701039-48800
; CURRENT APPLICATION NUMBER: US/09/583,638
; CURRENT FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US98/26127
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-583-638-11
```

```
Query Match          100.0%; Score 31; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      |||||
Db      2 CGPC 5
```

```
RESULT 26
US-09-579-420B-1
; Sequence 1, Application US/09579420B
; Patent No. 6777534
; GENERAL INFORMATION:
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Soker, Shay
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
```

```
; FILE REFERENCE: 701039-047875-C
; CURRENT APPLICATION NUMBER: US/09/579,420B
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: PCT/US98/26103
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-579-420B-1
```

```
Query Match          100.0%; Score 31; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      |||||
Db      2 CGPC 5
```

```
RESULT 27
US-09-579-420B-19
; Sequence 19, Application US/09579420B
; Patent No. 6777534
; GENERAL INFORMATION:
; APPLICANT: Klagsbrun, Michael
; APPLICANT: Soker, Shay
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
; FILE REFERENCE: 701039-047875-C
; CURRENT APPLICATION NUMBER: US/09/579,420B
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: PCT/US98/26103
; PRIOR FILING DATE: 1998-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-579-420B-19
```

```
Query Match          100.0%; Score 31; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      |||||
Db      2 CGPC 5
```

```
RESULT 28
US-09-513-999C-7252
; Sequence 7252, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Ducleart, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.RBG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
```


PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 7252
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 15
OTHER INFORMATION: Xaa= * or Glu or Gly or Trp
US-09-513-999C-7252

Query Match 100.0%; Score 31; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 8 CGPC 11

RESULT 29

US-09-513-999C-5904
Sequence 5904, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5904
LENGTH: 53
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa=Arg or Ser or Thr
US-09-513-999C-5904

Query Match 100.0%; Score 31; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 34 CGPC 37

RESULT 30

US-09-513-999C-5905
Sequence 5905, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5905
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 2
OTHER INFORMATION: Xaa=Ala or Ser
FEATURE:
NAME/KEY: UNSURE
LOCATION: 27
OTHER INFORMATION: Xaa=Arg or Ser or Thr
US-09-513-999C-5905

Query Match 100.0%; Score 31; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 34 CGPC 37

RESULT 31

US-09-902-540-11828
Sequence 11828, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 11828
LENGTH: 77
TYPE: PRT
ORGANISM: Myxococcus xanthus
US-09-902-540-11828

Query Match 100.0%; Score 31; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 32

US-09-630-273-2
Sequence 2, Application US/09630273
Patent No. 6521416
GENERAL INFORMATION:
APPLICANT: Birken et al, Steven
TITLE OF INVENTION: Determination Of The Amount Of h1h Beta Core Fragment
FILE REFERENCE: 54204-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/630,273
CURRENT FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US99/02279
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2

LENGTH: 80
TYPE: PRT
ORGANISM: Homo sapiens
US-09-630-273-2

Query Match 100.0%; Score 31; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 77 CGPC 80

RESULT 33
US-09-621-976-6168
Sequence 6168, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 6168
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-6168

Query Match 100.0%; Score 31; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 63 CGPC 66

RESULT 34
US-09-198-452A-697
Sequence 697, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Grifflais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198.452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 697
LENGTH: 102
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-198-452A-697

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 28 CGPC 31

RESULT 35
US-09-621-976-5629

Sequence 5629, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 5629
LENGTH: 102
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -35..-1
US-09-621-976-5629

Query Match 100.0%; Score 31; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 35 CGPC 38

RESULT 36
US-08-241-853-27
Sequence 27, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241.853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-241-853-27

Query Match 100.0%; Score 31; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 49 CGPC 52

RESULT 37

US-08-850-917-27
Sequence 27, Application US/08850917
Patent No. 5854045

GENERAL INFORMATION:

APPLICANT: Fang, Kathy S.
HANAFLISA, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/850,917

CLASSIFICATION: 435

FILING DATE: 02-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/241,853

FILING DATE: 12-MAY-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-078

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 103 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics

FILE REFERENCE: PATH00-07A

CURRENT APPLICATION NUMBER: US/09/563,110

CURRENT FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/107,433

PRIOR FILING DATE: 1998-06-30

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: US 60/051,553

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 3078

LENGTH: 104

TYPE: PRT

ORGANISM: Streptococcus pneumoniae

US-09-583-110-3078

Query Match 100.0%; Score 31; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 28 CGPC 31

RESULT 39

5210073-1

Patent No. 5210073

APPLICANT: YODOI, JUNJI;UCHIDA, ATSUSHI;TAGAWA, YUTAKA

MITSUI, AKIRA;HIRAKAWA, TADASHI

TITLE OF INVENTION: METHOD FOR TREATING CANCER THERAPY

RADIATION DAMAGE OR ARTERIOSCLEROSIS USING HUMAN ADP

NUMBER OF SEQUENCES: 1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/569,616

FILING DATE: 28-SEP-1990

SEQ ID NO:1;

LENGTH: 104

5210073-1

Query Match 100.0%; Score 31; DB 6; Length 104;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

Db 31 CGPC 34

RESULT 40

US-08-826-910-3

Sequence 3, Application US/08826910

Patent No. 5919657

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 339649
;
US-08-826-910-3

Query Match          100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
Db       32 CGPC 35

RESULT 41
US-08-826-910-4
; Sequence 4, Application US/08826910
; Patent No. 5919657
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: THIOREDUXIN-LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/826,910
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0268 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 453972
;
US-08-826-910-4

Query Match          100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
Db       32 CGPC 35

RESULT 42
US-09-601-144-68
; Sequence 68, Application US/09601144
; Patent No. 656514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDUXIN
; TITLE OF INVENTION: AND THIOREDUXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-1120S-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
;
US-09-601-144-68

Query Match          100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
Db       32 CGPC 35

RESULT 43
US-09-513-999C-8037
; Sequence 8037, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8037
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-513-999C-8037
```

```

;
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 453972
;
US-08-826-910-4

Query Match          100.0%; Score 31; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
Db       32 CGPC 35

RESULT 42
US-09-601-144-68
; Sequence 68, Application US/09601144
; Patent No. 656514
; GENERAL INFORMATION:
; APPLICANT: Wright, Jim A.
; APPLICANT: Young, Aiping H.
; APPLICANT: Lee, Yoon S.
; TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDUXIN
; TITLE OF INVENTION: AND THIOREDUXIN REDUCTASE GENES AND METHODS OF USING
; TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
; FILE REFERENCE: 683-1120S-A
; CURRENT APPLICATION NUMBER: US/09/601,144
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US 60/073,196
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Human
;
US-09-601-144-68

Query Match          100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
Db       32 CGPC 35

RESULT 43
US-09-513-999C-8037
; Sequence 8037, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8037
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-513-999C-8037
```

Query Match 100.0%; Score 31; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 44
US-08-386-729A-10
; Sequence 10, Application US/08386729A
; Patent No. 5753435
; GENERAL INFORMATION:
; APPLICANT: Aharonowitz, Yair
; APPLICANT: Van Der Voort, Lucia H. M.
; APPLICANT: Cohen, Gerald
; APPLICANT: Bovenberg, Roelof A. L.
; APPLICANT: Schreiber, Rachel
; APPLICANT: Argaman, Anat
; APPLICANT: Av-Gay, Yosef
; APPLICANT: Nan, Helena M.
; APPLICANT: Katsvilder, Alfred
; APPLICANT: Pallisa, Harriet
; TITLE OF INVENTION: An oxidoreductase enzyme system
; TITLE OF INVENTION: obtainable from P. chrysoenum, the set of genes
; TITLE OF INVENTION: encoding the same and the use of oxidoreductase enzyme
; TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weil, Gotshal & Manges
; STREET: 2882 Sand Hill Road, Ste. 280
; CITY: Menlo Park
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,729A
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/274,043
; FILING DATE: 12-JULY-1994
; APPLICATION NUMBER: US 07/820,688
; FILING DATE: 24-MARCH-1992
; APPLICATION NUMBER: PCT/NL91/000101
; FILING DATE: 18-JUNE-1991
; APPLICATION NUMBER: EP 90201598.1
; FILING DATE: 18-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Ventler, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: GBRO-024/02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 926-6200
; TELEFAX: (415) 854-3713
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-386-729A-10

Query Match 100.0%; Score 31; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 45
US-09-383-586-13
; Sequence 13, Application US/09383586
; Patent No. 6242419
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevil
; APPLICANT: Orrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compounds isolated from stromal cells
; TITLE OF INVENTION: and methods for their use
; FILE REFERENCE: 11000.1037c1
; CURRENT APPLICATION NUMBER: US/09/383,586
; CURRENT FILING DATE: 1999-08-26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
; US-09-383-586-13

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 46
US-09-823-038A-13
; Sequence 13, Application US/09823038A
; Patent No. 6797271
; GENERAL INFORMATION:
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Abernethy, Nevil
; APPLICANT: Orrust, Rene
; APPLICANT: Kumble, Anand
; APPLICANT: Murison, Greg
; TITLE OF INVENTION: Compositions isolated from Stromal Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1037c3
; CURRENT APPLICATION NUMBER: US/09/823,038A
; CURRENT FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Mouse
; US-09-823-038A-13

Query Match 100.0%; Score 31; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 47
US-07-745-382-22
Sequence 22, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioresdoxin and Thioresdoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cseer, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-382-22
Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 33 CGPC 36
RESULT 48
US-07-921-848-22
Sequence 22, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioresdoxin and Thioresdoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Cseer, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-22
Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CGPC 5
Db 33 CGPC 36
RESULT 49
US-08-165-301A-22
Sequence 22, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: G1 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-22

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 33 CGPC 36

RESULT 50
US-08-165-301A-26
Sequence 26, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-26

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 33 CGPC 36

RESULT 51
US-08-165-301A-28
Sequence 28, Application US/08165301A
Patent No. 5646016

GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-28

Query Match 100.0%; Score 31; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 33 CGPC 36

RESULT 52
US-08-810-436-22
Sequence 22, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-22

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 53
US-08-810-436-26
Sequence 26, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlaasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:

LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-26

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 54
US-08-810-436-28
Sequence 28, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlaasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-28

Query Match 100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 55
US-09-485-885-17


```
; Sequence 17, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchetkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-17

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      33 CGPC 36

RESULT 56
US-09-166-966E-10
; Sequence 10, Application US/09166366E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: thioredoxin
; LOCATION: 1..109
; OTHER INFORMATION: amino acid of thioredoxin
US-09-166-966E-10

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      33 CGPC 36

RESULT 57
US-09-248-796A-19911
; Sequence 19911, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
```

```
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19911
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19911

Query Match          100.0%; Score 31; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      36 CGPC 39

RESULT 58
PCT-US94-14179-22
; Sequence 22, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14179-22

Query Match          100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 CGPC 5
|||
Db 33 CGPC 36

RESULT 59
PCT-US94-14179-26
; Sequence 26, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBasilio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiner, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14179-26
Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 33 CGPC 36
RESULT 60
PCT-US94-14179-28
; Sequence 28, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBasilio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-28
Query Match 100.0%; Score 31; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 33 CGPC 36
RESULT 61
US-09-621-976-4028
; Sequence 4028, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4028
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -102...-1
US-09-621-976-4028
Query Match 100.0%; Score 31; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CGPC 5
|||
Db 74 CGPC 77
RESULT 62
US-09-264-419C-6
; Sequence 6, Application US/09264419C
; Patent No. 6174682
; GENERAL INFORMATION:

APPLICANT: Rhododouct, Mehran
TITLE OF INVENTION: No. 6174682a1 Thioresdoin Family Active Site Molecules and Uses
FILE OF INVENTION: Therefor
FILE REFERENCE: WNI-076
CURRENT APPLICATION NUMBER: US/09/264,419C
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 111
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-264-419C-6

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 111;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 63
US-09-134-001C-3859
Sequence 3859, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3859
LENGTH: 111
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3859

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 111;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 36 CGPC 39

RESULT 64
US-09-107-532A-6739
Sequence 6739, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSER: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6739:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...112
SEQUENCE DESCRIPTION: SEQ ID NO: 6739:
US-09-107-532A-6739

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 112;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 36 CGPC 39

RESULT 65
US-10-104-047-3199
Sequence 3199, Application US/10104047
Patent No. 6943241
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. 6943241a1 full length cDNA
FILE REFERENCE: HI-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3199
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-10-104-047-3199

Query Match
Best Local Similarity 100.0%; Score 31; DB 2; Length 113;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 37 CGPC 40

RESULT 66
US-08-918-288-71
Sequence 71, Application US/08918288
Patent No. 623890
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-71
Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 90 CGPC 93

RESULT 67
US-09-282-357-71
Sequence 71, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
City: Washington
STATE: DC

COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-357-71
Query Match 100.0%; Score 31; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 90 CGPC 93

RESULT 68
US-09-897-425-41
Sequence 41, Application US/09897425
Patent No. 6750046
GENERAL INFORMATION:
APPLICANT: MOLONEY, MAURICE M.
APPLICANT: DALMIA, BIPIN K.
TITLE OF INVENTION: PREPARATION OF THIOREDUXIN AND THIOREDUXIN REDUCTASE
TITLE OF INVENTION: PROTEINS ON OIL BODIES
FILE REFERENCE: 034547/0106
CURRENT APPLICATION NUMBER: US/09/897,425
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 09/210,843
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/846,021
PRIOR FILING DATE: 1997-04-25
PRIOR APPLICATION NUMBER: 08/366,783
PRIOR FILING DATE: 1994-12-30
PRIOR APPLICATION NUMBER: 08/142,418
PRIOR FILING DATE: 1993-11-16
PRIOR APPLICATION NUMBER: 07/659,835
PRIOR FILING DATE: 1991-02-22
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 114
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-897-425-41

Query Match 100.0%; Score 31; DB 2; Length 114;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
 ||||
 Db 40 CGPC 43

RESULT 69
 US-09-107-433-2930

; Sequence 2930, Application US/09107433
 ; Patent No. 6800744

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID

; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN
 THERAPEUTICS

; NUMBER OF SEQUENCES: 5206

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: <Unknown>

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: <Unknown>

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,433

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085131

; FILING DATE: May 12, 1998

; APPLICATION NUMBER: 60/051553

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Arinello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-011

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 2930:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 114 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus pneumoniae

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: (B) LOCATION 1...114

; SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

US-09-107-433-2930

Query Match 100.0%; Score 31; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
 ||||
 Db 38 CGPC 41

RESULT 70

US-09-786-715-11

; Sequence 11, Application US/09786715

; Patent No. 6897356
 ; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Lu, Albert

; APPLICANT: Thorpe, Cathy

; TITLE OF INVENTION: Thiolredoxin H Homologs

; FILE REFERENCE: BB-1246

; CURRENT APPLICATION NUMBER: US/09/786,715

; PRIOR FILING DATE: 2001-06-25

; PRIOR APPLICATION NUMBER: 60/099,501

; PRIOR FILING DATE: September 8, 1998

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Microsoft Office 97

; SEQ ID NO: 11

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-786-715-11

Query Match 100.0%; Score 31; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
 ||||
 Db 40 CGPC 43

Search completed: February 23, 2006, 00:43:45
 Job time : 44.5 secs

113 Page Blank (us910)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:47 ; Search time 116.5 Seconds
(without alignments)
21.519 Million cell updates/sec

Title: US-10-660-118a-2

Perfect score: 31

Sequence: 1 XGCPX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 41782326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA.Main:

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep.*
3: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep.*
4: /cgn2_6/prodata/1/pubppa/US10A_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep.*
6: /cgn2_6/prodata/1/pubppa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	4	US-10-286-516a-11	Sequence 11, Appl
2	31	100.0	4	US-10-234-319a-1	Sequence 1, Appl
3	31	100.0	4	US-10-369-094-1	Sequence 1, Appl
4	31	100.0	4	US-10-660-118a-1	Sequence 1, Appl
5	31	100.0	4	US-10-628-391-2	Sequence 2, Appl
6	31	100.0	4	US-10-776-933-149	Sequence 149, Appl
7	31	100.0	6	US-10-304-287-4	Sequence 4, Appl
8	31	100.0	6	US-10-290-072-233	Sequence 233, Appl
9	31	100.0	6	US-10-461-224-5	Sequence 5, Appl
10	31	100.0	6	US-10-660-118a-2	Sequence 3, Appl
11	31	100.0	6	US-10-660-118a-3	Sequence 17, Appl
12	31	100.0	6	US-10-735-577-4	Sequence 10, Appl
13	31	100.0	8	US-10-954-951-11	Sequence 11, Appl
14	31	100.0	10	US-09-572-404b-918	Sequence 918, Appl
15	31	100.0	10	US-09-572-404b-970	Sequence 970, Appl
16	31	100.0	14	US-10-615-343-2	Sequence 2, Appl
17	31	100.0	16	US-10-044-844-217	Sequence 217, Appl
18	31	100.0	16	US-10-846-079-217	Sequence 217, Appl
19	31	100.0	19	US-09-963-339-217	Sequence 10, Appl
20	31	100.0	19	US-10-145-586-59	Sequence 59, Appl
21	31	100.0	25	US-10-050-882-98	Sequence 98, Appl
22	31	100.0	25	US-10-963-903-98	Sequence 98, Appl
23	31	100.0	25	US-10-179-382-31	Sequence 31, Appl
24	31	100.0	28	US-09-881-572a-25	Sequence 25, Appl
25	31	100.0	30	US-09-881-572a-5	Sequence 5, Appl
26	31	100.0	32	US-09-864-761-40069	Sequence 40069, A
27	31	100.0	32	US-09-864-761-40069	Sequence 40069, A

28	31	100.0	32	US-10-424-599-160512	Sequence 160512,
29	31	100.0	35	US-10-044-359-26	Sequence 26, Appl
30	31	100.0	36	US-09-801-260-5	Sequence 5, Appl
31	31	100.0	36	US-10-145-586-44	Sequence 44, Appl
32	31	100.0	42	US-10-450-763-51435	Sequence 51435, A
33	31	100.0	43	US-09-864-761-35367	Sequence 35367, A
34	31	100.0	43	US-10-293-157-20	Sequence 20, Appl
35	31	100.0	43	US-10-424-599-255327	Sequence 255327, A
36	31	100.0	44	US-09-833-355A-3	Sequence 3, Appl
37	31	100.0	44	US-10-104-440-11	Sequence 11, Appl
38	31	100.0	44	US-10-104-610-15	Sequence 15, Appl
39	31	100.0	45	US-10-424-599-252212	Sequence 252212, A
40	31	100.0	47	US-10-425-115-210616	Sequence 210616, A
41	31	100.0	47	US-10-425-115-321622	Sequence 321622, A
42	31	100.0	47	US-11-097-143-37521	Sequence 37521, A
43	31	100.0	49	US-10-425-115-34172	Sequence 34172, A
44	31	100.0	52	US-09-801-260-4	Sequence 4, Appl
45	31	100.0	52	US-10-145-586-43	Sequence 43, Appl
46	31	100.0	52	US-10-437-963-164055	Sequence 164055, A
47	31	100.0	53	US-10-424-599-16951	Sequence 16951, A
48	31	100.0	55	US-09-864-761-42458	Sequence 42458, A
49	31	100.0	55	US-10-318-302-2	Sequence 2, Appl
50	31	100.0	55	US-10-425-115-307743	Sequence 307743, A
51	31	100.0	55	US-10-868-577a-28	Sequence 28, Appl
52	31	100.0	55	US-11-097-143-26469	Sequence 26469, A
53	31	100.0	56	US-10-425-115-219153	Sequence 219153, A
54	31	100.0	57	US-11-097-143-26490	Sequence 26490, A
55	31	100.0	57	US-10-029-386-28568	Sequence 28568, A
56	31	100.0	57	US-10-425-115-353222	Sequence 353222, A
57	31	100.0	58	US-10-424-599-185374	Sequence 185374, A
58	31	100.0	58	US-10-437-963-202381	Sequence 202381, A
59	31	100.0	59	US-10-424-599-176362	Sequence 176362, A
60	31	100.0	60	US-09-864-408a-7494	Sequence 7494, A
61	31	100.0	60	US-11-097-143-10200	Sequence 10200, A
62	31	100.0	62	US-10-424-599-278438	Sequence 278438, A
63	31	100.0	63	US-10-425-115-223772	Sequence 223772, A
64	31	100.0	64	US-11-097-143-26472	Sequence 26472, A
65	31	100.0	65	US-10-425-115-336734	Sequence 336734, A
66	31	100.0	65	US-10-424-599-180203	Sequence 180203, A
67	31	100.0	67	US-10-437-963-152827	Sequence 152827, A
68	31	100.0	67	US-10-425-115-26158	Sequence 26158, A
69	31	100.0	67	US-11-097-143-32565	Sequence 32565, A
70	31	100.0	68	US-10-243-552-978	Sequence 978, Appl
71	31	100.0	68	US-10-425-115-276302	Sequence 276302, A
72	31	100.0	68	US-10-450-763-46542	Sequence 46542, A
73	31	100.0	69	US-10-437-963-163370	Sequence 163370, A
74	31	100.0	69	US-10-437-963-165021	Sequence 165021, A
75	31	100.0	69	US-10-425-115-268198	Sequence 268198, A
76	31	100.0	70	US-10-424-599-261419	Sequence 261419, A
77	31	100.0	71	US-10-425-115-279845	Sequence 279845, A
78	31	100.0	71	US-09-764-875-1015	Sequence 1015, Appl
79	31	100.0	72	US-10-437-963-143715	Sequence 143715, A
80	31	100.0	72	US-10-437-963-199279	Sequence 199279, A
81	31	100.0	72	US-10-425-115-346964	Sequence 346964, A
82	31	100.0	72	US-11-097-143-26460	Sequence 26460, A
83	31	100.0	73	US-10-424-599-149108	Sequence 149108, A
84	31	100.0	73	US-10-424-599-179898	Sequence 179898, A
85	31	100.0	73	US-10-424-599-219036	Sequence 219036, A
86	31	100.0	74	US-10-425-115-341562	Sequence 341562, A
87	31	100.0	74	US-10-424-599-239804	Sequence 239804, A
88	31	100.0	74	US-10-424-599-258570	Sequence 258570, A
89	31	100.0	74	US-10-450-763-56818	Sequence 56818, A
90	31	100.0	74	US-11-097-143-26457	Sequence 26457, A
91	31	100.0	75	US-10-156-761-12390	Sequence 12390, A
92	31	100.0	77	US-10-424-599-276894	Sequence 276894, A
93	31	100.0	77	US-10-425-115-307289	Sequence 307289, A
94	31	100.0	78	US-10-424-599-159506	Sequence 159506, A
95	31	100.0	78	US-10-424-599-241960	Sequence 241960, A
96	31	100.0	78	US-10-450-763-48586	Sequence 48586, A
97	31	100.0	78	US-10-450-763-52656	Sequence 52656, A
98	31	100.0	79	US-09-764-878-149	Sequence 149, Appl
99	31	100.0	79	US-10-079-854-149	Sequence 149, Appl
100	31	100.0	79	US-10-437-963-147189	Sequence 147189, A

101	31	100.0	80	3	US-09-864-761-42788	Sequence 42788, A	174	31	100.0	104	4	US-10-032-201B-146	Sequence 146, App
102	31	100.0	80	4	US-10-159-354-2	Sequence 2, App1	175	31	100.0	104	4	US-10-032-201B-150	Sequence 150, App
103	31	100.0	80	4	US-10-373-617A-3	Sequence 3, App1	176	31	100.0	104	4	US-10-032-201B-152	Sequence 152, App
104	31	100.0	80	4	US-10-424-599-150482	Sequence 150482, A	177	31	100.0	104	4	US-10-032-201B-154	Sequence 154, App
105	31	100.0	80	4	US-10-361-652-2	Sequence 2, App1	178	31	100.0	104	4	US-10-032-201B-155	Sequence 155, App
106	31	100.0	80	6	US-11-097-143-30585	Sequence 30585, A	179	31	100.0	104	4	US-10-032-201B-158	Sequence 158, App
107	31	100.0	81	4	US-10-311-129-34	Sequence 34, App1	180	31	100.0	104	4	US-10-032-201B-159	Sequence 159, App
108	31	100.0	81	4	US-10-425-115-311489	Sequence 311489, A	181	31	100.0	104	4	US-10-032-201B-161	Sequence 161, App
109	31	100.0	82	4	US-10-425-115-351019	Sequence 351019, A	182	31	100.0	104	4	US-10-032-201B-166	Sequence 166, App
110	31	100.0	83	4	US-10-424-599-216631	Sequence 216631, A	183	31	100.0	104	4	US-10-424-599-173662	Sequence 173662, A
111	31	100.0	83	4	US-10-425-115-243739	Sequence 243739, A	184	31	100.0	104	4	US-10-424-599-282588	Sequence 282588, A
112	31	100.0	83	4	US-10-425-115-312478	Sequence 312478, A	185	31	100.0	104	4	US-10-474-776-712	Sequence 712, App
113	31	100.0	83	4	US-10-425-115-362195	Sequence 362195, A	186	31	100.0	104	4	US-10-437-963-191626	Sequence 191626, A
114	31	100.0	83	5	US-10-450-763-52658	Sequence 52658, A	187	31	100.0	104	4	US-10-660-118A-5	Sequence 5, App1
115	31	100.0	84	4	US-10-408-765A-312	Sequence 312, App	188	31	100.0	104	4	US-10-451-467A-188	Sequence 188, App
116	31	100.0	84	4	US-10-425-115-310941	Sequence 310941, A	189	31	100.0	104	5	US-10-472-928-3670	Sequence 3670, App
117	31	100.0	84	4	US-10-425-115-316596	Sequence 316596, A	190	31	100.0	105	3	US-09-954-342-61	Sequence 61, App1
118	31	100.0	85	3	US-09-925-301-1356	Sequence 1356, App	191	31	100.0	105	4	US-10-171-311-226	Sequence 226, App
119	31	100.0	85	4	US-10-437-963-103422	Sequence 103422, A	192	31	100.0	105	4	US-10-316-253-291	Sequence 291, App1
120	31	100.0	85	4	US-10-425-115-210889	Sequence 210889, A	193	31	100.0	105	4	US-10-032-201B-47	Sequence 47, App1
121	31	100.0	86	4	US-10-767-701-60198	Sequence 60198, A	194	31	100.0	105	4	US-10-032-201B-94	Sequence 94, App1
122	31	100.0	88	4	US-10-032-201B-115	Sequence 115, App	195	31	100.0	105	4	US-10-032-201B-106	Sequence 106, App
123	31	100.0	88	4	US-10-032-201B-116	Sequence 116, App	196	31	100.0	105	4	US-10-032-201B-114	Sequence 114, App
124	31	100.0	88	4	US-10-425-115-351023	Sequence 351023, A	197	31	100.0	105	4	US-10-032-201B-118	Sequence 118, App
125	31	100.0	89	4	US-10-437-963-150151	Sequence 150151, A	198	31	100.0	105	4	US-10-032-201B-135	Sequence 135, App
126	31	100.0	89	4	US-10-425-115-185286	Sequence 185286, A	199	31	100.0	105	4	US-10-032-201B-184	Sequence 184, App
127	31	100.0	90	4	US-10-424-599-208931	Sequence 208931, A	200	31	100.0	105	4	US-10-424-599-237784	Sequence 237784, A
128	31	100.0	90	4	US-10-424-599-267688	Sequence 267688, A	201	31	100.0	105	4	US-10-351-891-127	Sequence 127, App
129	31	100.0	90	4	US-10-424-599-280571	Sequence 280571, A	202	31	100.0	105	4	US-10-408-765A-2019	Sequence 2019, App
130	31	100.0	90	4	US-10-425-115-190527	Sequence 190527, A	203	31	100.0	105	4	US-10-660-118A-8	Sequence 8, App1
131	31	100.0	90	4	US-10-425-115-288823	Sequence 288823, A	204	31	100.0	105	4	US-10-660-118A-9	Sequence 9, App1
132	31	100.0	91	4	US-10-032-201B-143	Sequence 143, App	205	31	100.0	105	4	US-10-660-118A-10	Sequence 10, App1
133	31	100.0	92	4	US-10-437-963-162872	Sequence 162872, A	206	31	100.0	105	4	US-10-660-118A-11	Sequence 11, App1
134	31	100.0	92	4	US-10-437-963-151713	Sequence 151713, A	207	31	100.0	105	4	US-10-660-118A-12	Sequence 12, App1
135	31	100.0	93	4	US-10-425-115-253563	Sequence 253563, A	208	31	100.0	105	4	US-10-451-467A-684	Sequence 684, App
136	31	100.0	94	5	US-10-972-024-484	Sequence 484, App	209	31	100.0	105	4	US-10-425-115-241180	Sequence 241180, A
137	31	100.0	95	4	US-10-424-599-285034	Sequence 285034, A	210	31	100.0	105	4	US-10-425-115-241829	Sequence 241829, A
138	31	100.0	95	4	US-10-425-115-230911	Sequence 230911, A	211	31	100.0	105	5	US-10-699-113-32	Sequence 32, App1
139	31	100.0	96	4	US-10-425-115-191803	Sequence 191803, A	212	31	100.0	105	5	US-10-970-370-2	Sequence 2, App1
140	31	100.0	96	4	US-10-425-115-286533	Sequence 286533, A	213	31	100.0	105	5	US-10-970-370-6	Sequence 6, App1
141	31	100.0	96	4	US-10-425-115-334150	Sequence 334150, A	214	31	100.0	106	3	US-09-823-038A-13	Sequence 13, App1
142	31	100.0	98	4	US-10-424-599-277258	Sequence 277258, A	215	31	100.0	106	4	US-10-032-201B-58	Sequence 58, App1
143	31	100.0	98	4	US-10-425-115-314721	Sequence 314721, A	216	31	100.0	106	4	US-10-032-201B-70	Sequence 70, App1
144	31	100.0	99	3	US-09-730-617-41	Sequence 41, App1	217	31	100.0	106	4	US-10-032-201B-113	Sequence 113, App
145	31	100.0	99	4	US-10-425-115-211714	Sequence 211714, A	218	31	100.0	106	4	US-10-032-201B-123	Sequence 123, App
146	31	100.0	99	4	US-10-425-115-367170	Sequence 367170, A	219	31	100.0	106	4	US-10-032-201B-132	Sequence 132, App
147	31	100.0	101	4	US-10-457-963-132710	Sequence 132710, A	220	31	100.0	106	4	US-10-032-201B-137	Sequence 137, App
148	31	100.0	102	4	US-10-032-201B-72	Sequence 72, App1	221	31	100.0	106	4	US-10-032-201B-140	Sequence 140, App
149	31	100.0	102	4	US-10-032-201B-102	Sequence 102, App	222	31	100.0	106	4	US-10-032-201B-146	Sequence 146, App
150	31	100.0	102	4	US-10-032-201B-103	Sequence 103, App	223	31	100.0	106	4	US-10-424-599-249497	Sequence 249497, A
151	31	100.0	102	4	US-10-032-201B-104	Sequence 104, App	224	31	100.0	106	4	US-10-425-114-48446	Sequence 48446, A
152	31	100.0	102	4	US-10-032-201B-105	Sequence 105, App	225	31	100.0	106	4	US-10-335-977-6752	Sequence 6752, App
153	31	100.0	102	4	US-10-032-201B-126	Sequence 126, App	226	31	100.0	106	4	US-10-032-201B-2072	Sequence 2072, App
154	31	100.0	102	4	US-10-032-201B-128	Sequence 128, App	227	31	100.0	106	4	US-10-628-391-1	Sequence 1, App1
155	31	100.0	102	4	US-10-289-762-697	Sequence 697, App	228	31	100.0	106	6	US-10-425-115-365910	Sequence 365910, A
156	31	100.0	102	5	US-10-275-652-20	Sequence 20, App1	229	31	100.0	107	3	US-11-097-143-7479	Sequence 7479, App
157	31	100.0	102	5	US-10-501-282-3126	Sequence 3126, App	230	31	100.0	107	4	US-09-746-783-19	Sequence 19, App1
158	31	100.0	103	4	US-10-032-201B-96	Sequence 96, App1	231	31	100.0	107	4	US-10-032-201B-71	Sequence 71, App1
159	31	100.0	103	4	US-10-032-201B-124	Sequence 124, App	232	31	100.0	107	4	US-10-032-201B-74	Sequence 74, App1
160	31	100.0	103	4	US-10-032-585-7785	Sequence 7785, App	233	31	100.0	107	4	US-10-032-201B-75	Sequence 75, App1
161	31	100.0	103	4	US-10-660-118A-6	Sequence 6, App1	234	31	100.0	107	4	US-10-032-201B-109	Sequence 109, App
162	31	100.0	103	4	US-10-660-118A-7	Sequence 7, App1	235	31	100.0	107	4	US-10-032-201B-121	Sequence 121, App
163	31	100.0	103	4	US-10-451-467A-270	Sequence 270, App	236	31	100.0	107	4	US-10-032-201B-139	Sequence 139, App
164	31	100.0	103	4	US-10-451-467A-450	Sequence 450, App	237	31	100.0	107	4	US-10-032-201B-151	Sequence 151, App
165	31	100.0	103	4	US-10-451-467A-614	Sequence 614, App	238	31	100.0	107	4	US-10-335-977-6753	Sequence 6753, App
166	31	100.0	103	4	US-10-425-115-186849	Sequence 186849, A	239	31	100.0	107	4	US-10-437-963-136226	Sequence 136226, A
167	31	100.0	103	4	US-10-425-115-243742	Sequence 243742, A	240	31	100.0	107	4	US-10-425-115-231345	Sequence 231345, A
168	31	100.0	103	4	US-10-425-115-280404	Sequence 280404, A	241	31	100.0	107	4	US-10-425-115-280315	Sequence 280315, A
169	31	100.0	104	3	US-09-954-342-62	Sequence 62, App1	242	31	100.0	107	4	US-10-425-115-30506	Sequence 308506, A
170	31	100.0	104	3	US-09-954-342-63	Sequence 63, App1	243	31	100.0	107	4	US-10-425-115-363988	Sequence 363988, A
171	31	100.0	104	3	US-09-954-342-64	Sequence 64, App1	244	31	100.0	107	6	US-11-097-143-8226	Sequence 8226, App
172	31	100.0	104	3	US-09-954-342-65	Sequence 65, App1	245	31	100.0	108	3	US-09-812-777-16	Sequence 16, App1
173	31	100.0	104	4	US-10-032-201B-134	Sequence 134, App	246	31	100.0	108	4	US-10-032-201B-101	Sequence 101, App

247	31	100.0	108	4	US-10-032-201B-117	Sequence 117, App	320	31	100.0	117	4	US-10-424-599-262611	Sequence 262611,
248	31	100.0	108	4	US-10-032-201B-133	Sequence 133, App	321	31	100.0	117	4	US-10-424-599-283863	Sequence 283863,
249	31	100.0	108	4	US-10-032-201B-142	Sequence 142, App	322	31	100.0	118	4	US-10-032-201B-82	Sequence 82, App
250	31	100.0	108	4	US-10-264-237-2386	Sequence 2386, Ap	323	31	100.0	118	4	US-10-032-201B-91	Sequence 91, App
251	31	100.0	108	4	US-10-424-599-149659	Sequence 149659,	324	31	100.0	118	4	US-10-767-701-46089	Sequence 46089, A
252	31	100.0	109	3	US-09-927-876-40	Sequence 40, App	325	31	100.0	118	4	US-10-425-115-200792	Sequence 200792,
253	31	100.0	109	4	US-10-000-903-17	Sequence 17, App	326	31	100.0	118	4	US-10-425-115-316523	Sequence 316523,
254	31	100.0	109	4	US-10-128-714-3073	Sequence 3073, Ap	327	31	100.0	118	5	US-10-978-538-4	Sequence 4, App
255	31	100.0	109	4	US-10-128-714-8073	Sequence 8073, Ap	328	31	100.0	118	5	US-10-978-538-10	Sequence 10, App
256	31	100.0	109	4	US-10-194-885-24	Sequence 24, App	329	31	100.0	118	5	US-10-978-538-13	Sequence 13, App
257	31	100.0	109	4	US-10-032-201B-43	Sequence 43, App	330	31	100.0	119	5	US-10-032-201B-175	Sequence 175, App
258	31	100.0	109	4	US-10-032-201B-73	Sequence 73, App	331	31	100.0	119	4	US-10-424-599-227977	Sequence 227977,
259	31	100.0	109	4	US-10-032-201B-93	Sequence 93, App	332	31	100.0	119	4	US-10-425-115-216847	Sequence 216847,
260	31	100.0	109	4	US-10-032-201B-141	Sequence 141, App	333	31	100.0	119	5	US-10-450-763-33266	Sequence 33266, A
261	31	100.0	109	4	US-10-032-201B-185	Sequence 185, App	334	31	100.0	120	3	US-09-737-149-26	Sequence 26, App
262	31	100.0	109	4	US-10-360-149-40	Sequence 40, App	335	31	100.0	120	4	US-10-424-599-10543	Sequence 190543,
263	31	100.0	109	4	US-10-460-524-11	Sequence 11, App	336	31	100.0	120	4	US-10-701-283-26	Sequence 26, App
264	31	100.0	109	4	US-10-424-599-185105	Sequence 185105,	337	31	100.0	120	4	US-10-425-115-283693	Sequence 283693,
265	31	100.0	109	4	US-10-424-999-22	Sequence 22, App	338	31	100.0	120	5	US-10-978-538-6	Sequence 6, App
266	31	100.0	109	4	US-10-457-047-40	Sequence 40, App	339	31	100.0	121	4	US-10-360-101-251	Sequence 251, App
267	31	100.0	109	4	US-10-437-963-157435	Sequence 157435,	340	31	100.0	121	4	US-10-424-599-158010	Sequence 158010,
268	31	100.0	109	4	US-10-660-118A-4	Sequence 4, App	341	31	100.0	121	4	US-10-437-963-117121	Sequence 117121,
269	31	100.0	109	4	US-10-767-701-51831	Sequence 51831, A	342	31	100.0	121	4	US-10-425-115-283977	Sequence 283977,
270	31	100.0	109	5	US-10-899-771-17	Sequence 17, App	343	31	100.0	121	4	US-10-425-115-360486	Sequence 360486,
271	31	100.0	109	5	US-10-811-081-40	Sequence 40, App	344	31	100.0	122	3	US-09-813-398-4	Sequence 4, App
272	31	100.0	109	5	US-10-913-944-40	Sequence 40, App	345	31	100.0	122	4	US-10-159-354-1	Sequence 9, App
273	31	100.0	109	5	US-10-970-370-4	Sequence 4, App	346	31	100.0	122	4	US-10-194-885-9	Sequence 9, App
274	31	100.0	110	3	US-09-864-761-42215	Sequence 42215, A	347	31	100.0	122	4	US-10-194-885-19	Sequence 19, App
275	31	100.0	110	4	US-10-156-761-11840	Sequence 11840, A	348	31	100.0	122	4	US-10-091-841-2	Sequence 21, App
276	31	100.0	110	4	US-10-032-201B-77	Sequence 77, App	349	31	100.0	122	4	US-10-091-841-2	Sequence 21, App
277	31	100.0	110	4	US-10-032-201B-138	Sequence 138, App	350	31	100.0	122	4	US-10-032-201B-99	Sequence 89, App
278	31	100.0	110	4	US-10-424-599-241664	Sequence 241664,	351	31	100.0	122	4	US-10-361-655-1	Sequence 1, App
279	31	100.0	110	4	US-10-424-599-265070	Sequence 265070,	352	31	100.0	122	4	US-10-437-963-164982	Sequence 164982,
280	31	100.0	110	5	US-10-450-763-53132	Sequence 53132, A	353	31	100.0	122	4	US-10-425-115-280326	Sequence 280326,
281	31	100.0	111	4	US-10-437-963-182983	Sequence 182983,	354	31	100.0	122	4	US-10-425-115-28038	Sequence 28038,
282	31	100.0	111	4	US-10-724-972A-5631	Sequence 5631, Ap	355	31	100.0	122	4	US-10-425-115-280382	Sequence 280382,
283	31	100.0	111	4	US-10-425-115-197955	Sequence 197955,	356	31	100.0	122	5	US-10-826-324-1	Sequence 4, App
284	31	100.0	111	6	US-11-097-143-6207	Sequence 6207, Ap	357	31	100.0	122	5	US-10-810-160-25	Sequence 25, App
285	31	100.0	112	3	US-09-854-342-32	Sequence 32, App	358	31	100.0	122	5	US-10-978-538-2	Sequence 2, App
286	31	100.0	112	4	US-10-032-201B-87	Sequence 87, App	359	31	100.0	123	4	US-10-424-599-283484	Sequence 283484,
287	31	100.0	112	4	US-10-032-201B-129	Sequence 129, App	360	31	100.0	123	4	US-10-425-115-283692	Sequence 283692,
288	31	100.0	112	4	US-10-296-115-1167	Sequence 1167, Ap	361	31	100.0	123	4	US-10-425-115-283695	Sequence 283695,
289	31	100.0	112	4	US-10-767-701-33511	Sequence 33511, A	362	31	100.0	123	5	US-10-978-538-1	Sequence 8, App
290	31	100.0	112	4	US-10-425-115-201579	Sequence 201579,	363	31	100.0	124	3	US-09-738-628-6919	Sequence 6919, Ap
291	31	100.0	112	4	US-10-425-115-297320	Sequence 297320,	364	31	100.0	124	4	US-10-425-115-312480	Sequence 312480,
292	31	100.0	113	3	US-10-425-115-306849	Sequence 306849,	365	31	100.0	124	5	US-10-494-541-34	Sequence 34, App
293	31	100.0	113	3	US-09-963-339-8	Sequence 44, App	366	31	100.0	125	4	US-10-087-192-1314	Sequence 1314, Ap
294	31	100.0	113	3	US-09-963-339-8	Sequence 8, App	367	31	100.0	125	4	US-10-194-885-20	Sequence 20, App
295	31	100.0	113	4	US-10-145-586-57	Sequence 57, App	368	31	100.0	125	4	US-10-032-201B-90	Sequence 90, App
296	31	100.0	113	4	US-10-104-047-3199	Sequence 3199, Ap	369	31	100.0	125	4	US-10-437-963-112360	Sequence 112360,
297	31	100.0	113	4	US-10-108-260A-3146	Sequence 3146, Ap	370	31	100.0	125	4	US-10-437-963-153318	Sequence 153318,
298	31	100.0	113	4	US-10-425-115-324504	Sequence 324504,	371	31	100.0	125	4	US-10-767-701-55966	Sequence 55966, A
299	31	100.0	114	3	US-09-897-898-6	Sequence 6, App	372	31	100.0	126	4	US-10-194-885-22	Sequence 22, App
300	31	100.0	114	3	US-09-897-898-6	Sequence 41, App	373	31	100.0	126	4	US-10-032-201B-79	Sequence 79, App
301	31	100.0	114	4	US-10-194-885-23	Sequence 23, App	374	31	100.0	126	4	US-10-032-201B-92	Sequence 92, App
302	31	100.0	114	4	US-10-032-201B-15	Sequence 15, App	375	31	100.0	126	4	US-10-424-599-250281	Sequence 250281,
303	31	100.0	114	4	US-10-032-201B-39	Sequence 39, App	376	31	100.0	126	4	US-10-741-601-389	Sequence 389, App
304	31	100.0	114	4	US-10-032-201B-76	Sequence 76, App	377	31	100.0	126	4	US-10-425-115-342989	Sequence 342989,
305	31	100.0	114	5	US-10-617-320-2930	Sequence 2930, Ap	378	31	100.0	126	5	US-10-741-600-1162	Sequence 1162, Ap
306	31	100.0	115	5	US-10-978-538-11	Sequence 11, App	379	31	100.0	127	5	US-10-978-538-12	Sequence 12, App
307	31	100.0	115	4	US-10-032-201B-130	Sequence 130, App	380	31	100.0	127	4	US-10-091-841-4	Sequence 4, App
308	31	100.0	115	4	US-10-032-201B-148	Sequence 148, App	381	31	100.0	127	4	US-10-032-201B-131	Sequence 131, App
309	31	100.0	115	4	US-10-425-115-278817	Sequence 278817,	382	31	100.0	127	4	US-10-424-599-165012	Sequence 165012,
310	31	100.0	116	3	US-09-863-339-7	Sequence 7, App	383	31	100.0	127	4	US-10-425-114-60505	Sequence 60505, A
311	31	100.0	116	4	US-10-087-192-1311	Sequence 1311, Ap	384	31	100.0	127	4	US-10-425-115-204623	Sequence 204623,
312	31	100.0	116	4	US-10-145-586-49	Sequence 49, App	385	31	100.0	127	5	US-10-450-763-48663	Sequence 48663, A
313	31	100.0	116	4	US-10-145-586-56	Sequence 56, App	386	31	100.0	128	4	US-10-424-599-224915	Sequence 224915,
314	31	100.0	116	4	US-10-032-201B-88	Sequence 88, App	387	31	100.0	128	4	US-10-425-115-200323	Sequence 200323,
315	31	100.0	116	4	US-10-425-115-218496	Sequence 218496,	388	31	100.0	128	4	US-10-425-115-286769	Sequence 286769,
316	31	100.0	116	4	US-10-425-115-330782	Sequence 330782,	389	31	100.0	128	5	US-10-450-763-54097	Sequence 54097, A
317	31	100.0	116	4	US-10-425-115-349852	Sequence 349852,	390	31	100.0	129	4	US-10-156-761-14876	Sequence 14876, A
318	31	100.0	117	4	US-10-032-201B-98	Sequence 98, App	391	31	100.0	129	4	US-10-104-047-2145	Sequence 2145, Ap
319	31	100.0	117	4	US-10-424-599-261531	Sequence 261531,	392	31	100.0	129	4	US-10-320-797-3005	Sequence 3005, Ap

393	31	100.0	129	4	US-10-437-963-126907	Sequence 126907,	466	31	100.0	143	4	US-10-425-115-247348	Sequence 247348,
394	31	100.0	130	4	US-10-091-841-6	Sequence 6, App1	467	31	100.0	143	4	US-10-425-115-273032	Sequence 273032,
395	31	100.0	130	4	US-10-032-201B-136	Sequence 136, App	468	31	100.0	144	4	US-10-425-115-439225	Sequence 439225, A
396	31	100.0	130	4	US-10-425-115-344247	Sequence 344247,	469	31	100.0	144	4	US-10-767-701-40579	Sequence 40579, A
397	31	100.0	131	4	US-10-032-201B-170	Sequence 170, App	470	31	100.0	144	4	US-10-425-115-292694	Sequence 292694, A
398	31	100.0	131	4	US-10-032-201B-171	Sequence 171, App	471	31	100.0	145	4	US-10-032-201B-108	Sequence 108, App
399	31	100.0	131	4	US-10-032-201B-172	Sequence 172, App	472	31	100.0	145	4	US-10-437-963-147748	Sequence 147748,
400	31	100.0	131	4	US-10-032-201B-174	Sequence 174, App	473	31	100.0	146	4	US-10-156-761-12145	Sequence 12145, A
401	31	100.0	131	4	US-10-032-201B-193	Sequence 193, App	474	31	100.0	146	4	US-10-375-680-59	Sequence 59, App1
402	31	100.0	131	4	US-10-424-599-231070	Sequence 231070,	475	31	100.0	147	2	US-08-424-598-520	Sequence 520, App
403	31	100.0	131	4	US-10-425-115-320098	Sequence 320098,	476	31	100.0	147	4	US-10-424-599-282587	Sequence 282587,
404	31	100.0	131	4	US-10-425-115-342218	Sequence 342218,	477	31	100.0	147	4	US-10-425-115-44850	Sequence 44850, A
405	31	100.0	132	4	US-10-425-000-48	Sequence 48, App1	478	31	100.0	147	4	US-10-425-115-268135	Sequence 268135,
406	31	100.0	132	4	US-10-425-115-317382	Sequence 317382,	479	31	100.0	148	4	US-10-425-115-366408	Sequence 366408,
407	31	100.0	132	5	US-10-425-115-323035	Sequence 323035,	480	31	100.0	148	4	US-10-919-193B-33	Sequence 33, App1
408	31	100.0	132	5	US-10-450-763-44285	Sequence 44285, A	481	31	100.0	148	5	US-10-450-763-60323	Sequence 60323, A
409	31	100.0	133	4	US-10-032-201B-80	Sequence 80, App1	482	31	100.0	149	3	US-09-738-626-6793	Sequence 6793, Ap
410	31	100.0	133	4	US-10-424-599-194117	Sequence 194117,	483	31	100.0	149	3	US-10-437-963-174733	Sequence 174733,
411	31	100.0	133	4	US-10-425-114-61995	Sequence 61995, A	484	31	100.0	150	4	US-10-425-114-65385	Sequence 65385, A
412	31	100.0	133	4	US-10-239-656-3	Sequence 3, App1	485	31	100.0	150	4	US-10-767-701-41404	Sequence 41404, A
413	31	100.0	133	4	US-10-767-701-43666	Sequence 43666, A	486	31	100.0	151	4	US-10-050-786-10	Sequence 10, App1
414	31	100.0	133	4	US-10-767-701-52028	Sequence 52028, A	487	31	100.0	151	4	US-10-156-763-14771	Sequence 14771, A
415	31	100.0	133	4	US-10-425-115-192971	Sequence 192971,	488	31	100.0	151	4	US-10-032-201B-168	Sequence 168, App
416	31	100.0	133	4	US-10-425-115-311941	Sequence 311941,	489	31	100.0	151	4	US-10-423-115-225181	Sequence 225181,
417	31	100.0	134	4	US-10-424-599-237789	Sequence 237789,	490	31	100.0	152	4	US-10-425-114-62447	Sequence 62447, A
418	31	100.0	134	4	US-10-660-118A-13	Sequence 13, App1	491	31	100.0	153	4	US-10-424-599-178292	Sequence 178292,
419	31	100.0	134	4	US-10-425-115-247611	Sequence 247611,	492	31	100.0	153	4	US-10-425-114-50553	Sequence 50553, A
420	31	100.0	134	4	US-10-425-115-329434	Sequence 329434,	493	31	100.0	155	4	US-10-425-115-196289	Sequence 196289,
421	31	100.0	135	3	US-09-864-761-34782	Sequence 34782, A	494	31	100.0	157	4	US-10-029-386-32603	Sequence 32603, A
422	31	100.0	135	4	US-10-424-599-201417	Sequence 201417,	495	31	100.0	157	5	US-10-450-763-42358	Sequence 42358, A
423	31	100.0	135	4	US-10-425-115-237035	Sequence 237035,	496	31	100.0	157	5	US-10-450-763-52892	Sequence 52892, A
424	31	100.0	136	4	US-10-425-114-62450	Sequence 62450, A	497	31	100.0	158	4	US-10-425-115-311179	Sequence 311179,
425	31	100.0	137	4	US-09-765-272-40	Sequence 40, App1	498	31	100.0	160	4	US-10-032-201B-181	Sequence 181, App
426	31	100.0	137	4	US-10-424-599-182536	Sequence 182536,	499	31	100.0	160	4	US-10-425-115-314782	Sequence 314782,
427	31	100.0	137	4	US-10-424-599-259824	Sequence 259824,	500	31	100.0	161	4	US-10-437-963-113912	Sequence 113912,
428	31	100.0	137	4	US-10-425-114-48233	Sequence 48233, A	501	31	100.0	162	4	US-10-239-656-90	Sequence 90, App1
429	31	100.0	137	4	US-10-425-114-53102	Sequence 53102, A	502	31	100.0	162	4	US-10-437-963-104684	Sequence 104684,
430	31	100.0	137	4	US-10-425-114-60594	Sequence 60594, A	503	31	100.0	163	4	US-10-425-114-41500	Sequence 41500, A
431	31	100.0	137	4	US-10-425-114-64437	Sequence 64437, A	504	31	100.0	163	4	US-10-425-114-52657	Sequence 52657, A
432	31	100.0	137	4	US-10-425-114-65475	Sequence 65475, A	505	31	100.0	164	4	US-10-264-049-2874	Sequence 2874, Ap
433	31	100.0	137	4	US-10-425-115-272549	Sequence 272549,	506	31	100.0	165	4	US-10-200-050-3	Sequence 3, App1
434	31	100.0	137	4	US-10-425-115-272551	Sequence 272551,	507	31	100.0	165	4	US-10-318-302-1	Sequence 1, App1
435	31	100.0	137	6	US-11-106-649-40	Sequence 40, App1	508	31	100.0	165	4	US-10-417-923-20	Sequence 20, App1
436	31	100.0	138	4	US-10-424-599-157666	Sequence 157666,	509	31	100.0	165	4	US-10-437-963-131521	Sequence 131521,
437	31	100.0	138	4	US-10-437-963-161970	Sequence 161970,	510	31	100.0	165	5	US-10-429-485-2	Sequence 2, App1
438	31	100.0	139	4	US-10-032-201B-119	Sequence 119, App	511	31	100.0	165	5	US-10-429-635-2	Sequence 2, App1
439	31	100.0	139	4	US-10-424-599-237785	Sequence 237785,	512	31	100.0	165	5	US-10-429-635-2	Sequence 2, App1
440	31	100.0	139	6	US-11-097-143-31419	Sequence 31419, A	513	31	100.0	165	5	US-10-429-653-2	Sequence 2, App1
441	31	100.0	140	4	US-10-032-201B-64	Sequence 64, App1	514	31	100.0	165	5	US-10-429-653-2	Sequence 2, App1
442	31	100.0	140	4	US-10-032-201B-163	Sequence 163, App	515	31	100.0	165	5	US-10-429-661-2	Sequence 2, App1
443	31	100.0	140	4	US-10-425-114-60597	Sequence 60597, A	516	31	100.0	165	5	US-10-429-660-2	Sequence 2, App1
444	31	100.0	140	4	US-10-425-114-60597	Sequence 47, App1	517	31	100.0	165	5	US-10-429-665-2	Sequence 2, App1
445	31	100.0	141	3	US-09-730-617-47	Sequence 47, App1	518	31	100.0	165	5	US-10-429-655-2	Sequence 2, App1
446	31	100.0	141	3	US-09-730-617-48	Sequence 48, App1	519	31	100.0	165	5	US-10-429-654-2	Sequence 2, App1
447	31	100.0	141	3	US-09-927-876-6	Sequence 6, App1	520	31	100.0	165	5	US-10-714-449-1	Sequence 1, App1
448	31	100.0	141	4	US-10-360-149-6	Sequence 6, App1	521	31	100.0	165	5	US-10-919-193B-32	Sequence 32, App1
449	31	100.0	141	4	US-10-424-599-226954	Sequence 226954,	522	31	100.0	165	5	US-10-954-311-8	Sequence 8, App1
450	31	100.0	141	4	US-10-425-114-48043	Sequence 48043, A	523	31	100.0	166	4	US-10-032-201B-147	Sequence 147, App
451	31	100.0	141	4	US-10-425-114-48133	Sequence 48133, A	524	31	100.0	166	4	US-10-032-201B-153	Sequence 153, App
452	31	100.0	141	4	US-10-425-114-60598	Sequence 60598, A	525	31	100.0	166	4	US-10-032-201B-156	Sequence 156, App
453	31	100.0	141	4	US-10-425-114-61985	Sequence 61985, A	526	31	100.0	166	4	US-10-032-201B-160	Sequence 160, App
454	31	100.0	141	4	US-10-457-047-6	Sequence 6, App1	527	31	100.0	166	4	US-10-264-049-3110	Sequence 3110, Ap
455	31	100.0	141	4	US-10-425-115-338893	Sequence 338893,	528	31	100.0	166	5	US-10-970-370-8	Sequence 8, App1
456	31	100.0	141	5	US-10-357-819-26	Sequence 26, App1	529	31	100.0	167	3	US-09-764-860-527	Sequence 527, App
457	31	100.0	141	5	US-10-811-081-6	Sequence 6, App1	530	31	100.0	167	4	US-10-074-095-527	Sequence 527, App
458	31	100.0	141	5	US-10-913-944-6	Sequence 6, App1	531	31	100.0	167	4	US-10-032-201B-65	Sequence 65, App1
459	31	100.0	142	4	US-10-378-029-75	Sequence 75, App1	532	31	100.0	167	4	US-10-212-872-527	Sequence 527, App
460	31	100.0	142	4	US-10-425-115-227007	Sequence 227007,	533	31	100.0	167	4	US-10-437-963-137652	Sequence 137652,
461	31	100.0	142	4	US-10-425-115-325859	Sequence 325859,	534	31	100.0	167	4	US-10-660-118A-14	Sequence 14, App1
462	31	100.0	143	3	US-09-978-360A-641	Sequence 641, App	535	31	100.0	167	4	US-10-767-701-46497	Sequence 46297, A
463	31	100.0	143	4	US-10-239-656-2	Sequence 2, App1	536	31	100.0	167	4	US-10-425-115-196292	Sequence 196292,
464	31	100.0	143	4	US-10-437-963-122996	Sequence 122996,	537	31	100.0	167	4	US-10-425-115-249938	Sequence 249938,
465	31	100.0	143	4	US-10-425-115-247344	Sequence 247344,	538	31	100.0	168	4	US-10-425-115-196290	Sequence 196290,

539	31	100.0	168	4	US-10-425-115-249786	Sequence 249786,	612	31	100.0	187	4	US-10-437-963-183458	Sequence 183458,
540	31	100.0	169	3	US-09-897-898-9	Sequence 9, Appl1	613	31	100.0	188	3	US-09-893-737-16	Sequence 16,
541	31	100.0	169	3	US-09-897-425-44	Sequence 44, Appl1	614	31	100.0	188	4	US-10-425-115-360038	Sequence 360038,
542	31	100.0	169	4	US-10-032-201B-18	Sequence 18, Appl1	615	31	100.0	188	5	US-10-970-713-16	Sequence 16, Appl1
543	31	100.0	169	4	US-10-424-599-176516	Sequence 176516,	616	31	100.0	189	4	US-10-094-744-2776	Sequence 2776, Ap
544	31	100.0	170	3	US-09-935-127-4	Sequence 4, Appl1	617	31	100.0	189	4	US-10-437-963-105917	Sequence 105917,
545	31	100.0	170	4	US-10-418-242-4	Sequence 4, Appl1	618	31	100.0	189	4	US-10-437-963-204688	Sequence 204688,
546	31	100.0	170	5	US-10-450-763-35332	Sequence 35332, A	619	31	100.0	189	5	US-10-919-193B-30	Sequence 30, Appl1
547	31	100.0	171	4	US-10-425-114-59988	Sequence 59988, A	620	31	100.0	190	3	US-09-813-398-8	Sequence 8, Appl1
548	31	100.0	171	4	US-10-425-114-63526	Sequence 63526, A	621	31	100.0	190	4	US-10-177-488-4	Sequence 4, Appl1
549	31	100.0	172	4	US-10-032-201B-66	Sequence 66, Appl1	622	31	100.0	190	4	US-10-155-492-4	Sequence 4, Appl1
550	31	100.0	172	4	US-10-032-201B-67	Sequence 67, Appl1	623	31	100.0	190	5	US-10-032-201B-57	Sequence 57, Appl1
551	31	100.0	172	4	US-10-437-963-137025	Sequence 137025,	624	31	100.0	190	4	US-10-826-324-8	Sequence 8, Appl1
552	31	100.0	172	4	US-10-660-118A-15	Sequence 15, Appl1	625	31	100.0	190	6	US-11-052-721-1	Sequence 1, Appl1
553	31	100.0	172	4	US-10-767-701-33148	Sequence 33148, A	626	31	100.0	191	3	US-09-349-954A-2	Sequence 2, Appl1
554	31	100.0	173	4	US-10-032-201B-61	Sequence 61, Appl1	627	31	100.0	191	3	US-09-932-451A-2	Sequence 2, Appl1
555	31	100.0	173	4	US-10-437-963-108195	Sequence 108195,	628	31	100.0	191	3	US-09-907-007-2	Sequence 2, Appl1
556	31	100.0	173	4	US-10-425-115-187390	Sequence 187390,	629	31	100.0	191	3	US-09-795-006A-2	Sequence 2, Appl1
557	31	100.0	173	4	US-10-425-115-187392	Sequence 187392,	630	31	100.0	191	3	US-09-870-759-122	Sequence 122, App
558	31	100.0	174	3	US-09-764-868-633	Sequence 633, App	631	31	100.0	191	4	US-09-751-708A-122	Sequence 122, App
559	31	100.0	174	4	US-10-767-701-32096	Sequence 32096, A	632	31	100.0	191	4	US-10-083-817-3	Sequence 3, Appl1
560	31	100.0	174	4	US-10-425-115-317875	Sequence 317875,	633	31	100.0	191	4	US-10-200-050-2	Sequence 2, Appl1
561	31	100.0	175	4	US-10-032-201B-69	Sequence 69, Appl1	634	31	100.0	191	4	US-10-201-388-56	Sequence 56, Appl1
562	31	100.0	175	4	US-10-032-201B-166	Sequence 166, App	635	31	100.0	191	4	US-10-268-447-6	Sequence 6, Appl1
563	31	100.0	175	4	US-10-424-599-177899	Sequence 177899,	636	31	100.0	191	4	US-10-262-538-20	Sequence 20, Appl1
564	31	100.0	175	4	US-10-424-599-282483	Sequence 282483,	637	31	100.0	191	4	US-10-277-184-2	Sequence 2, Appl1
565	31	100.0	175	4	US-10-425-114-50857	Sequence 50857, A	638	31	100.0	191	4	US-10-207-655-51	Sequence 51, Appl1
566	31	100.0	175	4	US-10-767-701-40803	Sequence 40803, A	639	31	100.0	191	4	US-10-207-655-53	Sequence 53, Appl1
567	31	100.0	175	4	US-10-425-115-256814	Sequence 256814,	640	31	100.0	191	4	US-10-032-201B-55	Sequence 55, Appl1
568	31	100.0	176	4	US-10-425-115-260475	Sequence 260475,	641	31	100.0	191	4	US-10-131-988-17	Sequence 17, Appl1
569	31	100.0	177	4	US-10-032-201B-63	Sequence 63, Appl1	642	31	100.0	191	4	US-10-170-385-227	Sequence 227, App
570	31	100.0	177	4	US-10-425-114-41212	Sequence 41212, A	643	31	100.0	191	4	US-10-246-091-32	Sequence 32, Appl1
571	31	100.0	177	4	US-10-425-115-348412	Sequence 348412,	644	31	100.0	191	4	US-10-352-155-4	Sequence 4, Appl1
572	31	100.0	178	3	US-09-764-891-3869	Sequence 3869, Ap	645	31	100.0	191	4	US-10-116-275-227	Sequence 227, App
573	31	100.0	178	4	US-10-032-201B-52	Sequence 52, Appl1	646	31	100.0	191	4	US-10-418-529-6	Sequence 6, Appl1
574	31	100.0	178	4	US-10-424-599-262936	Sequence 262936,	647	31	100.0	191	4	US-10-370-291-4	Sequence 4, Appl1
575	31	100.0	179	4	US-10-323-362-4	Sequence 4, Appl1	648	31	100.0	191	4	US-10-440-464-127	Sequence 127, App
576	31	100.0	179	4	US-10-032-201B-59	Sequence 59, Appl1	649	31	100.0	191	4	US-10-424-599-275952	Sequence 275952,
577	31	100.0	179	4	US-10-424-599-225033	Sequence 225033,	650	31	100.0	191	4	US-10-673-708-2	Sequence 2, Appl1
578	31	100.0	179	4	US-10-425-114-62266	Sequence 62266, A	651	31	100.0	191	4	US-10-474-776-661	Sequence 661, App
579	31	100.0	179	4	US-10-425-114-66811	Sequence 66811, A	652	31	100.0	191	4	US-10-792-480-56	Sequence 56, Appl1
580	31	100.0	179	4	US-10-425-115-280370	Sequence 280370,	653	31	100.0	191	4	US-10-792-461-56	Sequence 56, Appl1
581	31	100.0	179	4	US-10-425-115-305796	Sequence 305796,	654	31	100.0	191	4	US-10-793-094-14	Sequence 14, Appl1
582	31	100.0	180	4	US-10-425-114-48070	Sequence 48070, A	655	31	100.0	191	4	US-10-770-668-32	Sequence 32, Appl1
583	31	100.0	180	4	US-10-425-114-52471	Sequence 52471, A	656	31	100.0	191	4	US-10-425-115-305799	Sequence 305799,
584	31	100.0	180	4	US-10-425-114-66813	Sequence 66813, A	657	31	100.0	191	4	US-10-669-176-20	Sequence 20, Appl1
585	31	100.0	180	4	US-10-437-963-147191	Sequence 147191,	658	31	100.0	191	4	US-10-428-817A-118	Sequence 118, App
586	31	100.0	180	4	US-10-437-963-154824	Sequence 154824,	659	31	100.0	191	5	US-10-749-706-3	Sequence 3, Appl1
587	31	100.0	180	4	US-10-425-115-314784	Sequence 314784,	660	31	100.0	191	5	US-10-772-927A-12	Sequence 12, Appl1
588	31	100.0	181	4	US-10-032-201B-68	Sequence 68, Appl1	661	31	100.0	191	5	US-10-615-345-21	Sequence 21, Appl1
589	31	100.0	181	4	US-10-424-599-178291	Sequence 178291,	662	31	100.0	191	5	US-10-901-417-17	Sequence 17, Appl1
590	31	100.0	181	4	US-10-424-599-178934	Sequence 178934,	663	31	100.0	191	5	US-10-868-577A-7	Sequence 7, Appl1
591	31	100.0	181	4	US-10-424-599-279345	Sequence 279345,	664	31	100.0	191	5	US-10-868-549-18	Sequence 18, Appl1
592	31	100.0	181	4	US-10-424-599-280573	Sequence 280573,	665	31	100.0	191	5	US-10-937-758A-99	Sequence 99, Appl1
593	31	100.0	181	4	US-10-437-963-127106	Sequence 127106,	666	31	100.0	191	5	US-10-756-149-4876	Sequence 4876, Ap
594	31	100.0	181	4	US-10-437-963-204686	Sequence 204686,	667	31	100.0	191	5	US-09-852-209A-8	Sequence 8, Appl1
595	31	100.0	182	4	US-10-032-201B-54	Sequence 54, Appl1	668	31	100.0	192	4	US-10-131-600-8	Sequence 8, Appl1
596	31	100.0	182	4	US-10-032-201B-56	Sequence 56, Appl1	669	31	100.0	192	4	US-10-303-997B-8	Sequence 8, Appl1
597	31	100.0	182	4	US-10-424-599-250227	Sequence 250227,	670	31	100.0	192	4	US-10-439-337A-8	Sequence 8, Appl1
598	31	100.0	182	4	US-10-425-114-67114	Sequence 67114, A	671	31	100.0	192	4	US-10-767-701-46126	Sequence 46126, A
599	31	100.0	182	4	US-10-437-963-111424	Sequence 111424,	672	31	100.0	192	5	US-10-485-539-17	Sequence 17, Appl1
600	31	100.0	182	4	US-10-767-701-42070	Sequence 42070, A	673	31	100.0	193	4	US-10-032-201B-62	Sequence 62, Appl1
601	31	100.0	182	4	US-10-425-115-256661	Sequence 256661,	674	31	100.0	194	4	US-10-437-963-104337	Sequence 104337,
602	31	100.0	182	4	US-10-425-115-314786	Sequence 314786,	675	31	100.0	194	4	US-10-437-963-204634	Sequence 204634,
603	31	100.0	183	4	US-10-424-599-225032	Sequence 225032,	676	31	100.0	194	5	US-10-617-320-5104	Sequence 5104, Ap
604	31	100.0	183	4	US-10-767-701-46296	Sequence 46296, A	677	31	100.0	195	4	US-10-424-599-262247	Sequence 262247,
605	31	100.0	183	4	US-10-425-115-229688	Sequence 229688,	678	31	100.0	196	4	US-10-180-120-2	Sequence 2, Appl1
606	31	100.0	183	5	US-10-919-193B-31	Sequence 31, Appl1	679	31	100.0	196	4	US-10-437-963-195282	Sequence 195282,
607	31	100.0	185	4	US-10-032-201B-53	Sequence 53, Appl1	680	31	100.0	197	4	US-10-767-701-33489	Sequence 33489, A
608	31	100.0	185	5	US-10-739-930-6217	Sequence 6217, Ap	681	31	100.0	198	4	US-10-425-115-212572	Sequence 212572,
609	31	100.0	185	5	US-10-739-930-6865	Sequence 6865, Ap	682	31	100.0	201	4	US-10-425-114-42331	Sequence 42331, A
610	31	100.0	185	5	US-10-472-928-1980	Sequence 1980, Ap	683	31	100.0	204	4	US-10-425-114-47113	Sequence 47113, A
611	31	100.0	186	4	US-10-032-201B-60	Sequence 60, Appl1	684	31	100.0	206	5	US-10-872-198-103	Sequence 103, App

685	31	100.0	206	5	US-10-919-193B-29	Sequence 29, Appl	758	31	100.0	232	5	US-10-868-577A-57	Sequence 57, Appl
686	31	100.0	206	6	US-11-021-951-103	Sequence 103, App	759	31	100.0	232	5	US-10-868-549-11	Sequence 11, Appl
687	31	100.0	208	4	US-10-293-157-26	Sequence 26, Appl	760	31	100.0	232	5	US-10-980-815-7	Sequence 7, Appl
688	31	100.0	209	4	US-10-423-000-54	Sequence 54, Appl	761	31	100.0	232	5	US-10-978-107-33	Sequence 33, Appl
689	31	100.0	211	3	US-09-877-156-20	Sequence 20, Appl	762	31	100.0	232	5	US-10-971-643-2	Sequence 2, Appl
690	31	100.0	211	6	US-11-097-143-5826	Sequence 5826, Ap	763	31	100.0	232	5	US-10-992-196-7	Sequence 7, Appl
691	31	100.0	213	4	US-10-425-000-62	Sequence 62, Appl	764	31	100.0	232	5	US-10-992-195-7	Sequence 7, Appl
692	31	100.0	213	3	US-09-963-156A-1	Sequence 1, Appl	765	31	100.0	232	6	US-11-067-015-7	Sequence 7, Appl
693	31	100.0	214	4	US-10-425-000-58	Sequence 58, Appl	766	31	100.0	232	6	US-11-078-507-7	Sequence 7, Appl
694	31	100.0	214	4	US-10-425-000-66	Sequence 58, Appl	767	31	100.0	234	4	US-10-029-386-32351	Sequence 32351, A
695	31	100.0	214	4	US-10-749-832-1	Sequence 66, Appl	768	31	100.0	236	3	US-09-777-789-62	Sequence 62, Appl
696	31	100.0	215	3	US-09-244-694-3	Sequence 3, Appl	769	31	100.0	237	3	US-09-746-284-5	Sequence 5, Appl
697	31	100.0	215	3	US-10-418-529-8	Sequence 8, Appl	770	31	100.0	237	3	US-10-425-114-66489	Sequence 66489, A
698	31	100.0	215	4	US-10-370-291-6	Sequence 6, Appl	771	31	100.0	241	4	US-10-425-115-260478	Sequence 260478, A
699	31	100.0	215	4	US-10-425-000-56	Sequence 56, Appl	772	31	100.0	242	3	US-09-919-603-5	Sequence 5, Appl
700	31	100.0	215	5	US-10-615-343-15	Sequence 15, Appl	773	31	100.0	243	5	US-10-491-213-46	Sequence 46, Appl
701	31	100.0	215	5	US-10-868-577A-10	Sequence 10, Appl	774	31	100.0	247	4	US-10-369-493-9470	Sequence 9470, Ap
702	31	100.0	215	5	US-10-868-549-19	Sequence 19, Appl	775	31	100.0	247	5	US-10-450-763-59922	Sequence 59922, A
703	31	100.0	215	5	US-10-926-806-4	Sequence 4, Appl	776	31	100.0	249	4	US-10-177-293-148	Sequence 148, App
704	31	100.0	215	5	US-10-924-025A-105	Sequence 105, App	777	31	100.0	249	4	US-10-479-284-15	Sequence 15, Appl
705	31	100.0	215	5	US-10-970-698A-56	Sequence 56, Appl	778	31	100.0	249	4	US-10-755-889-130	Sequence 130, App
706	31	100.0	215	5	US-10-450-763-41147	Sequence 41147, A	779	31	100.0	249	5	US-10-450-763-53065	Sequence 53065, A
707	31	100.0	215	5	US-10-798-896-7	Sequence 7, Appl	780	31	100.0	250	3	US-09-764-868-1063	Sequence 1063, Ap
708	31	100.0	215	6	US-11-019-829-87	Sequence 87, Appl	781	31	100.0	250	3	US-09-955-999-77	Sequence 77, Appl
709	31	100.0	216	4	US-10-335-009-8	Sequence 8, Appl	782	31	100.0	251	4	US-10-437-963-128810	Sequence 128810, A
710	31	100.0	216	4	US-10-425-114-66365	Sequence 6365, A	783	31	100.0	252	4	US-10-423-156-7	Sequence 7, Appl
711	31	100.0	216	5	US-10-723-860-613	Sequence 613, App	784	31	100.0	252	4	US-10-423-156-8	Sequence 8, Appl
712	31	100.0	216	5	US-10-756-149-4881	Sequence 4881, Ap	785	31	100.0	252	4	US-10-423-156-7	Sequence 8, Appl
713	31	100.0	216	5	US-10-512-181-10	Sequence 10, Appl	786	31	100.0	259	4	US-10-437-963-135706	Sequence 135706, A
714	31	100.0	217	4	US-10-425-114-63276	Sequence 63276, A	787	31	100.0	261	4	US-10-012-542-413	Sequence 413, App
715	31	100.0	217	4	US-10-425-000-70	Sequence 70, Appl	788	31	100.0	261	4	US-10-115-123-413	Sequence 413, App
716	31	100.0	217	4	US-10-424-999-38	Sequence 38, Appl	789	31	100.0	263	4	US-10-800-834-413	Sequence 413, App
717	31	100.0	218	4	US-10-282-122A-55347	Sequence 55347, A	790	31	100.0	263	5	US-10-108-260A-2809	Sequence 2809, Ap
718	31	100.0	218	4	US-10-425-000-50	Sequence 50, Appl	791	31	100.0	263	5	US-10-732-923-13421	Sequence 13421, A
719	31	100.0	219	4	US-10-220-120-514	Sequence 34, App	792	31	100.0	264	4	US-10-767-701-47316	Sequence 47316, A
720	31	100.0	219	4	US-10-425-000-52	Sequence 52, Appl	793	31	100.0	265	6	US-10-457-372-17	GENERAL INFO
721	31	100.0	219	4	US-10-425-000-60	Sequence 60, Appl	794	31	100.0	265	6	US-11-097-143-27600	Sequence 27600, A
722	31	100.0	219	4	US-10-425-000-72	Sequence 72, Appl	795	31	100.0	266	4	US-10-437-963-125623	Sequence 125623, A
723	31	100.0	219	4	US-10-424-999-40	Sequence 40, Appl	796	31	100.0	270	4	US-10-437-963-125901	Sequence 125901, A
724	31	100.0	221	4	US-10-424-999-34	Sequence 34, Appl	797	31	100.0	271	4	US-10-129-709-1	Sequence 1, Appl
725	31	100.0	221	4	US-10-424-999-36	Sequence 36, Appl	798	31	100.0	271	4	US-10-417-923-4	Sequence 4, Appl
726	31	100.0	222	4	US-10-425-114-53092	Sequence 53092, A	799	31	100.0	271	4	US-10-793-269-6	Sequence 6, Appl
727	31	100.0	223	4	US-10-276-774-2216	Sequence 2216, Ap	800	31	100.0	271	4	US-10-793-269-8	Sequence 8, Appl
728	31	100.0	223	4	US-10-437-963-182799	Sequence 182799, A	801	31	100.0	271	4	US-10-466-786-1	Sequence 1, Appl
729	31	100.0	223	4	US-10-159-357A-175	Sequence 175, App	802	31	100.0	271	5	US-10-775-180-139	Sequence 139, App
730	31	100.0	223	5	US-10-128-558-389	Sequence 389, App	803	31	100.0	271	5	US-10-775-180-140	Sequence 140, App
731	31	100.0	224	4	US-10-104-047-3343	Sequence 3343, App	804	31	100.0	271	5	US-10-775-180-141	Sequence 141, App
732	31	100.0	225	4	US-10-002-631C-106	Sequence 106, App	805	31	100.0	271	5	US-10-775-180-142	Sequence 142, App
733	31	100.0	225	4	US-10-425-000-64	Sequence 64, Appl	806	31	100.0	271	5	US-10-775-180-143	Sequence 143, App
734	31	100.0	226	4	US-10-002-631C-295	Sequence 295, App	807	31	100.0	271	5	US-10-775-180-144	Sequence 144, App
735	31	100.0	226	4	US-10-425-115-334048	Sequence 334048, A	808	31	100.0	271	5	US-10-775-180-146	Sequence 146, App
736	31	100.0	226	5	US-10-450-763-39815	Sequence 39815, A	809	31	100.0	271	5	US-10-775-180-147	Sequence 147, App
737	31	100.0	227	5	US-10-934-998-59	Sequence 59, Appl	810	31	100.0	271	5	US-10-775-180-148	Sequence 148, App
738	31	100.0	227	4	US-10-029-386-34096	Sequence 34096, A	811	31	100.0	271	5	US-10-775-180-149	Sequence 149, App
739	31	100.0	229	4	US-10-425-115-207582	Sequence 207582, A	812	31	100.0	271	5	US-10-775-180-150	Sequence 150, App
740	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	813	31	100.0	271	5	US-10-775-180-156	Sequence 156, App
741	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	814	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
742	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	815	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
743	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	816	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
744	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	817	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
745	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	818	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
746	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	819	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
747	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	820	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
748	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	821	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
749	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	822	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
750	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	823	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
751	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	824	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
752	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	825	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
753	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	826	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
754	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	827	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
755	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	828	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
756	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	829	31	100.0	271	5	US-10-775-180-159	Sequence 159, App
757	31	100.0	232	3	US-09-897-898-11	Sequence 11, Appl	830	31	100.0	271	5	US-10-775-180-159	Sequence 159, App

831	-31	100.0	277	3	US-09-808-602-50	Sequence 50, Appl	904	-31	100.0	303	5	US-10-450-763-56753	Sequence 56753, A
832	-31	100.0	277	4	US-09-800-198-40	Sequence 40, Appl	905	-31	100.0	304	5	US-10-902-531-16	Sequence 16, Appl
833	-31	100.0	277	4	US-10-236-031B-66	Sequence 66, Appl	906	-31	100.0	306	4	US-10-267-430-13	Sequence 13, Appl
834	-31	100.0	278	4	US-10-287-971-36	Sequence 36, Appl	907	-31	100.0	309	4	US-10-369-499-18683	Sequence 19683, A
835	-31	100.0	279	5	US-10-739-930-8419	Sequence 8419, Ap	908	-31	100.0	314	4	US-10-408-768A-2474	Sequence 2474, Ap
836	-31	100.0	280	5	US-10-450-763-36182	Sequence 36182, A	909	-31	100.0	314	4	US-10-479-284-16	Sequence 16, Appl
837	-31	100.0	281	3	US-09-808-602-49	Sequence 49, Appl	910	-31	100.0	317	4	US-10-276-774-2644	Sequence 2644, Ap
838	-31	100.0	281	3	US-09-808-602-51	Sequence 51, Appl	911	-31	100.0	318	4	US-09-771-730-20	Sequence 20, Appl
839	-31	100.0	281	3	US-09-800-198-39	Sequence 39, Appl	912	-31	100.0	318	4	US-10-437-963-132260	Sequence 132260, A
840	-31	100.0	281	3	US-09-800-198-41	Sequence 41, Appl	913	-31	100.0	318	5	US-10-732-922-9556	Sequence 9556, Ap
841	-31	100.0	281	4	US-10-418-064-3	Sequence 3, Appl1	914	-31	100.0	320	5	US-10-774-358A-2225	Sequence 2225, Ap
842	-31	100.0	282	3	US-09-808-602-52	Sequence 52, Appl	915	-31	100.0	321	4	US-09-771-730-43	Sequence 43, Appl
843	-31	100.0	282	3	US-09-877-843-14	Sequence 14, Appl	916	-31	100.0	321	4	US-10-023-601-46	Sequence 46, Appl
844	-31	100.0	282	3	US-09-800-198-42	Sequence 42, Appl	917	-31	100.0	321	4	US-10-023-601-48	Sequence 48, Appl
845	-31	100.0	282	4	US-10-301-822-85	Sequence 85, Appl	918	-31	100.0	321	4	US-10-023-601-50	Sequence 50, Appl
846	-31	100.0	282	4	US-10-418-064-5	Sequence 5, Appl1	919	-31	100.0	321	4	US-10-023-601-52	Sequence 52, Appl
847	-31	100.0	282	4	US-10-240-240A-12	Sequence 12, Appl	920	-31	100.0	321	4	US-10-024-399-28	Sequence 28, Appl
848	-31	100.0	282	4	US-10-706-791-19	Sequence 19, Appl	921	-31	100.0	321	4	US-10-024-399-30	Sequence 30, Appl
849	-31	100.0	282	4	US-10-734-564-101	Sequence 101, App	922	-31	100.0	321	4	US-10-041-615-70	Sequence 70, Appl
850	-31	100.0	282	5	US-10-887-229A-14	Sequence 14, Appl	923	-31	100.0	321	4	US-10-041-615-71	Sequence 71, Appl
851	-31	100.0	283	5	US-10-888-805-28	Sequence 28, Appl	924	-31	100.0	321	4	US-10-282-122A-75634	Sequence 75634, A
852	-31	100.0	283	5	US-10-888-805-30	Sequence 30, Appl	925	-31	100.0	321	5	US-10-774-358A-1807	Sequence 1807, Ap
853	-31	100.0	283	5	US-10-888-805-32	Sequence 32, Appl	926	-31	100.0	322	4	US-10-292-798-542	Sequence 542, App
854	-31	100.0	283	5	US-10-888-805-34	Sequence 34, Appl	927	-31	100.0	323	4	US-10-141-531-28	Sequence 28, Appl
855	-31	100.0	284	4	US-10-032-201B-189	Sequence 189, App	928	-31	100.0	323	4	US-10-290-072-28	Sequence 28, Appl
856	-31	100.0	287	4	US-10-032-201B-190	Sequence 190, App	929	-31	100.0	323	4	US-10-024-212-106	Sequence 106, App
857	-31	100.0	287	6	US-11-097-143-11535	Sequence 11535, A	930	-31	100.0	323	4	US-10-343-650A-2	Sequence 2, Appl1
858	-31	100.0	289	4	US-10-032-201B-191	Sequence 191, App	931	-31	100.0	323	5	US-10-902-531-17	Sequence 17, Appl
859	-31	100.0	289	4	US-10-197-962B-5	Sequence 5, Appl1	932	-31	100.0	325	3	US-09-800-095A-96	Sequence 96, Appl
860	-31	100.0	290	4	US-10-032-201B-186	Sequence 186, App	933	-31	100.0	325	3	US-09-978-360A-406	Sequence 406, App
861	-31	100.0	291	5	US-10-450-763-30874	Sequence 30874, A	934	-31	100.0	325	4	US-10-267-430-4	Sequence 4, Appl1
862	-31	100.0	292	4	US-10-424-599-245742	Sequence 245742, A	935	-31	100.0	325	4	US-10-315-664-74	Sequence 74, Appl1
863	-31	100.0	294	4	US-10-335-977-7130	Sequence 7130, Ap	936	-31	100.0	325	4	US-10-295-072-1174	Sequence 1374, Ap
864	-31	100.0	296	4	US-10-032-201B-173	Sequence 173, App	937	-31	100.0	325	4	US-10-367-978-23	Sequence 23, Appl
865	-31	100.0	296	4	US-10-437-963-104806	Sequence 104806, A	938	-31	100.0	325	5	US-10-357-819-28	Sequence 28, Appl
866	-31	100.0	299	3	US-09-877-156-17	Sequence 17, Appl	939	-31	100.0	325	5	US-10-631-467-726	Sequence 726, App
867	-31	100.0	299	3	US-09-771-156-98	Sequence 98, Appl	940	-31	100.0	326	3	US-09-921-301-1449	Sequence 1449, Ap
868	-31	100.0	300	3	US-09-896-096A-1	Sequence 1, Appl1	941	-31	100.0	326	4	US-10-264-049-3112	Sequence 3112, Ap
869	-31	100.0	300	3	US-09-894-924-1	Sequence 1, Appl1	942	-31	100.0	326	4	US-10-033-585-7827	Sequence 7827, Ap
870	-31	100.0	300	3	US-09-919-603-7	Sequence 7, Appl1	943	-31	100.0	327	4	US-10-276-774-2140	Sequence 2140, Ap
871	-31	100.0	300	3	US-09-840-795-2	Sequence 2, Appl1	944	-31	100.0	329	5	US-10-732-923-9551	Sequence 9551, Ap
872	-31	100.0	300	3	US-09-935-727-2	Sequence 2, Appl1	945	-31	100.0	330	5	US-10-437-963-154386	Sequence 154386, A
873	-31	100.0	300	4	US-10-129-709-3	Sequence 3, Appl1	946	-31	100.0	330	4	US-10-250-615-23	Sequence 23, Appl
874	-31	100.0	300	4	US-10-125-985-2	Sequence 2, Appl1	947	-31	100.0	330	5	US-10-774-355A-2471	Sequence 2471, Ap
875	-31	100.0	300	4	US-10-310-793-6	Sequence 6, Appl1	948	-31	100.0	330	5	US-10-774-355A-2525	Sequence 2525, Ap
876	-31	100.0	300	4	US-10-369-300-19	Sequence 19, Appl	949	-31	100.0	330	5	US-10-774-355A-2528	Sequence 2528, Ap
877	-31	100.0	300	4	US-10-375-680-52	Sequence 52, Appl	950	-31	100.0	330	5	US-10-774-355A-2528	Sequence 2528, Ap
878	-31	100.0	300	4	US-10-418-242-2	Sequence 2, Appl1	951	-31	100.0	331	4	US-10-732-923-13423	Sequence 13423, A
879	-31	100.0	300	4	US-10-456-819-1	Sequence 1, Appl1	952	-31	100.0	331	4	US-10-017-161-618	Sequence 618, App
880	-31	100.0	300	4	US-10-467-259-9	Sequence 9, Appl1	953	-31	100.0	331	5	US-10-450-763-36089	Sequence 36089, A
881	-31	100.0	300	4	US-10-600-815-5	Sequence 5, Appl1	954	-31	100.0	331	5	US-10-450-763-52652	Sequence 52652, A
882	-31	100.0	300	4	US-10-793-269-2	Sequence 2, Appl1	955	-31	100.0	332	4	US-10-839-882-39	Sequence 39, Appl
883	-31	100.0	300	4	US-10-793-269-4	Sequence 4, Appl1	956	-31	100.0	332	5	US-10-631-467-1495	Sequence 1495, Ap
884	-31	100.0	300	4	US-10-688-132-1	Sequence 1, Appl1	957	-31	100.0	334	4	US-10-839-882-1	Sequence 1, Appl1
885	-31	100.0	300	4	US-10-466-786-3	Sequence 3, Appl1	958	-31	100.0	341	6	US-11-097-143-2163	Sequence 2163, Ap
886	-31	100.0	300	4	US-10-425-115-256815	Sequence 256815, A	959	-31	100.0	341	4	US-10-106-698-4514	Sequence 4514, Ap
887	-31	100.0	300	5	US-10-871-907-1	Sequence 1, Appl1	960	-31	100.0	341	5	US-10-643-795A-158	Sequence 158, App
888	-31	100.0	300	5	US-10-500-428-4	Sequence 4, Appl	961	-31	100.0	341	5	US-10-948-518-158	Sequence 158, App
889	-31	100.0	300	5	US-10-775-180-145	Sequence 145, App	962	-31	100.0	342	5	US-10-948-518-158	Sequence 158, App
890	-31	100.0	300	5	US-10-775-180-151	Sequence 151, App	963	-31	100.0	342	3	US-09-938-864-332	Sequence 332, App
891	-31	100.0	300	5	US-10-775-180-157	Sequence 157, App	964	-31	100.0	342	3	US-09-785-019-332	Sequence 332, App
892	-31	100.0	300	5	US-10-775-180-158	Sequence 158, App	965	-31	100.0	342	4	US-10-125-635A-332	Sequence 332, App
893	-31	100.0	300	5	US-10-775-180-158	Sequence 158, App	966	-31	100.0	342	4	US-10-002-603-332	Sequence 332, App
894	-31	100.0	300	5	US-10-943-197-49	Sequence 49, Appl	967	-31	100.0	342	4	US-10-195-835-332	Sequence 332, App
895	-31	100.0	300	5	US-10-773-204-439	Sequence 439, App	968	-31	100.0	342	4	US-10-286-333-332	Sequence 332, App
896	-31	100.0	300	5	US-10-775-204-452	Sequence 452, App	969	-31	100.0	342	4	US-10-244-830-332	Sequence 332, App
897	-31	100.0	300	5	US-10-775-204-491	Sequence 491, App	970	-31	100.0	342	4	US-10-427-717-332	Sequence 332, App
898	-31	100.0	301	4	US-10-775-204-494	Sequence 494, App	971	-31	100.0	344	4	US-10-648-780-332	Sequence 332, App
899	-31	100.0	301	4	US-10-309-629-4	Sequence 4, Appl1	972	-31	100.0	345	4	US-10-648-780-39850	Sequence 39850, A
900	-31	100.0	301	4	US-10-437-963-103918	Sequence 103918, A	973	-31	100.0	345	4	US-10-225-567A-619	Sequence 619, App
901	-31	100.0	301	4	US-10-479-284-31	Sequence 31, Appl	974	-31	100.0	345	4	US-10-467-252-8	Sequence 8, Appl1
902	-31	100.0	302	4	US-10-767-701-45068	Sequence 45068, A	975	-31	100.0	345	5	US-10-600-816-4	Sequence 4, Appl1
903	-31	100.0	302	3	US-09-833-245-1155	Sequence 1155, Ap	976	-31	100.0	345	5	US-10-500-428-2	Sequence 2, Appl1
					US-09-833-245-1156	Sequence 1156, Ap						US-10-732-923-9550	Sequence 9550, Ap

```
977 31 100.0 348 4 US-10-424-599-181709 Sequence 181709,
978 31 100.0 350 5 US-10-902-531-18 Sequence 18, App1
979 31 100.0 352 3 US-09-886-055-441 Sequence 441, App
980 31 100.0 352 3 US-09-804-291-441 Sequence 441, App
981 31 100.0 352 4 US-10-343-650A-448 Sequence 448, App
982 31 100.0 352 5 US-10-819-316-441 Sequence 441, App
983 31 100.0 354 4 US-10-099-322-58 Sequence 58, App1
984 31 100.0 354 4 US-10-369-493-297 Sequence 297, App
985 31 100.0 354 4 US-10-369-493-21120 Sequence 21120, A
986 31 100.0 354 4 US-10-044-564-58 Sequence 58, App1
987 31 100.0 355 4 US-10-012-896-1011 Sequence 1011, App
988 31 100.0 355 4 US-10-144-678A-1011 Sequence 1011, App
989 31 100.0 355 4 US-10-294-025-1011 Sequence 1011, App
990 31 100.0 356 4 US-10-369-493-23509 Sequence 23509, A
991 31 100.0 356 5 US-10-450-763-54715 Sequence 54715, A
992 31 100.0 360 4 US-10-425-114-41585 Sequence 41585, A
993 31 100.0 361 4 US-10-435-696-52 Sequence 52, App1
994 31 100.0 362 4 US-10-182-822A-14 Sequence 14, App1
995 31 100.0 363 4 US-10-425-115-326082 Sequence 326082,
996 31 100.0 366 5 US-10-928-992-162 Sequence 162, App
997 31 100.0 371 3 US-09-878-178-2235 Sequence 2235, App
998 31 100.0 371 4 US-10-046-935-2235 Sequence 2235, App
999 31 100.0 371 4 US-10-146-502-2235 Sequence 2235, App
1000 31 100.0 371 4 US-10-066-543-1422 Sequence 1422, App
```

ALIGNMENTS

```
RESULT 1
US-10-286-516A-11
; Sequence 11, Application US/10286516A
; Publication No. US20030092087A1
; GENERAL INFORMATION:
; APPLICANT: McBridge, Jere W.
; APPLICANT: Walker, David H.
; TITLE OF INVENTION: Bhrilichia Disulfide Bond Formation
; FILE REFERENCE: D6428
; CURRENT APPLICATION NUMBER: US/10/286, 516A
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/335, 611
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; OTHER INFORMATION: Escherichia coli conserved cysteine
; OTHER INFORMATION: motif in active site of thiredoxin
; OTHER INFORMATION: protein
US-10-286-516A-11

Query Match          100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
      ||||
Db      1 CGPC 4

RESULT 2
US-10-234-319A-1
; Sequence 1, Application US/10234319A
; Publication No. US20030109457A1
; GENERAL INFORMATION:
; APPLICANT: Atlas, Daphne
; TITLE OF INVENTION: MULTI-COMPONENT ANTIOXIDANT COMPOUNDS, PHARMACEUTICAL COMPOSITION
; TITLE OF INVENTION: CONTAINING SAME AND THEIR USE FOR REDUCING OR PREVENTING OXIDATI
; FILE REFERENCE: 24890
; CURRENT APPLICATION NUMBER: US/10/234, 319A
```

```
; CURRENT FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-(1)
; OTHER INFORMATION: ACETYLATION
; NAME/KEY: MOD_RES
; LOCATION: (4)-(4)
; OTHER INFORMATION: AMIDATION
US-10-234-319A-1
```

```
Query Match          100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      ||||
Db      1 CGPC 4
```

```
RESULT 3
US-10-369-094-1
; Sequence 1, Application US/10369094
; Publication No. US20030235588A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria M.
; APPLICANT: Marks, Paul A.
; APPLICANT: Rifkind, Richard A.
; APPLICANT: Butler, Lisa M.
; TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
; FILE REFERENCE: 3254.1005-001
; CURRENT APPLICATION NUMBER: US/10/369, 094
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/357, 383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-369-094-1
```

```
Query Match          100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
      ||||
Db      1 CGPC 4
```

```
RESULT 4
US-10-660-118A-1
; Sequence 1, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660, 118A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409, 960
; PRIOR FILING DATE: 2002-09-10
; CURRENT APPLICATION NUMBER: 60/462, 082
```

;; PRIOR FILING DATE: 2003-04-11
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-1

Query Match 100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 5
US-10-628-391-2
;; Sequence 2, Application US/10628391
;; Publication No. US20040146526A1
;; GENERAL INFORMATION:
;; APPLICANT: WINDLE, Henry J.
;; APPLICANT: O'TOOLE, Dermot
;; APPLICANT: KELLEHER, Dermot
;; APPLICANT: ABDEL-LATIF, Mohamed M.
;; TITLE OF INVENTION: INHIBITION OF NF-kappaB ACTIVATION
;; FILE REFERENCE: P69048USO
;; CURRENT APPLICATION NUMBER: US/10/628,391
;; PRIOR FILING DATE: 2003-07-29
;; PRIOR APPLICATION NUMBER: PCT/IE02/00011
;; PRIOR FILING DATE: 2002-01-30
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 2
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: the redox active peptide sequence
US-10-628-391-2

Query Match 100.0%; Score 31; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 6
US-10-776-933-149
;; Sequence 149, Application US/10776933
;; Publication No. US20040241717A1
;; GENERAL INFORMATION:
;; APPLICANT: HANSEN, BO
;; APPLICANT: THRIE, CHARLOTTE ALBAEK
;; APPLICANT: WESTERGAARD, MAJKEN
;; APPLICANT: PETERSEN, KAMILLE DUMONG
;; APPLICANT: MISENBACH, MARGIT
;; TITLE OF INVENTION: OLIGOMERIC COMPOUNDS FOR THE MODULATION OF THIOREDUXIN
;; FILE REFERENCE: 58614(71432)
;; CURRENT APPLICATION NUMBER: US/10/776,933
;; PRIOR FILING DATE: 2004-02-10
;; PRIOR APPLICATION NUMBER: 60/446,374
;; PRIOR FILING DATE: 2003-02-10
;; NUMBER OF SEQ ID NOS: 150
;; SOFTWARE: PatentIn Ver. 3.2

;; SEQ ID NO 149
;; LENGTH: 4
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-10-776-933-149

Query Match 100.0%; Score 31; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 7
US-10-304-287-4
;; Sequence 4, Application US/10304287
;; Publication No. US20030083234A1
;; GENERAL INFORMATION:
;; APPLICANT: Walsman, David M.
;; APPLICANT: Kwon, Mijung
;; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
;; FILE REFERENCE: ME02-001
;; CURRENT APPLICATION NUMBER: US/10/304,287
;; PRIOR FILING DATE: 2002-11-26
;; PRIOR APPLICATION NUMBER: US 60/333,866
;; PRIOR FILING DATE: 2001-11-28
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: Microsoft Word
;; SEQ ID NO 4
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: mammalian
US-10-304-287-4

Query Match 100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 2 CGPC 5

RESULT 8
US-10-290-072-233
;; Sequence 233, Application US/10290072
;; Publication No. US2003021151A1
;; GENERAL INFORMATION:
;; APPLICANT: Briggs, Steven P.
;; APPLICANT: Dalma, Bipin K.
;; APPLICANT: del Val, Greg
;; APPLICANT: Desjarlais, John R.
;; APPLICANT: Heiletz, Peter
;; APPLICANT: Lugibuhl, Peter
;; APPLICANT: Muchhal, Umesh
;; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity
;; FILE REFERENCE: A-71457-3
;; CURRENT APPLICATION NUMBER: US/10/290,072
;; PRIOR FILING DATE: 2002-11-06
;; PRIOR APPLICATION NUMBER: US 60/370,609
;; PRIOR FILING DATE: 2002-04-05
;; PRIOR APPLICATION NUMBER: US 60/376,682
;; PRIOR FILING DATE: 2002-04-29
;; PRIOR APPLICATION NUMBER: US 10/141,531
;; PRIOR FILING DATE: 2002-05-06
;; PRIOR APPLICATION NUMBER: US 60/289,029
;; PRIOR FILING DATE: 2001-05-04
;; NUMBER OF SEQ ID NOS: 239

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: active site consensus sequence
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(1)
; OTHER INFORMATION: "Xaa" at position 1 can be any amino acid, preferably a
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: "Xaa" at position 6 can be any amino acid, preferably polar amino
; OTHER INFORMATION: acids
US-10-290-072-233

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 9
US-10-461-224-5
; Sequence 5, Application US/10461224
; Publication No. US20040019104A1
; GENERAL INFORMATION:
; APPLICANT: Edright, Richard H.
; FILE OF INVENTION: Reagents and Procedures for High Specificity Labeling
; TITLE REFERENCE: 744-34
; CURRENT APPLICATION NUMBER: US/10/461,224
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/388,699
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target sequence.
US-10-461-224-5

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 10
US-10-660-118A-2
; Sequence 2, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; FILE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; TITLE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
```

```
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
; NAME/KEY: misc_feature
; LOCATION: (1)..(6)
; OTHER INFORMATION: Xaa = any amino acid
US-10-660-118A-2

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 11
US-10-660-118A-3
; Sequence 3, Application US/10660118A
; Publication No. US20040131606A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; FILE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; TITLE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-3

Query Match          100.0%; Score 31; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
DB      2 CGPC 5

RESULT 12
US-10-735-577-4
; Sequence 4, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metasta
; FILE REFERENCE: ME03-003
; CURRENT APPLICATION NUMBER: US/10/735,577
; PRIOR FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
```



```

; TYPE: PRT
; ORGANISM: mammalian
US-10-735-577-4

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 2 CGPC 5

RESULT 13
US-10-461-224-10
; Sequence 10, Application US/10461224
; Publication No. US20040019104A1
; GENERAL INFORMATION:
; APPLICANT: EdBright, Richard H.
; TITLE OF INVENTION: Reagents and Procedures for High Specificity Labeling
; FILE REFERENCE: 744-34
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/388,699
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Target sequence.
US-10-461-224-10

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 1 CGPC 4

RESULT 14
US-10-954-951-11
; Sequence 11, Application US/10954951
; Publication No. US20050136449A1
; GENERAL INFORMATION:
; APPLICANT: Hanson, George
; APPLICANT: Kudlicki, Wieslaw Antoni
; APPLICANT: Kepestipola, Shrinanthi
; TITLE OF INVENTION: Compositions and Methods for Synthesizing, Purifying and
; FILE REFERENCE: 0942.6650001
; CURRENT APPLICATION NUMBER: US/10/954,951
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: US 60/508,142
; PRIOR FILING DATE: 2003-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: C terminal of Cam Ortho expressed in PRESETB
US-10-954-951-11

Query Match
Best Local Similarity 100.0%; Score 31; DB 5; Length 8;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 CGPC 5
   ||||
Db 1 CGPC 4

RESULT 15
US-09-572-404B-918
; Sequence 918, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 918
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LHB at 105-114 and may interact with Sequence
US-09-572-404B-918

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 6 CGPC 9

RESULT 16
US-09-572-404B-970
; Sequence 970, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 970
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in LHB at 105-114 and may interact with Sequence
US-09-572-404B-970

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 6 CGPC 9

RESULT 17
US-10-615-343-2
; Sequence 2, Application US/10615343
; Publication No. US20050009110A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, XIAO-JIA
; TITLE OF INVENTION: METHODS OF PRODUCING ANTIBODIES FOR DIAGNOSTICS AND THERAPEUTICS
```

FILE REFERENCE: IGA-003.01
CURRENT APPLICATION NUMBER: US/10/615,343
CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-615-343-2

Query Match 100.0%; Score 31; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 9 CGPC 12

RESULT 18

US-10-044-844-217
Sequence 217, Application US/10044844
Publication No. US2004009904A1
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
Margulis, David M.
Jones, David S.
Yu, Lin
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND
METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED PATHOLOGIES
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,844
FILING DATE: 10-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-044-844-217

Query Match 100.0%; Score 31; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 19

US-10-846-079-217
Sequence 217, Application US/10846079
Publication No. US20050208480A1
GENERAL INFORMATION:
APPLICANT: Victoria, Edward J.
Margulis, David M.
Jones, David S.
Yu, Lin
TITLE OF INVENTION: APL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND
METHODS OF TREATMENT FOR APL ANTIBODY-MEDIATED PATHOLOGIES
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER LLP
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/846,079
FILING DATE: 13-May-2004
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: CATHERINE M. POLIZZI
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 25231-20061.03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-10-846-079-217

Query Match 100.0%; Score 31; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 4 CGPC 7

RESULT 20

US-09-963-339-10
Sequence 10, Application US/09963339
Publication No. US20030049700A1
GENERAL INFORMATION:
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: 22108 AND 47916, NOVEL HUMAN THIOREDOXIN
FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-090001
CURRENT APPLICATION NUMBER: US/09/963,339
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/235,049
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10

LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-09-963-339-10

Query Match 100.0%; Score 31; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 21
US-10-145-586-59

Sequence 59, Application US/10145586
Publication No. US20030138890A1
GENERAL INFORMATION:
APPLICANT: Alexandra Glucksmann, Maria
APPLICANT: Silos-Santiago, Immaculada
APPLICANT: M. Galvin, Katherine
APPLICANT: Weich, Nadine
APPLICANT: Curtis, Rory A.J.
APPLICANT: Bandaru, Rajasekhar
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS, HUMAN LEUCINE-RICH
TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
FILE REFERENCE: 10448-188001
CURRENT APPLICATION NUMBER: US/10/145,586
CURRENT FILING DATE: 2002-05-14
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 95
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-145-586-59

Query Match 100.0%; Score 31; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 22
US-10-050-882-98

Sequence 98, Application US/10050882
Publication No. US20030104400A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 27 Human secreted proteins
FILE REFERENCE: P2038P1
CURRENT APPLICATION NUMBER: US/10/050,882
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/661,453
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/US00/06783
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/125,055
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-10-050-882-98

Query Match 100.0%; Score 31; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 19 CGPC 22

RESULT 23
US-10-963-903-98

Sequence 98, Application US/10963903
Publication No. US20050239099A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 27 Human secreted proteins
FILE REFERENCE: P2038P1C2
CURRENT APPLICATION NUMBER: US/10/963,903
CURRENT FILING DATE: 2004-10-14
PRIOR APPLICATION NUMBER: US 10/050,882
PRIOR FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: US 09/661,453
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/US00/06783
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: US 60/125,055
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 98
LENGTH: 25
TYPE: PRT
ORGANISM: Homo sapiens
US-10-963-903-98

Query Match 100.0%; Score 31; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 19 CGPC 22

RESULT 24
US-10-179-382-31

Sequence 31, Application US/10179382
Publication No. US2003016235A1
GENERAL INFORMATION:
APPLICANT: THIREOS, GEORGE
APPLICANT: KAFETZPOULOS, DIMITRIS
TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
CURRENT APPLICATION NUMBER: US/10/179,382
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US/09/230,041
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 28
TYPE: PRT
ORGANISM: Rhizobium leguminosarum
US-10-179-382-31

Query Match 100.0%; Score 31; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

```
RESULT 25
US-09-881-572A-25
; Sequence 25, Application US/09881572A
; Patent No. US20020164583A1
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: BUDD, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 29
; TYPE: PRF
; ORGANISM: Amphotrophic Murine Leukemia Virus
US-09-881-572A-25

Query Match          100.0%; Score 31; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
DB      11 CGPC 14

RESULT 26
US-09-881-572A-5
; Sequence 5, Application US/09881572A
; Patent No. US20020164583A1
; GENERAL INFORMATION:
; APPLICANT: Roth, Monica;
; APPLICANT: BUDD, Keith;
; APPLICANT: University of Medicine and Dentistry of New Jersey
; TITLE OF INVENTION: Targeting Viral Vectors to Specific Cells
; FILE REFERENCE: 601-1-095
; CURRENT APPLICATION NUMBER: US/09/881,572A
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: 60/212,239
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRF
; ORGANISM: amphotrophic murine leukemia virus
US-09-881-572A-5

Query Match          100.0%; Score 31; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
DB      11 CGPC 14

RESULT 27
US-09-864-761-40069
; Sequence 40069, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
```

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 40069
; LENGTH: 32
; TYPE: PRF
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC003681.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4
; OTHER INFORMATION: EST HUMAN HIT: BF446535.1, EVALU6 6.00e-12
; OTHER INFORMATION: SWISSPROT HIT: Q02597, EVALU6 1.70e+00
US-09-864-761-40069

Query Match          100.0%; Score 31; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
DB      8 CGPC 11

RESULT 28
US-10-424-599-160512
; Sequence 160512, Application US/10424599
```

```
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160512
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_115960C.1.pep
US-10-424-599-160512
```

```
Query Match          100.0%; Score 31; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       23 CGPC 26
```

```
RESULT 29
US-10-044-359-26
; Sequence 26, Application US/10044359
; Publication No. US20020160454A1
; GENERAL INFORMATION:
; APPLICANT: Herriman, Rafael
; APPLICANT: Wong, James F.
; APPLICANT: Lee, Jian-Ming
; TITLE OF INVENTION: SCORPION TOXINS
; FILE REFERENCE: B1367 US NA
; CURRENT APPLICATION NUMBER: US/10/044,359
; CURRENT FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 09/599,416
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,227
; PRIOR FILING DATE: 1999-06-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Androctonus mauretanicus
US-10-044-359-26
```

```
Query Match          100.0%; Score 31; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       1 CGPC 4
```

```
RESULT 30
US-09-801-260-5
; Sequence 5, Application US/09801260
; Patent No. US20020034801A1
; GENERAL INFORMATION:
; APPLICANT: Cutlis, Roy A.J.
; TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE REFERENCE: 10448-022001
; CURRENT APPLICATION NUMBER: US/09/801,260
; CURRENT FILING DATE: 2001-03-06
```

```
; PRIOR APPLICATION NUMBER: US 60/187,447
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-260-5
```

```
Query Match          100.0%; Score 31; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       33 CGPC 36
```

```
RESULT 31
US-10-145-586-44
; Sequence 44, Application US/10145586
; Publication No. US20030138890A1
; GENERAL INFORMATION:
; APPLICANT: Alexandra Glucksmann, Maria
; APPLICANT: Silos-Santiago, Imaculada
; APPLICANT: M. Galvin, Katherine
; APPLICANT: Welch, Nadine
; APPLICANT: Curtis, Roy A.J.
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Liberman, Rosana
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS
; TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LECTIVE-RICH
; FILE REFERENCE: 10448-188001
; CURRENT APPLICATION NUMBER: US/10/145,586
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-10-145-586-44
```

```
Query Match          100.0%; Score 31; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       33 CGPC 36
```

```
RESULT 32
US-10-450-763-51435
; Sequence 51435, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
```

```

; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 51435
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-51435

Query Match          100.0%; Score 31; DB 5; Length 42;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        1 CGPC 4

Db

RESULT 33
US-09-864-761-35367
; Sequence 35367, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmlca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24262.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35367
; LENGTH: 43
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011297.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3
; OTHER INFORMATION: EST HUMAN HIT: AW65671.1, EVALUE 3.00e-03
; OTHER INFORMATION: SWISSPROT HIT: Q14990, EVALUE 4.00e-04
US-09-864-761-35367

Query Match          100.0%; Score 31; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        1 CGPC 20

Db

RESULT 34
US-10-293-157-20
; Sequence 20, Application US/10293157
; Publication No. US20030144200A1
; GENERAL INFORMATION:
; APPLICANT: BAIRD, ANDREW
; APPLICANT: ANDREASON, GRAI
; TITLE OF INVENTION: NOVEL FORMS OF THE ANGIOGENIC FACTOR
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL CELL GROWTH FACTOR: VEGF
; FILE REFERENCE: 240/086
; CURRENT APPLICATION NUMBER: US/10/293,157
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/244,583
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 60/073,979
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-293-157-20

Query Match          100.0%; Score 31; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
        ||||
        2 CGPC 5

Db

RESULT 35
US-10-424-599-255327
; Sequence 255327, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
```

```

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 255327
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_72582C.1.pep
US-10-424-599-255327

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 43;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPC 5
    ||||
DB 18 CGPC 21

```

```

RESULT 36
US-09-832-355A-3
; Sequence 3, Application US/09832355A
; Publication No. US20030027751A1
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Kessler, Paul
; TITLE OF INVENTION: VEGF FUSION PROTEINS
; FILE REFERENCE: 205654
; CURRENT APPLICATION NUMBER: US/09/832,355A
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-355A-3

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPC 5
    ||||
DB 2 CGPC 5

```

```

RESULT 37
US-10-104-440-11
; Sequence 11, Application US/10104440
; Publication No. US2002013274A1
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, Michael
; APPLICANT: SOKER, Shay
; APPLICANT: MIAO, Hua Quan
; TITLE OF INVENTION: ANTAGONISTS OF NEUROPILIN RECEPTOR FUNCTION AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 48802 C
; CURRENT APPLICATION NUMBER: US/10/104,440
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/580,803
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-29
; PRIOR APPLICATION NUMBER: 60/078,541
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 44
; TYPE: PRT

```

```

; ORGANISM: human
US-10-104-440-11

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPC 5
    ||||
DB 2 CGPC 5

```

```

RESULT 38
US-10-104-610-15
; Sequence 15, Application US/10104610
; Publication No. US20030104532A1
; GENERAL INFORMATION:
; APPLICANT: KLAGSBRUN, Michael
; APPLICANT: SOKER, Shay
; APPLICANT: GAGNON, Michael L.
; TITLE OF INVENTION: SOLUBLE INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH
; TITLE OF INVENTION: AND USE THEREOF
; FILE REFERENCE: 48801 C
; CURRENT APPLICATION NUMBER: US/10/104,610
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/580,989
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 60/069,155
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/069,687
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 44
; TYPE: PRT
; ORGANISM: human
US-10-104-610-15

```

```

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 44;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPC 5
    ||||
DB 2 CGPC 5

```

```

RESULT 39
US-10-424-599-252212
; Sequence 252212, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 252212
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(45)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

```

OTHER INFORMATION: Clone ID: PAT_MRT3847_6976C.1.pep
US-10-424-599-252212

Query Match 100.0%; Score 31; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 15 CGPC 18

RESULT 40

US-10-425-115-210616
Sequence 210616, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425, 115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 210616
LENGTH: 47
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_12367C.1.pep
US-10-425-115-210616

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 18 CGPC 21

RESULT 41

US-10-425-115-321622
Sequence 321622, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425, 115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 321622
LENGTH: 47
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(47)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_56384C.1.pep
US-10-425-115-321622

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 1 CGPC 4

RESULT 42

US-11-097-143-37521
Sequence 37521, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37521
LENGTH: 47
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-37521

Query Match 100.0%; Score 31; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 43

US-10-425-115-334172
Sequence 334172, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53222)B
CURRENT APPLICATION NUMBER: US/10/425, 115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 334172
LENGTH: 49
TYPE: PRT
ORGANISM: Zea mays
FEATURE:

Query Match 100.0%; Score 31; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 6e+02;


```
/ NAME/KEY: unsure
/ LOCATION: (1)..(49)
/ OTHER INFORMATION: unsure at all Xaa locations
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_6787C.1.pdp
US-10-425-115-334172

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 10 CGPC 13

RESULT 44
US-09-801-260-4
/ Sequence 4, Application US/09801260
/ Patent No. US20020034801A1
/ GENERAL INFORMATION:
/ APPLICANT: Curtis, Roy A.J.
/ TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
/ FILE REFERENCE: 10448-022001
/ CURRENT APPLICATION NUMBER: US/09/801,260
/ PRIOR FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: US 60/187,447
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus sequence
US-09-801-260-4

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

RESULT 45
US-10-145-586-43
/ Sequence 43, Application US/10145586
/ Publication No. US20030138890A1
/ GENERAL INFORMATION:
/ APPLICANT: Alexandra Glucksmann, Maria
/ APPLICANT: Silos-Santiago, Immaculada
/ APPLICANT: M. Galvin, Katherine
/ APPLICANT: Weich, Nadine
/ APPLICANT: Curtis, Roy A.J.
/ APPLICANT: Bandaru, Rajasekhar
/ APPLICANT: Kapeller-Lieberman, Rosana
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
/ TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH
/ FILE REFERENCE: 10448-188001
/ CURRENT APPLICATION NUMBER: US/10/145,586
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 95
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 43
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: consensus sequence
US-10-145-586-43

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 21 CGPC 24

RESULT 46
US-10-437-963-164055
/ Sequence 164055, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 164055
/ LENGTH: 52
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_62993C.1.pdp
US-10-437-963-164055

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 5 CGPC 8

RESULT 47
US-10-424-599-166951
/ Sequence 166951, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 166951
/ LENGTH: 53
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_121771C.1.pdp
US-10-424-599-166951

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 53;
```

Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 33 CGPC 36

RESULT 48

US-09-864-761-42458
; Sequence 42458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42458
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011510.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EST HUMAN HIT: BE148597.1, EVALUE 2.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P03204, EVALUE 3.50e+00
US-09-864-761-42458

Query Match 100.0%; Score 31; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 9 CGPC 12

RESULT 49

US-10-318-302-2
; Sequence 2, Application US/10318302
; Publication No. US20030171556A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH FOUNDATION
; APPLICANT: Chae, Chi-Bom
; APPLICANT: Gho, Yong Seng
; APPLICANT: Yang, Seung-Pil
; APPLICANT: Kwon, Byung Oh
; APPLICANT: Bae, Dong-Goo
; APPLICANT: Haeng, Sewook
; TITLE OF INVENTION: BETA-AMYLOID BINDING FACTORS AND INHIBITORS THEREOF
; FILE REFERENCE: 10011-00001
; CURRENT APPLICATION NUMBER: US/10/318,302
; CURRENT FILING DATE: 2002-12-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-302-2

Query Match 100.0%; Score 31; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 7 CGPC 10

RESULT 50

US-10-425-115-307743
; Sequence 307743, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovall, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 307743
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MR4577_43730C.1.pep
US-10-425-115-307743

Query Match 100.0%; Score 31; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 40 CGPC 43

RESULT 51
US-10-868-577A-28
; Sequence 28; Application US/10868577A
; Publication No. US2005032697A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-28

Query Match 100.0%; Score 31; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 7 CGPC 10

RESULT 52
US-11-097-143-26469
; Sequence 26469; Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26469
; LENGTH: 55
; TYPE: PRT
; ORGANISM: DROSOPHILA

US-11-097-143-26469

Query Match 100.0%; Score 31; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 3 CGPC 6

RESULT 53
US-10-425-115-219153
; Sequence 219153; Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 219153
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_131459C.1.pap
US-10-425-115-219153

Query Match 100.0%; Score 31; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
Db 45 CGPC 48

RESULT 54
US-11-097-143-26490
; Sequence 26490; Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26490
; LENGTH: 56
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26490

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 3 CGPC 6

RESULT 55
US-10-029-386-28568
; Sequence 28568; Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 28568
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: SWISSPROT HIT: P00203, EVALUATE 1.20e+00
US-10-029-386-28568

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 6 CGPC 9

RESULT 56
US-10-425-115-353222
; Sequence 353222; Application US/10425115
; Publication No. US2004021272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 353222
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Zea mays
```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_85311C.1.pep
US-10-425-115-353222

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 29 CGPC 32

RESULT 57
US-10-424-599-185374
; Sequence 185374; Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185374
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_138407C.1.pep
US-10-424-599-185374

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 58;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 38 CGPC 41

RESULT 58
US-10-437-963-202381
; Sequence 202381; Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 202381
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_97667C.1.pep
US-10-437-963-202381

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 58;
```

Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 17 CGPC 20

RESULT 59

US-10-424-599-176362
; Sequence 176362, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 176362
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_130272C.1.pep
US-10-424-599-176362

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 41 CGPC 44

RESULT 60

US-09-864-408A-7494
; Sequence 7494, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enc
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7494
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-408A-7494

Query Match
Best Local Similarity 100.0%; Score 31; DB 3; Length 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 4 CGPC 7

RESULT 61
US-11-097-143-10200
; Sequence 10200, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10200
; LENGTH: 60
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-10200

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 41 CGPC 44

RESULT 62

US-10-424-599-278438
; Sequence 278438, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278438
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93452C.1.pep
US-10-424-599-278438

Query Match
Best Local Similarity 100.0%; Score 31; DB 4; Length 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
DB 28 CGPC 31

RESULT 63
US-10-423-115-233772
; Sequence 233772, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 233772
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144792C.1.pep
US-10-425-115-233772

Query Match 100.0%; Score 31; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 40 CGPC 43

RESULT 64
US-11-097-143-26472
; Sequence 26472, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26472
; LENGTH: 63
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26472

Query Match 100.0%; Score 31; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 17 CGPC 20

RESULT 65
US-10-425-115-336734
; Sequence 336734, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 336734
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(64)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_70240C.1.pep
US-10-425-115-336734

Query Match 100.0%; Score 31; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 40 CGPC 43

RESULT 66
US-10-424-599-180203
; Sequence 180203, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 180203
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(65)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133738C.1.pep
US-10-424-599-180203

Query Match 100.0%; Score 31; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 28 CGPC 31

RESULT 67
US-10-437-963-152827
; Sequence 152827, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152827
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_5283C.1.pcp
US-10-437-963-152827

Query Match 100.0%; Score 31; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 21 CGPC 24

RESULT 68
US-10-425-115-256158
; Sequence 256158, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256158
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165207C.1.pcp
US-10-425-115-256158

Query Match 100.0%; Score 31; DB 4; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 10 CGPC 13

RESULT 69
US-11-097-143-32565
; Sequence 32565, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: C1000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32565
; LENGTH: 67
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32565

Query Match 100.0%; Score 31; DB 6; Length 67;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 8 CGPC 11

RESULT 70
US-10-243-552-978
; Sequence 978, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yunding
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404

```
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 978
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-243-552-978
```

```
Query Match          100.0%; Score 31; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
         ||||
Db       53 CGPC 56
```

Search completed: February 23, 2006, 00:47:46
Job time : 128.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:44:02 ; Search time 11.5 Seconds
(without alignments)
7.767 Million cell updates/sec

Title: US-10-660-118a-2
Perfect score: 31
Sequence: 1 XGCPX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 1000 summaries

Database :

Published Applications AA.New:*
1: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubppa/US09_NEW_PUB.pep:*
5: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubppa/US12_NEW_PUB.pep:*
8: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	4	US-11-090-916-1	Sequence 1, App11
2	31	100.0	4	US-11-144-301A-8	Sequence 8, App11
3	31	100.0	4	US-11-223-405-1	Sequence 1, App11
4	31	100.0	4	US-11-223-547-1	Sequence 1, App11
5	31	100.0	4	US-11-058-926-2	Sequence 2, App11
6	31	100.0	6	US-11-090-916-2	Sequence 2, App11
7	31	100.0	6	US-11-090-916-3	Sequence 3, App11
8	31	100.0	75	US-11-131-744-2	Sequence 2, App11
9	31	100.0	84	US-10-467-657-5372	Sequence 5372, App
10	31	100.0	91	US-11-131-744-1	Sequence 1, App11
11	31	100.0	103	US-11-074-176-286	Sequence 286, App1
12	31	100.0	103	US-11-090-916-6	Sequence 9, App11
13	31	100.0	103	US-11-090-916-7	Sequence 7, App11
14	31	100.0	104	US-11-090-916-5	Sequence 5, App11
15	31	100.0	105	US-10-821-234-1371	Sequence 1371, App
16	31	100.0	105	US-11-090-916-8	Sequence 8, App11
17	31	100.0	105	US-11-090-916-9	Sequence 9, App11
18	31	100.0	105	US-11-090-916-10	Sequence 10, App11
19	31	100.0	105	US-11-090-916-11	Sequence 11, App11
20	31	100.0	105	US-11-090-916-12	Sequence 12, App11
21	31	100.0	105	US-11-106-796-13	Sequence 13, App11
22	31	100.0	105	US-11-144-301A-9	Sequence 9, App11
23	31	100.0	105	US-11-144-301A-10	Sequence 10, App11
24	31	100.0	105	US-11-032-773-943	Sequence 943, App
25	31	100.0	107	US-10-689-742-19	Sequence 19, App1

26	31	100.0	107	US-11-098-686-10612	Sequence 10612, A
27	31	100.0	109	US-11-090-916-4	Sequence 4, App11
28	31	100.0	113	US-11-072-512-3199	Sequence 1199, App
29	31	100.0	122	US-11-195-459-12	Sequence 12, App1
30	31	100.0	122	US-11-195-459-16	Sequence 16, App1
31	31	100.0	122	US-11-195-459-19	Sequence 19, App1
32	31	100.0	123	US-11-195-459-10	Sequence 10, App1
33	31	100.0	126	US-10-995-561-703	Sequence 703, App
34	31	100.0	127	US-11-106-796-10	Sequence 10, App1
35	31	100.0	127	US-11-106-796-11	Sequence 11, App1
36	31	100.0	127	US-11-106-796-12	Sequence 12, App1
37	31	100.0	129	US-10-467-657-4354	Sequence 4354, App
38	31	100.0	129	US-11-072-512-2145	Sequence 2145, App
39	31	100.0	134	US-11-090-916-13	Sequence 13, App11
40	31	100.0	134	US-11-195-459-8	Sequence 8, App11
41	31	100.0	143	US-09-978-360A-641	Sequence 641, App
42	31	100.0	167	US-11-090-916-14	Sequence 14, App1
43	31	100.0	172	US-11-090-916-15	Sequence 15, App1
44	31	100.0	177	US-11-131-744-3	Sequence 3, App11
45	31	100.0	183	US-10-467-962B-6	Sequence 6, App11
46	31	100.0	189	US-10-995-561-643	Sequence 643, App
47	31	100.0	191	US-10-995-561-642	Sequence 642, App
48	31	100.0	191	US-11-064-774A-2	Sequence 2, App11
49	31	100.0	191	US-11-075-400-2	Sequence 2, App11
50	31	100.0	191	US-11-226-005-4	Sequence 4, App11
51	31	100.0	191	US-11-129-076-9	Sequence 9, App11
52	31	100.0	191	US-11-145-494-2	Sequence 2, App11
53	31	100.0	191	US-11-075-047A-81	Sequence 81, App1
54	31	100.0	197	US-11-098-686-11017	Sequence 11017, A
55	31	100.0	209	US-10-467-657-8494	Sequence 8494, App
56	31	100.0	215	US-10-995-561-640	Sequence 640, App
57	31	100.0	215	US-10-995-561-645	Sequence 645, App
58	31	100.0	215	US-10-995-561-646	Sequence 646, App
59	31	100.0	215	US-11-149-462-3	Sequence 3, App11
60	31	100.0	216	US-11-106-399-8	Sequence 8, App11
61	31	100.0	224	US-11-072-512-3343	Sequence 3343, App
62	31	100.0	232	US-10-995-561-641	Sequence 641, App
63	31	100.0	232	US-10-995-561-644	Sequence 644, App
64	31	100.0	232	US-11-153-880-7	Sequence 7, App11
65	31	100.0	232	US-11-064-774A-147	Sequence 147, App
66	31	100.0	232	US-11-211-724-5	Sequence 5, App11
67	31	100.0	232	US-11-233-119-7	Sequence 7, App11
68	31	100.0	273	US-11-075-047A-91	Sequence 91, App1
69	31	100.0	273	US-11-131-744-6	Sequence 6, App11
70	31	100.0	282	US-11-186-284-85	Sequence 85, App1
71	31	100.0	294	US-11-055-822-480	Sequence 480, App
72	31	100.0	294	US-11-055-822-880	Sequence 880, App
73	31	100.0	300	US-11-154-257-2	Sequence 2, App11
74	31	100.0	325	US-09-978-360A-406	Sequence 406, App
75	31	100.0	354	US-11-054-281-58	Sequence 58, App1
76	31	100.0	373	US-11-186-284-16	Sequence 16, App1
77	31	100.0	373	US-11-054-281-59	Sequence 59, App1
78	31	100.0	380	US-11-090-439-52	Sequence 52, App1
79	31	100.0	380	US-11-090-439-54	Sequence 54, App1
80	31	100.0	380	US-11-054-281-60	Sequence 60, App1
81	31	100.0	430	US-11-072-512-2204	Sequence 2204, App
82	31	100.0	440	US-11-131-744-7	Sequence 7, App11
83	31	100.0	447	US-10-967-527A-14	Sequence 14, App1
84	31	100.0	448	US-10-967-527A-16	Sequence 16, App1
85	31	100.0	448	US-11-182-016-24	Sequence 24, App1
86	31	100.0	450	US-11-186-284-14	Sequence 14, App1
87	31	100.0	502	US-10-966-483-23	Sequence 23, App1
88	31	100.0	502	US-11-021-441-17	Sequence 7, App11
89	31	100.0	509	US-11-124-367A-447	Sequence 447, App
90	31	100.0	539	US-11-043-788-464	Sequence 464, App
91	31	100.0	549	US-11-043-788-467	Sequence 467, App
92	31	100.0	549	US-11-043-788-468	Sequence 468, App
93	31	100.0	563	US-10-966-483-25	Sequence 25, App1
94	31	100.0	563	US-11-021-441-9	Sequence 9, App11
95	31	100.0	572	US-10-763-712A-10	Sequence 10, App1
96	31	100.0	572	US-10-763-712A-11	Sequence 11, App1
97	31	100.0	572	US-10-763-712A-37	Sequence 37, App1
98	31	100.0	572	US-10-763-712A-109	Sequence 109, App

99	31	100.0	572	6	US-10-763-712A-110	Sequence 110, App	172	25	80.6	355	6	US-10-967-527A-22	Sequence 22, App1
100	31	100.0	574	6	US-10-763-712A-1	Sequence 1, App1	173	25	80.6	355	7	US-11-182-946-14	Sequence 14, App1
101	31	100.0	574	6	US-10-763-712A-6	Sequence 6, App1	174	25	80.6	380	7	US-11-144-236-1	Sequence 1, App1
102	31	100.0	574	6	US-10-763-712A-102	Sequence 102, App	175	25	80.6	386	6	US-10-131-826A-340	Sequence 340, App
103	31	100.0	574	6	US-10-966-483-31	Sequence 31, App1	176	25	80.6	386	7	US-11-183-878-2	Sequence 2, App1
104	31	100.0	574	6	US-11-021-441-15	Sequence 15, App1	177	25	80.6	386	7	US-11-099-135-1	Sequence 1, App1
105	31	100.0	581	6	US-10-966-483-27	Sequence 27, App1	178	25	80.6	398	7	US-11-072-512-2769	Sequence 2769, App
106	31	100.0	581	6	US-10-966-483-29	Sequence 29, App1	179	25	80.6	400	6	US-10-948-053-4	Sequence 4, App1
107	31	100.0	581	7	US-11-021-441-11	Sequence 11, App1	180	25	80.6	400	6	US-10-948-053-5	Sequence 5, App1
108	31	100.0	581	7	US-11-021-441-13	Sequence 13, App1	181	25	80.6	401	6	US-10-949-720-419	Sequence 419, App
109	31	100.0	654	6	US-10-510-947-6	Sequence 6, App1	182	25	80.6	401	6	US-10-510-876-2	Sequence 2, App1
110	31	100.0	654	6	US-10-055-877-255	Sequence 255, App	183	25	80.6	401	6	US-10-510-876-4	Sequence 4, App1
111	31	100.0	660	6	US-10-055-877-254	Sequence 254, App	184	25	80.6	401	6	US-10-948-053-8	Sequence 8, App1
112	31	100.0	747	6	US-10-131-826A-426	Sequence 426, App	185	25	80.6	404	6	US-10-948-053-7	Sequence 7, App1
113	31	100.0	755	7	US-11-067-121-6	Sequence 6, App1	186	25	80.6	406	6	US-10-948-053-6	Sequence 6, App1
114	31	100.0	757	7	US-11-067-121-16	Sequence 16, App1	187	25	80.6	406	7	US-11-098-686-10564	Sequence 10564, A
115	31	100.0	757	7	US-11-186-284-41	Sequence 41, App1	188	25	80.6	407	6	US-10-948-053-3	Sequence 3, App1
116	31	100.0	780	6	US-10-878-556A-197	Sequence 197, App	189	25	80.6	431	6	US-10-949-720-410	Sequence 410, App
117	31	100.0	884	7	US-11-098-686-11426	Sequence 11426, A	190	25	80.6	466	7	US-11-127-877-41	Sequence 41, App1
118	31	100.0	885	6	US-10-467-657-2302	Sequence 2302, App	191	25	80.6	502	7	US-11-127-877-41	Sequence 4, App1
119	31	100.0	905	7	US-11-072-512-2728	Sequence 2728, App	192	25	80.6	514	6	US-10-498-026-97	Sequence 97, App1
120	31	100.0	954	6	US-10-467-9628-31	Sequence 31, App1	193	25	80.6	514	6	US-10-498-026-98	Sequence 98, App1
121	31	100.0	961	6	US-10-831-997-4	Sequence 4, App1	194	25	80.6	522	6	US-10-949-720-425	Sequence 425, App
122	31	100.0	976	6	US-10-966-483-2	Sequence 2, App1	195	25	80.6	537	6	US-11-144-236-6	Sequence 424, App
123	31	100.0	976	6	US-10-511-273-1	Sequence 1, App1	196	25	80.6	537	7	US-11-144-236-6	Sequence 6, App1
124	31	100.0	976	7	US-11-233-796-2	Sequence 2, App1	197	25	80.6	555	6	US-10-949-720-387	Sequence 387, App
125	31	100.0	976	7	US-11-072-175-138	Sequence 138, App	198	25	80.6	570	6	US-10-949-720-386	Sequence 386, App
126	31	100.0	1035	6	US-10-966-483-20	Sequence 20, App1	199	25	80.6	570	6	US-10-949-720-412	Sequence 412, App
127	31	100.0	1035	7	US-11-021-441-4	Sequence 4, App1	200	25	80.6	645	7	US-11-072-512-2588	Sequence 2588, App
128	31	100.0	1075	7	US-11-174-150-34	Sequence 34, App1	201	25	80.6	655	7	US-11-072-512-2502	Sequence 2502, App
129	31	100.0	1114	7	US-11-174-150-35	Sequence 35, App1	202	25	80.6	698	7	US-11-177-506-46	Sequence 46, App1
130	31	100.0	1857	6	US-10-055-877-252	Sequence 252, App	203	25	80.6	771	6	US-10-949-720-389	Sequence 389, App
131	31	100.0	2084	6	US-10-055-877-73	Sequence 73, App1	204	25	80.6	794	7	US-11-218-986-2	Sequence 2, App1
132	31	100.0	2098	6	US-10-055-877-253	Sequence 253, App	205	25	80.6	820	6	US-10-821-234-1176	Sequence 1176, App
133	31	100.0	2109	6	US-10-055-877-251	Sequence 251, App	206	25	80.6	985	7	US-11-113-424-61	Sequence 61, App1
134	25	80.6	47	7	US-11-116-746-8	Sequence 8, App1	207	25	80.6	987	6	US-10-949-720-395	Sequence 395, App
135	25	80.6	57	6	US-10-467-657-7390	Sequence 7390, App	208	25	80.6	990	6	US-10-821-234-1201	Sequence 1201, App
136	25	80.6	88	7	US-11-018-868-8	Sequence 8627, App	209	25	80.6	1049	6	US-10-821-234-958	Sequence 358, App
137	25	80.6	88	7	US-11-072-512-2975	Sequence 8, App1	210	25	80.6	1187	6	US-10-821-234-955	Sequence 955, App
138	25	80.6	106	7	US-11-072-512-2975	Sequence 2975, App	211	25	80.6	2143	6	US-10-453-372-1188	Sequence 1188, App
139	25	80.6	114	6	US-10-986-501-190	Sequence 190, App	212	25	80.6	2764	6	US-10-995-561-691	Sequence 691, App
140	25	80.6	117	7	US-11-103-957-74	Sequence 74, App1	213	25	80.6	2813	6	US-10-995-561-688	Sequence 688, App
141	25	80.6	120	6	US-10-793-626-2214	Sequence 2214, App	214	25	80.6	3219	6	US-10-821-234-1133	Sequence 1133, App
142	25	80.6	132	7	US-11-072-512-3315	Sequence 3315, App	215	25	80.6	3335	7	US-11-019-711-47	Sequence 47, App1
143	25	80.6	161	7	US-11-154-257-3	Sequence 3, App1	216	25	80.6	3712	7	US-11-019-711-48	Sequence 48, App1
144	25	80.6	167	7	US-11-072-512-3290	Sequence 3290, App	217	25	80.6	3712	7	US-11-019-711-51	Sequence 51, App1
145	25	80.6	170	6	US-10-467-657-104	Sequence 104, App	218	25	80.6	4374	7	US-11-128-572-2	Sequence 2, App1
146	25	80.6	170	6	US-10-467-657-8078	Sequence 8078, App	219	25	80.6	4961	6	US-10-453-372-1142	Sequence 1142, App
147	25	80.6	204	7	US-11-080-991-8	Sequence 8, App1	220	25	80.6	4961	6	US-10-453-372-1132	Sequence 1132, App
148	25	80.6	211	7	US-11-072-512-3219	Sequence 3219, App	221	24	77.4	46	7	US-11-188-552-69	Sequence 69, App1
149	25	80.6	228	6	US-10-793-626-1862	Sequence 1862, App	222	24	77.4	50	7	US-11-174-854-2	Sequence 2, App1
150	25	80.6	229	5	US-09-978-360A-753	Sequence 753, App	223	24	77.4	50	7	US-11-174-854-2	Sequence 2, App1
151	25	80.6	229	6	US-10-131-826A-522	Sequence 522, App	224	24	77.4	115	6	US-10-467-657-2032	Sequence 2032, App
152	25	80.6	241	6	US-10-467-657-4474	Sequence 4474, App	225	24	77.4	131	6	US-10-518-955-2	Sequence 2, App1
153	25	80.6	246	7	US-11-072-512-2232	Sequence 2232, App	226	24	77.4	132	6	US-10-518-955-4	Sequence 4, App1
154	25	80.6	247	7	US-11-072-512-2243	Sequence 2243, App	227	24	77.4	136	6	US-10-498-026-37	Sequence 37, App1
155	25	80.6	255	6	US-11-072-512-2790	Sequence 2790, App	228	24	77.4	144	6	US-10-498-026-37	Sequence 37, App1
156	25	80.6	255	6	US-10-170-997-2	Sequence 2, App1	229	24	77.4	146	7	US-11-026-657-80	Sequence 80, App1
157	25	80.6	255	7	US-11-182-946-11	Sequence 11, App1	230	24	77.4	260	7	US-11-182-946-8	Sequence 8, App1
158	25	80.6	255	7	US-11-108-257-2	Sequence 2, App1	231	24	77.4	331	7	US-11-185-878-3	Sequence 3, App1
159	25	80.6	259	6	US-10-131-826A-300	Sequence 300, App	232	24	77.4	334	6	US-10-514-057-6	Sequence 6, App1
160	25	80.6	259	6	US-10-821-234-1561	Sequence 1561, App	233	24	77.4	335	7	US-11-182-946-7	Sequence 7, App1
161	25	80.6	259	7	US-11-182-946-2	Sequence 2, App1	234	24	77.4	393	7	US-11-100-352-3	Sequence 3, App1
162	25	80.6	259	7	US-11-116-746-1	Sequence 1, App1	235	24	77.4	393	7	US-11-103-957-55	Sequence 55, App1
163	25	80.6	277	7	US-11-132-285-3	Sequence 3, App1	236	24	77.4	393	7	US-11-018-868-24	Sequence 24, App1
164	25	80.6	277	7	US-11-182-946-12	Sequence 12, App1	237	24	77.4	622	6	US-10-453-372-1186	Sequence 1186, App
165	25	80.6	280	6	US-10-131-826A-458	Sequence 458, App	238	24	77.4	669	7	US-11-076-187-3	Sequence 3, App1
166	25	80.6	280	6	US-10-689-742-160	Sequence 160, App	239	24	77.4	710	7	US-11-169-041-203	Sequence 203, App
167	25	80.6	299	7	US-11-116-746-3	Sequence 3, App1	240	24	77.4	843	7	US-11-129-104-89	Sequence 89, App1
168	25	80.6	336	6	US-10-467-657-5848	Sequence 5848, App	241	24	77.4	1544	6	US-10-453-372-1186	Sequence 1186, App
169	25	80.6	349	7	US-11-182-946-13	Sequence 13, App1	242	24	77.4	1565	6	US-10-453-372-1180	Sequence 1180, App
170	25	80.6	350	7	US-11-132-285-41	Sequence 41, App1	243	24	77.4	1566	6	US-10-453-372-1150	Sequence 1190, App
171	25	80.6	353	7	US-11-072-512-2052	Sequence 2052, App	244	24	77.4	2053	6	US-10-453-372-1174	Sequence 1174, App

245	23	74.2	4	7	US-11-029-003-90	Sequence 90, Appl	318	23	74.2	52	7	US-11-233-683-34	Sequence 34, Appl
246	23	74.2	5	6	US-11-058-926-3	Sequence 3, Appl1	319	23	74.2	53	6	US-10-914-391A-7	Sequence 7, Appl1
247	23	74.2	5	7	US-10-895-064-153	Sequence 153, App	320	23	74.2	54	6	US-10-467-657-2264	Sequence 2264, Ap
248	23	74.2	5	7	US-11-129-741-153	Sequence 153, App	321	23	74.2	55	7	US-11-000-463-303	Sequence 303, App
249	23	74.2	5	7	US-11-129-741-3086	Sequence 3086, Ap	322	23	74.2	55	7	US-11-000-463-775	Sequence 775, App
250	23	74.2	6	7	US-11-029-003-88	Sequence 88, Appl	323	23	74.2	56	7	US-11-042-814-6	Sequence 6, Appl1
251	23	74.2	7	7	US-11-029-003-87	Sequence 87, Appl	324	23	74.2	58	6	US-10-914-391A-4	Sequence 4, Appl1
252	23	74.2	7	7	US-11-029-003-89	Sequence 89, Appl	325	23	74.2	63	7	US-11-174-996A-93	Sequence 93, Appl
253	23	74.2	8	7	US-11-142-327-5	Sequence 5, Appl1	326	23	74.2	64	7	US-11-174-996A-69	Sequence 69, Appl
254	23	74.2	9	7	US-11-040-159-122	Sequence 122, App	327	23	74.2	66	7	US-11-172-536-7	Sequence 7, Appl1
255	23	74.2	10	6	US-10-929-988-48	Sequence 48, Appl	328	23	74.2	67	7	US-10-922-232B-20	Sequence 20, Appl
256	23	74.2	10	6	US-11-192-219-44	Sequence 44, Appl	329	23	74.2	68	6	US-11-123-896-164	Sequence 164, App
257	23	74.2	12	6	US-10-901-576-2	Sequence 2, Appl1	330	23	74.2	72	7	US-11-198-847-14	Sequence 14, Appl
258	23	74.2	15	6	US-10-925-366A-11	Sequence 11, Appl	331	23	74.2	72	7	US-11-198-847-221	Sequence 221, App
259	23	74.2	15	6	US-10-909-769-31	Sequence 31, Appl	332	23	74.2	72	7	US-11-174-996A-55	Sequence 55, Appl
260	23	74.2	15	7	US-11-198-847-336	Sequence 336, App	333	23	74.2	74	7	US-11-174-996A-77	Sequence 77, Appl
261	23	74.2	15	7	US-11-198-847-337	Sequence 337, App	334	23	74.2	75	6	US-10-478-345-10	Sequence 10, Appl
262	23	74.2	16	6	US-10-929-988-301	Sequence 301, App	335	23	74.2	75	6	US-10-478-345-14	Sequence 14, Appl
263	23	74.2	16	7	US-11-142-327-1	Sequence 1, Appl1	336	23	74.2	75	6	US-11-174-996A-91	Sequence 91, Appl
264	23	74.2	16	7	US-11-142-327-2	Sequence 2, Appl1	337	23	74.2	75	7	US-11-174-996A-73	Sequence 73, Appl
265	23	74.2	16	7	US-11-142-327-3	Sequence 3, Appl1	338	23	74.2	75	7	US-11-174-996A-83	Sequence 83, Appl
266	23	74.2	16	7	US-11-142-327-4	Sequence 4, Appl1	339	23	74.2	75	7	US-11-174-996A-87	Sequence 87, Appl
267	23	74.2	17	7	US-11-198-847-334	Sequence 334, App	340	23	74.2	75	7	US-11-174-996A-91	Sequence 91, Appl
268	23	74.2	17	7	US-11-198-847-335	Sequence 335, App	341	23	74.2	75	7	US-11-174-996A-95	Sequence 95, Appl
269	23	74.2	19	7	US-11-198-847-235	Sequence 235, App	342	23	74.2	75	7	US-11-174-996A-97	Sequence 97, Appl
270	23	74.2	21	7	US-11-198-847-236	Sequence 236, App	343	23	74.2	77	7	US-11-174-996A-53	Sequence 53, Appl
271	23	74.2	21	7	US-11-233-683-28	Sequence 28, App	344	23	74.2	77	7	US-11-174-996A-69	Sequence 69, Appl
272	23	74.2	24	6	US-10-895-861-26	Sequence 26, Appl	345	23	74.2	80	6	US-10-467-657-3504	Sequence 3504, Ap
273	23	74.2	27	6	US-10-895-861-73	Sequence 73, Appl	346	23	74.2	81	6	US-10-131-826A-150	Sequence 150, App
274	23	74.2	27	6	US-10-895-861-83	Sequence 83, Appl	347	23	74.2	84	5	US-09-978-360A-716	Sequence 716, Appl
275	23	74.2	28	7	US-11-120-501-31	Sequence 31, Appl	348	23	74.2	91	7	US-11-042-814-7	Sequence 7, Appl1
276	23	74.2	29	6	US-10-986-501-269	Sequence 269, App	349	23	74.2	92	6	US-10-821-230-1505	Sequence 1505, Ap
277	23	74.2	32	6	US-10-895-064-976	Sequence 976, App	350	23	74.2	93	7	US-11-230-180-112	Sequence 12, Appl
278	23	74.2	32	7	US-11-129-741-976	Sequence 976, App	351	23	74.2	96	6	US-10-467-657-4198	Sequence 4198, Ap
279	23	74.2	32	7	US-11-129-741-3972	Sequence 3972, Ap	352	23	74.2	97	6	US-10-467-657-4214	Sequence 4214, Ap
280	23	74.2	34	6	US-10-532-480-13	Sequence 13, Appl	353	23	74.2	97	6	US-11-054-281-299	Sequence 299, App
281	23	74.2	35	7	US-11-233-683-49	Sequence 49, Appl	354	23	74.2	102	6	US-11-172-536-8	Sequence 8, Appl1
282	23	74.2	35	7	US-11-233-683-50	Sequence 50, Appl	355	23	74.2	106	6	US-10-467-657-796	Sequence 796, App
283	23	74.2	35	7	US-11-233-683-53	Sequence 53, Appl	356	23	74.2	106	6	US-10-453-372-1178	Sequence 1178, Ap
284	23	74.2	35	7	US-11-233-683-54	Sequence 54, Appl	357	23	74.2	106	7	US-11-073-222-6	Sequence 6, Appl1
285	23	74.2	35	7	US-11-233-683-55	Sequence 55, Appl	358	23	74.2	106	7	US-11-072-512-2828	Sequence 2828, Appl
286	23	74.2	39	6	US-10-895-064-295	Sequence 295, App	359	23	74.2	107	6	US-11-253-881-6	Sequence 6, Appl1
287	23	74.2	39	7	US-11-129-741-295	Sequence 295, App	360	23	74.2	107	6	US-10-467-657-6644	Sequence 6644, Ap
288	23	74.2	39	7	US-11-129-741-3227	Sequence 3227, Ap	361	23	74.2	112	7	US-11-129-741-4223	Sequence 4223, Ap
289	23	74.2	40	6	US-10-979-871-4	Sequence 4, Appl1	362	23	74.2	115	7	US-11-155-288-11	Sequence 11, Appl
290	23	74.2	40	6	US-10-979-871-5	Sequence 5, Appl1	363	23	74.2	116	7	US-11-072-512-2094	Sequence 2094, Ap
291	23	74.2	40	6	US-10-979-871-6	Sequence 6, Appl1	364	23	74.2	124	5	US-09-995-493-84	Sequence 84, Appl
292	23	74.2	40	6	US-10-979-871-7	Sequence 7, Appl1	365	23	74.2	124	5	US-11-119-098-2	Sequence 2, Appl1
293	23	74.2	40	6	US-10-979-871-8	Sequence 8, Appl1	366	23	74.2	127	6	US-10-763-712A-82	Sequence 82, Appl
294	23	74.2	40	6	US-10-979-871-9	Sequence 9, Appl1	367	23	74.2	127	6	US-11-072-512-3790	Sequence 3790, Ap
295	23	74.2	40	6	US-10-979-871-10	Sequence 10, Appl	368	23	74.2	127	7	US-11-195-459-2	Sequence 2, Appl1
296	23	74.2	40	6	US-10-979-871-11	Sequence 11, Appl	369	23	74.2	128	7	US-11-195-459-4	Sequence 4, Appl1
297	23	74.2	40	6	US-10-979-871-12	Sequence 12, Appl	370	23	74.2	129	7	US-11-183-205-14	Sequence 14, Appl
298	23	74.2	40	6	US-10-979-871-13	Sequence 13, Appl	371	23	74.2	130	7	US-11-008-727-8	Sequence 8, Appl1
299	23	74.2	40	6	US-10-895-861-32	Sequence 32, Appl	372	23	74.2	130	7	US-11-135-855-27	Sequence 27, Appl
300	23	74.2	41	7	US-11-326-657-206	Sequence 206, App	373	23	74.2	130	7	US-11-073-222-5	Sequence 5, Appl1
301	23	74.2	41	7	US-11-233-683-30	Sequence 30, Appl	374	23	74.2	130	7	US-11-072-512-2940	Sequence 2940, Ap
302	23	74.2	41	7	US-11-233-683-35	Sequence 35, Appl	375	23	74.2	130	7	US-11-253-881-5	Sequence 5, Appl1
303	23	74.2	41	7	US-11-233-683-36	Sequence 36, Appl	376	23	74.2	137	6	US-10-821-234-1242	Sequence 1242, Appl
304	23	74.2	41	7	US-11-233-683-44	Sequence 44, Appl	377	23	74.2	138	7	US-11-008-727-2	Sequence 2, Appl1
305	23	74.2	41	7	US-11-233-683-47	Sequence 47, Appl	378	23	74.2	142	6	US-10-182-908-22	Sequence 22, Appl
306	23	74.2	42	6	US-11-233-683-47	Sequence 47, Appl	379	23	74.2	145	6	US-10-821-234-1231	Sequence 1231, Ap
307	23	74.2	42	6	US-10-895-861-42	Sequence 42, Appl	380	23	74.2	146	7	US-11-226-657-63	Sequence 63, Appl
308	23	74.2	42	6	US-10-895-861-44	Sequence 44, Appl	381	23	74.2	149	7	US-11-226-657-205	Sequence 205, App
309	23	74.2	45	7	US-11-123-896-165	Sequence 165, App	382	23	74.2	150	7	US-11-036-797-35	Sequence 35, Appl
310	23	74.2	47	7	US-11-000-463-756	Sequence 756, App	383	23	74.2	156	6	US-10-821-234-1397	Sequence 1397, Ap
311	23	74.2	48	6	US-10-895-861-39	Sequence 39, Appl	384	23	74.2	156	6	US-11-132-839-9	Sequence 9, Appl1
312	23	74.2	48	6	US-10-895-861-56	Sequence 56, Appl	385	23	74.2	157	6	US-10-793-626-1720	Sequence 1720, Ap
313	23	74.2	49	6	US-10-967-527A-15	Sequence 57, Appl	386	23	74.2	159	7	US-11-132-285-7	Sequence 7, Appl1
314	23	74.2	51	6	US-10-895-861-49	Sequence 49, Appl	387	23	74.2	160	6	US-10-924-074-10	Sequence 10, Appl
315	23	74.2	52	6	US-10-914-391A-9	Sequence 9, Appl1	388	23	74.2	163	6	US-10-510-386-126	Sequence 126, App
316	23	74.2	52	6	US-10-914-391A-9	Sequence 9, Appl1	389	23	74.2	165	7	US-11-069-856-23	Sequence 23, Appl
317	23	74.2	52	7	US-11-233-683-29	Sequence 29, Appl	390	23	74.2	165	7	US-11-069-856-23	Sequence 23, Appl

391	23	74.2	166	7	US-11-226-657-204	Sequence 204, App	464	23	74.2	240	7	US-11-218-234-23	Sequence 23, Appl
392	23	74.2	174	7	US-11-072-512-2144	Sequence 2144, Ap	465	23	74.2	243	7	US-11-098-686-10149	Sequence 10149, A
393	23	74.2	178	5	US-09-810-501-71	Sequence 71, Appl	466	23	74.2	244	6	US-10-924-074-2	Sequence 2, Appl1
394	23	74.2	182	5	US-09-978-860A-717	Sequence 717, App	467	23	74.2	245	7	US-11-029-003-20	Sequence 20, Appl
395	23	74.2	182	6	US-10-131-826A-174	Sequence 174, App	468	23	74.2	247	7	US-11-072-512-1998	Sequence 1998, Ap
396	23	74.2	183	5	US-09-978-960A-680	Sequence 680, App	469	23	74.2	249	7	US-11-010-239-107	Sequence 107, App
397	23	74.2	183	5	US-09-810-501-77	Sequence 77, Appl	470	23	74.2	250	7	US-11-242-294-35	Sequence 35, Appl1
398	23	74.2	183	6	US-10-821-234-1485	Sequence 1485, Ap	471	23	74.2	251	7	US-11-242-294-6	Sequence 6, Appl1
399	23	74.2	183	6	US-10-467-657-6906	Sequence 6906, Ap	472	23	74.2	251	7	US-11-242-294-29	Sequence 29, Appl
400	23	74.2	183	7	US-11-186-284-111	Sequence 111, App	473	23	74.2	251	7	US-11-242-294-31	Sequence 31, Appl
401	23	74.2	183	7	US-11-186-284-113	Sequence 113, App	474	23	74.2	251	7	US-11-242-294-33	Sequence 33, Appl
402	23	74.2	184	7	US-11-072-512-2477	Sequence 2477, Ap	475	23	74.2	251	7	US-11-242-294-37	Sequence 37, Appl
403	23	74.2	185	6	US-10-967-527A-10	Sequence 10, Appl	476	23	74.2	251	7	US-11-242-294-39	Sequence 39, Appl
404	23	74.2	186	6	US-10-467-657-470	Sequence 470, App	477	23	74.2	254	5	US-09-810-501-69	Sequence 69, Appl
405	23	74.2	188	7	US-11-024-959-304	Sequence 304, App	478	23	74.2	255	6	US-10-660-499A-2	Sequence 2, Appl1
406	23	74.2	188	7	US-11-024-959-307	Sequence 307, App	479	23	74.2	255	7	US-11-057-923-5	Sequence 5, Appl1
407	23	74.2	188	7	US-11-072-512-2380	Sequence 2380, Ap	480	23	74.2	256	7	US-11-029-003-14	Sequence 14, Appl
408	23	74.2	191	6	US-10-924-074-4	Sequence 4, Appl1	481	23	74.2	258	6	US-10-467-657-4130	Sequence 4130, Ap
409	23	74.2	191	6	US-10-055-877-42	Sequence 42, Appl	482	23	74.2	259	6	US-10-763-712A-116	Sequence 116, App
410	23	74.2	195	7	US-11-132-839-11	Sequence 11, Appl	483	23	74.2	259	7	US-11-057-923-6	Sequence 6, Appl
411	23	74.2	195	7	US-11-182-908-19	Sequence 19, Appl	484	23	74.2	259	7	US-11-098-686-11421	Sequence 11421, A
412	23	74.2	200	6	US-10-454-437-246	Sequence 246, App	485	23	74.2	262	6	US-10-498-026-46	Sequence 46, Appl
413	23	74.2	201	7	US-11-072-512-3518	Sequence 3518, Ap	486	23	74.2	263	6	US-10-498-026-31	Sequence 31, Appl
414	23	74.2	203	7	US-11-132-839-10	Sequence 10, Appl	487	23	74.2	263	6	US-10-498-026-45	Sequence 45, Appl
415	23	74.2	203	7	US-11-069-856-1	Sequence 1, Appl1	488	23	74.2	263	7	US-11-033-039-193	Sequence 193, App
416	23	74.2	207	7	US-11-072-512-2278	Sequence 2278, Ap	489	23	74.2	264	7	US-11-072-513-3558	Sequence 3558, Ap
417	23	74.2	207	7	US-11-072-512-2607	Sequence 2607, Ap	490	23	74.2	264	6	US-10-778-636-3	Sequence 3, Appl1
418	23	74.2	210	5	US-09-995-493-204	Sequence 204, App	491	23	74.2	264	6	US-10-778-636-4	Sequence 4, Appl1
419	23	74.2	211	6	US-10-821-234-1372	Sequence 1372, Ap	492	23	74.2	265	6	US-10-689-742-188	Sequence 188, App
420	23	74.2	211	6	US-10-498-026-107	Sequence 107, App	493	23	74.2	266	5	US-09-995-493-6	Sequence 6, Appl1
421	23	74.2	211	6	US-10-498-026-108	Sequence 108, App	494	23	74.2	267	6	US-10-841-956A-4	Sequence 4, Appl1
422	23	74.2	211	6	US-10-498-026-109	Sequence 109, App	495	23	74.2	269	6	US-10-841-956A-8	Sequence 8, Appl1
423	23	74.2	211	7	US-11-132-839-12	Sequence 12, Appl	496	23	74.2	269	7	US-11-072-512-3305	Sequence 3305, Ap
424	23	74.2	212	6	US-10-498-026-110	Sequence 110, App	497	23	74.2	270	6	US-10-841-956A-5	Sequence 5, Appl1
425	23	74.2	216	6	US-10-821-234-1033	Sequence 1033, Ap	498	23	74.2	270	7	US-11-008-727-24	Sequence 24, Appl
426	23	74.2	220	6	US-10-995-561-976	Sequence 976, App	499	23	74.2	277	6	US-10-924-074-24	Sequence 24, Appl
427	23	74.2	220	6	US-10-670-009-3	Sequence 3, Appl1	500	23	74.2	277	7	US-11-182-924-10	Sequence 10, Appl
428	23	74.2	222	6	US-10-746-909-2	Sequence 2, Appl1	501	23	74.2	277	7	US-11-127-046-2	Sequence 2, Appl1
429	23	74.2	223	6	US-10-746-909-3	Sequence 3, Appl1	502	23	74.2	277	7	US-11-169-041-196	Sequence 196, App
430	23	74.2	224	6	US-10-131-826A-86	Sequence 86, Appl	503	23	74.2	280	6	US-10-511-538-41	Sequence 41, Appl
431	23	74.2	225	6	US-10-670-009-5	Sequence 6, Appl1	504	23	74.2	280	7	US-11-098-686-10511	Sequence 10511, A
432	23	74.2	225	6	US-11-092-353-9	Sequence 9, Appl1	505	23	74.2	281	6	US-10-841-956A-7	Sequence 7, Appl1
433	23	74.2	225	7	US-11-128-937-9	Sequence 9, Appl1	506	23	74.2	282	6	US-10-841-956A-6	Sequence 6, Appl1
434	23	74.2	226	7	US-11-132-285-5	Sequence 5, Appl1	507	23	74.2	282	7	US-11-183-205-40	Sequence 40, Appl
435	23	74.2	227	6	US-10-467-657-2624	Sequence 2624, Ap	508	23	74.2	283	6	US-10-987-663-4	Sequence 4, Appl1
436	23	74.2	227	6	US-10-670-009-4	Sequence 4, Appl1	509	23	74.2	291	6	US-10-821-234-1560	Sequence 1560, Ap
437	23	74.2	227	6	US-10-670-009-7	Sequence 7, Appl1	510	23	74.2	292	7	US-11-055-822-940	Sequence 940, App
438	23	74.2	227	6	US-10-841-956A-17	Sequence 17, Appl	511	23	74.2	293	6	US-10-131-826A-422	Sequence 422, App
439	23	74.2	227	7	US-11-008-727-14	Sequence 14, Appl	512	23	74.2	293	6	US-10-841-956A-9	Sequence 9, Appl1
440	23	74.2	227	7	US-11-201-825-67	Sequence 67, Appl	513	23	74.2	296	6	US-10-954-468-9	Sequence 9, Appl1
441	23	74.2	228	6	US-10-670-009-2	Sequence 2, Appl1	514	23	74.2	297	6	US-10-967-527A-17	Sequence 17, Appl
442	23	74.2	228	6	US-10-841-956A-16	Sequence 16, Appl	515	23	74.2	299	7	US-11-098-686-11010	Sequence 11010, A
443	23	74.2	229	6	US-10-924-074-8	Sequence 8, Appl1	516	23	74.2	301	6	US-11-979-871-2	Sequence 2, Appl1
444	23	74.2	229	7	US-11-072-512-3781	Sequence 3781, Ap	517	23	74.2	307	6	US-11-024-959-291	Sequence 291, App
445	23	74.2	231	7	US-11-132-285-61	Sequence 61, Appl	518	23	74.2	308	7	US-11-072-512-3715	Sequence 3715, Ap
446	23	74.2	232	6	US-10-821-234-1023	Sequence 1023, Ap	519	23	74.2	309	6	US-10-714-887-42	Sequence 42, Appl
447	23	74.2	232	6	US-10-636-320-4	Sequence 4, Appl1	520	23	74.2	310	6	US-10-485-517-409	Sequence 409, App
448	23	74.2	232	6	US-10-948-053-1	Sequence 1, Appl1	521	23	74.2	314	6	US-10-689-742-116	Sequence 116, App
449	23	74.2	232	7	US-11-128-059-66	Sequence 66, Appl	522	23	74.2	316	7	US-11-072-512-2079	Sequence 2079, Ap
450	23	74.2	232	7	US-11-227-340-7	Sequence 7, Appl1	523	23	74.2	318	6	US-10-821-234-1117	Sequence 1117, Ap
451	23	74.2	232	7	US-11-201-825-66	Sequence 66, Appl	524	23	74.2	318	7	US-11-021-305-168	Sequence 168, App
452	23	74.2	233	6	US-10-923-327-18	Sequence 18, Appl	525	23	74.2	319	6	US-10-498-026-21	Sequence 21, Appl
453	23	74.2	233	6	US-10-923-327-19	Sequence 19, Appl	526	23	74.2	320	6	US-10-498-026-13	Sequence 13, Appl
454	23	74.2	233	7	US-11-150-533-45	Sequence 45, Appl	527	23	74.2	320	7	US-11-102-883-20	Sequence 20, Appl
455	23	74.2	235	7	US-11-126-126-16	Sequence 16, Appl	528	23	74.2	320	7	US-11-152-811-3	Sequence 3, Appl1
456	23	74.2	236	6	US-10-763-712A-115	Sequence 115, App	529	23	74.2	320	7	US-11-183-205-50	Sequence 50, Appl
457	23	74.2	236	7	US-11-008-727-4	Sequence 4, Appl1	530	23	74.2	321	6	US-10-478-345-8	Sequence 8, Appl1
458	23	74.2	237	6	US-10-924-074-6	Sequence 6, Appl1	531	23	74.2	321	6	US-11-072-512-2235	Sequence 2235, Ap
459	23	74.2	238	6	US-10-841-956A-20	Sequence 20, Appl	532	23	74.2	325	6	US-10-467-657-3036	Sequence 3036, Ap
460	23	74.2	238	7	US-11-008-727-26	Sequence 26, Appl	533	23	74.2	326	6	US-10-999-866-36	Sequence 36, Appl
461	23	74.2	238	7	US-11-029-003-4	Sequence 4, Appl1	534	23	74.2	326	6	US-10-493-909-22	Sequence 22, Appl
462	23	74.2	238	7	US-11-098-686-11045	Sequence 11045, A	535	23	74.2	326	7	US-11-144-248-28	Sequence 28, Appl
463	23	74.2	240	7	US-11-089-803-23	Sequence 23, Appl	536	23	74.2	326	7	US-11-061-821-36	Sequence 36, Appl

537	23	74.2	326	7	US-11-102-621-2	Sequence 2, Appl1	610	23	74.2	330	6	US-10-982-440-68	Sequence 68, Appl1
538	23	74.2	326	7	US-11-102-621-10	Sequence 10, Appl1	611	23	74.2	330	7	US-11-022-289-1	Sequence 11, Appl1
539	23	74.2	326	7	US-11-102-621-11	Sequence 11, Appl1	612	23	74.2	330	7	US-11-022-289-11	Sequence 11, Appl1
540	23	74.2	326	7	US-11-102-621-12	Sequence 12, Appl1	613	23	74.2	330	7	US-11-075-351-1	Sequence 1, Appl1
541	23	74.2	326	7	US-11-102-621-13	Sequence 13, Appl1	614	23	74.2	330	7	US-11-165-141-15	Sequence 15, Appl1
542	23	74.2	326	7	US-11-102-621-14	Sequence 14, Appl1	615	23	74.2	330	7	US-11-102-621-3	Sequence 3, Appl1
543	23	74.2	326	7	US-11-102-621-15	Sequence 15, Appl1	616	23	74.2	330	7	US-11-102-621-7	Sequence 7, Appl1
544	23	74.2	326	7	US-11-102-621-16	Sequence 16, Appl1	617	23	74.2	330	7	US-11-102-621-67	Sequence 67, Appl1
545	23	74.2	326	7	US-11-102-621-17	Sequence 17, Appl1	618	23	74.2	330	7	US-11-102-621-68	Sequence 68, Appl1
546	23	74.2	326	7	US-11-102-621-18	Sequence 18, Appl1	619	23	74.2	330	7	US-11-102-621-69	Sequence 69, Appl1
547	23	74.2	326	7	US-11-102-621-19	Sequence 19, Appl1	620	23	74.2	330	7	US-11-102-621-70	Sequence 70, Appl1
548	23	74.2	326	7	US-11-102-621-20	Sequence 20, Appl1	621	23	74.2	330	7	US-11-102-621-71	Sequence 71, Appl1
549	23	74.2	326	7	US-11-102-621-21	Sequence 21, Appl1	622	23	74.2	330	7	US-11-102-621-75	Sequence 75, Appl1
550	23	74.2	326	7	US-11-102-621-22	Sequence 22, Appl1	623	23	74.2	330	7	US-11-102-621-76	Sequence 76, Appl1
551	23	74.2	326	7	US-11-102-621-23	Sequence 23, Appl1	624	23	74.2	330	7	US-11-005-726-164	Sequence 164, Appl1
552	23	74.2	326	7	US-11-102-621-24	Sequence 24, Appl1	625	23	74.2	330	7	US-11-124-620-1	Sequence 1, Appl1
553	23	74.2	326	7	US-11-102-621-25	Sequence 25, Appl1	626	23	74.2	330	7	US-11-233-683-1	Sequence 1, Appl1
554	23	74.2	326	7	US-11-102-621-26	Sequence 26, Appl1	627	23	74.2	330	7	US-11-201-825-55	Sequence 55, Appl1
555	23	74.2	326	7	US-11-102-621-27	Sequence 27, Appl1	628	23	74.2	331	6	US-10-995-561-977	Sequence 977, Appl1
556	23	74.2	326	7	US-11-102-621-28	Sequence 28, Appl1	629	23	74.2	331	6	US-10-995-561-978	Sequence 978, Appl1
557	23	74.2	326	7	US-11-102-621-29	Sequence 29, Appl1	630	23	74.2	331	7	US-11-185-877-8	Sequence 8, Appl1
558	23	74.2	326	7	US-11-102-621-30	Sequence 30, Appl1	631	23	74.2	332	6	US-10-949-720-405	Sequence 405, Appl1
559	23	74.2	326	7	US-11-102-621-31	Sequence 31, Appl1	632	23	74.2	332	7	US-11-242-294-62	Sequence 62, Appl1
560	23	74.2	326	7	US-11-102-621-32	Sequence 32, Appl1	633	23	74.2	333	6	US-10-131-826A-132	Sequence 132, Appl1
561	23	74.2	326	7	US-11-102-621-33	Sequence 33, Appl1	634	23	74.2	333	6	US-10-821-233-1672	Sequence 1672, Appl1
562	23	74.2	326	7	US-11-102-621-34	Sequence 34, Appl1	635	23	74.2	333	7	US-11-185-877-9	Sequence 9, Appl1
563	23	74.2	326	7	US-11-102-621-35	Sequence 35, Appl1	636	23	74.2	334	6	US-10-131-826A-12	Sequence 12, Appl1
564	23	74.2	326	7	US-11-102-621-36	Sequence 36, Appl1	637	23	74.2	334	7	US-11-072-512-2440	Sequence 2440, Appl1
565	23	74.2	326	7	US-11-102-621-37	Sequence 37, Appl1	638	23	74.2	335	6	US-10-995-561-866	Sequence 866, Appl1
566	23	74.2	326	7	US-11-102-621-38	Sequence 38, Appl1	639	23	74.2	335	7	US-11-024-251-35	Sequence 35, Appl1
567	23	74.2	326	7	US-11-102-621-39	Sequence 39, Appl1	640	23	74.2	335	7	US-11-185-877-10	Sequence 10, Appl1
568	23	74.2	326	7	US-11-102-621-40	Sequence 40, Appl1	641	23	74.2	336	6	US-10-793-628-1858	Sequence 1858, Appl1
569	23	74.2	326	7	US-11-102-621-41	Sequence 41, Appl1	642	23	74.2	336	6	US-10-467-656-4390	Sequence 4390, Appl1
570	23	74.2	326	7	US-11-102-621-42	Sequence 42, Appl1	643	23	74.2	339	6	US-10-878-565A-18	Sequence 18, Appl1
571	23	74.2	326	7	US-11-102-621-43	Sequence 43, Appl1	644	23	74.2	339	6	US-10-999-866-35	Sequence 35, Appl1
572	23	74.2	326	7	US-11-102-621-44	Sequence 44, Appl1	645	23	74.2	339	6	US-10-995-561-661	Sequence 661, Appl1
573	23	74.2	326	7	US-11-102-621-45	Sequence 45, Appl1	646	23	74.2	339	6	US-10-995-561-662	Sequence 662, Appl1
574	23	74.2	326	7	US-11-102-621-46	Sequence 46, Appl1	647	23	74.2	339	6	US-10-995-561-664	Sequence 664, Appl1
575	23	74.2	326	7	US-11-102-621-47	Sequence 47, Appl1	648	23	74.2	339	6	US-10-995-561-665	Sequence 665, Appl1
576	23	74.2	326	7	US-11-102-621-48	Sequence 48, Appl1	649	23	74.2	339	6	US-10-995-561-667	Sequence 667, Appl1
577	23	74.2	326	7	US-11-102-621-49	Sequence 49, Appl1	650	23	74.2	339	6	US-10-995-561-687	Sequence 687, Appl1
578	23	74.2	326	7	US-11-102-621-50	Sequence 50, Appl1	651	23	74.2	339	7	US-11-061-821-35	Sequence 35, Appl1
579	23	74.2	326	7	US-11-102-621-51	Sequence 51, Appl1	652	23	74.2	339	7	US-11-186-284-43	Sequence 43, Appl1
580	23	74.2	326	7	US-11-102-621-52	Sequence 52, Appl1	653	23	74.2	339	7	US-11-185-877-11	Sequence 11, Appl1
581	23	74.2	326	7	US-11-102-621-53	Sequence 53, Appl1	654	23	74.2	339	7	US-11-177-648-81	Sequence 81, Appl1
582	23	74.2	326	7	US-11-102-621-54	Sequence 54, Appl1	655	23	74.2	342	7	US-11-098-686-10943	Sequence 10943, Appl1
583	23	74.2	326	7	US-11-102-621-55	Sequence 55, Appl1	656	23	74.2	344	6	US-10-821-234-923	Sequence 923, Appl1
584	23	74.2	326	7	US-11-102-621-56	Sequence 56, Appl1	657	23	74.2	344	7	US-11-242-294-52	Sequence 52, Appl1
585	23	74.2	326	7	US-11-102-621-57	Sequence 57, Appl1	658	23	74.2	344	7	US-11-098-686-10460	Sequence 10460, Appl1
586	23	74.2	326	7	US-11-102-621-58	Sequence 58, Appl1	659	23	74.2	346	7	US-11-077-386-24	Sequence 24, Appl1
587	23	74.2	326	7	US-11-102-621-59	Sequence 59, Appl1	660	23	74.2	347	7	US-11-224-624-136	Sequence 136, Appl1
588	23	74.2	326	7	US-11-102-621-60	Sequence 60, Appl1	661	23	74.2	347	7	US-11-098-686-10337	Sequence 10337, Appl1
589	23	74.2	326	7	US-11-102-621-61	Sequence 61, Appl1	662	23	74.2	348	7	US-11-242-294-54	Sequence 54, Appl1
590	23	74.2	326	7	US-11-102-621-62	Sequence 62, Appl1	663	23	74.2	349	7	US-11-098-686-10281	Sequence 10281, Appl1
591	23	74.2	326	7	US-11-102-621-63	Sequence 63, Appl1	664	23	74.2	350	6	US-10-063-703-8	Sequence 8, Appl1
592	23	74.2	326	7	US-11-102-621-64	Sequence 64, Appl1	665	23	74.2	350	7	US-11-102-240-8	Sequence 8, Appl1
593	23	74.2	326	7	US-11-102-621-65	Sequence 65, Appl1	666	23	74.2	350	7	US-11-108-528-54	Sequence 54, Appl1
594	23	74.2	326	7	US-11-102-621-66	Sequence 66, Appl1	667	23	74.2	350	7	US-11-119-351-4	Sequence 4, Appl1
595	23	74.2	326	7	US-11-102-621-72	Sequence 72, Appl1	668	23	74.2	350	7	US-11-072-512-2500	Sequence 2500, Appl1
596	23	74.2	326	7	US-11-102-621-73	Sequence 73, Appl1	669	23	74.2	351	7	US-11-108-528-52	Sequence 52, Appl1
597	23	74.2	326	7	US-11-102-621-74	Sequence 74, Appl1	670	23	74.2	351	7	US-11-102-683-28	Sequence 28, Appl1
598	23	74.2	326	7	US-11-144-222-28	Sequence 28, Appl1	671	23	74.2	353	6	US-10-131-826A-396	Sequence 396, Appl1
599	23	74.2	326	7	US-11-182-343-28	Sequence 28, Appl1	672	23	74.2	354	6	US-10-478-345-2	Sequence 2, Appl1
600	23	74.2	326	7	US-11-124-620-2	Sequence 2, Appl1	673	23	74.2	354	6	US-10-467-657-6058	Sequence 6058, Appl1
601	23	74.2	326	7	US-11-233-683-2	Sequence 2, Appl1	674	23	74.2	354	7	US-11-108-528-50	Sequence 50, Appl1
602	23	74.2	327	7	US-11-452-811-5	Sequence 5, Appl1	675	23	74.2	354	7	US-11-072-512-3151	Sequence 3151, Appl1
603	23	74.2	327	7	US-11-072-512-2508	Sequence 2508, Appl1	676	23	74.2	355	7	US-11-072-512-3556	Sequence 3556, Appl1
604	23	74.2	328	7	US-11-169-041-2227	Sequence 2227, Appl1	677	23	74.2	356	7	US-11-072-512-3544	Sequence 3544, Appl1
605	23	74.2	328	7	US-11-072-175-232	Sequence 232, Appl1	678	23	74.2	357	6	US-10-478-345-6	Sequence 6, Appl1
606	23	74.2	329	7	US-11-185-877-2	Sequence 2, Appl1	679	23	74.2	357	7	US-11-072-512-3308	Sequence 3308, Appl1
607	23	74.2	329	7	US-11-185-877-7	Sequence 7, Appl1	680	23	74.2	357	7	US-11-242-294-36	Sequence 36, Appl1
608	23	74.2	330	6	US-10-686-383-6	Sequence 6, Appl1	681	23	74.2	359	6	US-10-763-712A-74	Sequence 74, Appl1
609	23	74.2	330	6	US-10-493-909-20	Sequence 20, Appl1	682	23	74.2	359	7	US-11-105-172-2	Sequence 2, Appl1

683	23	74.2	360	6	US-10-467-657-7666	Sequence 7666, Ap	756	23	74.2	435	7	US-11-077-386-19	Sequence 19, Appl
684	23	74.2	360	7	US-11-112-240-1	Sequence 1, Appl1	757	23	74.2	436	7	US-11-042-814-4	Sequence 40, Appl1
685	23	74.2	360	7	US-11-112-304A-1	Sequence 1, Appl1	758	23	74.2	437	7	US-11-183-136-40	Sequence 40, Appl1
686	23	74.2	362	7	US-11-102-883-8	Sequence 8, Appl1	759	23	74.2	439	6	US-10-763-712A-39	Sequence 39, Appl
687	23	74.2	362	7	US-11-072-512-2384	Sequence 2384, Ap	760	23	74.2	442	7	US-11-102-621-124	Sequence 124, App
688	23	74.2	365	7	US-11-087-177-5	Sequence 5, Appl1	761	23	74.2	442	7	US-11-102-621-125	Sequence 125, App
689	23	74.2	366	7	US-11-075-351-38	Sequence 38, Appl	762	23	74.2	442	7	US-11-102-621-126	Sequence 126, App
690	23	74.2	369	6	US-10-763-712A-42	Sequence 42, Appl	763	23	74.2	442	7	US-11-102-621-127	Sequence 127, App
691	23	74.2	369	6	US-10-763-712A-43	Sequence 43, Appl	764	23	74.2	442	7	US-11-102-621-128	Sequence 128, App
692	23	74.2	369	6	US-10-763-712A-45	Sequence 45, Appl	765	23	74.2	444	7	US-11-172-320-6	Sequence 6, Appl1
693	23	74.2	369	6	US-10-763-712A-106	Sequence 106, App	766	23	74.2	444	7	US-11-173-969-6	Sequence 6, Appl1
694	23	74.2	374	7	US-11-075-351-42	Sequence 42, Appl	767	23	74.2	444	7	US-11-004-590-232	Sequence 232, App
695	23	74.2	376	6	US-10-523-503-52	Sequence 52, Appl	768	23	74.2	444	7	US-11-004-590-233	Sequence 233, App
696	23	74.2	378	7	US-11-201-825-60	Sequence 60, Appl	769	23	74.2	446	7	US-11-102-621-119	Sequence 119, App
697	23	74.2	379	6	US-10-763-712A-40	Sequence 40, Appl	770	23	74.2	446	7	US-11-102-621-120	Sequence 120, App
698	23	74.2	379	7	US-11-012-522-7	Sequence 7, Appl1	771	23	74.2	446	7	US-11-102-621-121	Sequence 121, App
699	23	74.2	379	7	US-11-054-281-45	Sequence 45, Appl	772	23	74.2	446	7	US-11-102-621-122	Sequence 122, App
700	23	74.2	381	6	US-10-641-678-74	Sequence 74, Appl	773	23	74.2	446	7	US-11-102-621-123	Sequence 123, App
701	23	74.2	381	6	US-10-641-678-74	Sequence 74, Appl	774	23	74.2	446	7	US-11-102-621-136	Sequence 136, App
702	23	74.2	381	7	US-10-453-372-224	Sequence 224, App	775	23	74.2	446	7	US-11-102-621-137	Sequence 137, App
703	23	74.2	381	7	US-11-054-281-2	Sequence 2, Appl1	776	23	74.2	446	7	US-11-102-621-138	Sequence 138, App
704	23	74.2	381	7	US-11-054-281-41	Sequence 41, Appl	777	23	74.2	446	7	US-11-102-621-139	Sequence 139, App
705	23	74.2	381	7	US-11-054-281-42	Sequence 42, Appl	778	23	74.2	446	7	US-11-102-621-140	Sequence 140, App
706	23	74.2	381	7	US-11-054-281-43	Sequence 43, Appl	779	23	74.2	447	7	US-11-102-621-131	Sequence 130, App
707	23	74.2	381	7	US-11-054-281-44	Sequence 44, Appl	780	23	74.2	447	7	US-11-102-621-131	Sequence 131, App
708	23	74.2	381	7	US-11-169-041-152	Sequence 152, App	781	23	74.2	447	7	US-11-102-621-132	Sequence 132, App
709	23	74.2	384	7	US-11-075-351-12	Sequence 12, Appl	782	23	74.2	447	7	US-11-102-621-133	Sequence 133, App
710	23	74.2	384	7	US-11-075-351-32	Sequence 32, Appl	783	23	74.2	447	7	US-11-102-621-134	Sequence 134, App
711	23	74.2	391	7	US-11-105-172-4	Sequence 4, Appl1	784	23	74.2	447	7	US-11-004-590-230	Sequence 230, App
712	23	74.2	392	7	US-11-242-294-50	Sequence 50, Appl	785	23	74.2	447	7	US-11-004-590-231	Sequence 231, App
713	23	74.2	397	7	US-11-192-219-47	Sequence 47, Appl	786	23	74.2	447	7	US-11-158-505-8	Sequence 8, Appl1
714	23	74.2	397	7	US-11-192-219-47	Sequence 47, Appl	787	23	74.2	448	7	US-11-158-505-16	Sequence 16, Appl
715	23	74.2	398	7	US-11-024-959-336	Sequence 336, App	788	23	74.2	448	7	US-11-158-505-32	Sequence 32, Appl
716	23	74.2	400	7	US-11-077-386-18	Sequence 18, Appl	789	23	74.2	448	7	US-11-158-505-32	Sequence 32, Appl
717	23	74.2	401	7	US-11-072-175-224	Sequence 26, Appl	790	23	74.2	448	7	US-11-182-908-16	Sequence 16, Appl
718	23	74.2	402	7	US-11-024-251-31	Sequence 31, Appl	791	23	74.2	448	7	US-11-182-908-16	Sequence 16, Appl
719	23	74.2	404	7	US-11-075-351-23	Sequence 23, Appl	792	23	74.2	449	6	US-10-763-712A-21	Sequence 21, Appl
720	23	74.2	404	7	US-11-098-686-11329	Sequence 25, Appl	793	23	74.2	449	6	US-10-763-712A-104	Sequence 104, App
721	23	74.2	405	6	US-10-467-657-4964	Sequence 11329, A	794	23	74.2	449	7	US-11-080-587-6	Sequence 6, Appl1
722	23	74.2	406	7	US-11-072-512-3010	Sequence 3010, Ap	795	23	74.2	449	7	US-11-154-337-15	Sequence 15, Appl
723	23	74.2	410	6	US-10-821-234-952	Sequence 952, App	796	23	74.2	449	7	US-11-154-337-17	Sequence 17, Appl
724	23	74.2	410	6	US-10-763-712A-85	Sequence 85, Appl	797	23	74.2	449	7	US-11-182-908-14	Sequence 14, Appl
725	23	74.2	411	7	US-11-075-351-47	Sequence 47, Appl	798	23	74.2	449	7	US-11-182-908-24	Sequence 24, Appl
726	23	74.2	413	6	US-10-821-234-989	Sequence 989, App	799	23	74.2	449	7	US-11-177-506-32	Sequence 32, Appl
727	23	74.2	414	6	US-10-131-826A-418	Sequence 418, App	800	23	74.2	450	7	US-11-025-512-12	Sequence 12, Appl
728	23	74.2	415	7	US-11-182-946-6	Sequence 6, Appl1	801	23	74.2	450	7	US-11-077-386-20	Sequence 20, Appl
729	23	74.2	415	7	US-11-029-003-12	Sequence 12, Appl	802	23	74.2	450	7	US-11-005-726-161	Sequence 161, App
730	23	74.2	417	7	US-11-072-175-333	Sequence 233, App	803	23	74.2	450	7	US-11-049-536-7	Sequence 701, App
731	23	74.2	418	6	US-10-512-325-3	Sequence 3, Appl1	804	23	74.2	451	6	US-10-923-327-7	Sequence 7, Appl1
732	23	74.2	418	7	US-11-196-919-2	Sequence 2, Appl1	805	23	74.2	451	6	US-10-923-327-9	Sequence 9, Appl1
733	23	74.2	419	7	US-11-113-302-2	Sequence 2, Appl1	806	23	74.2	451	6	US-10-923-327-11	Sequence 11, Appl
734	23	74.2	419	7	US-11-113-302-4	Sequence 4, Appl1	807	23	74.2	451	7	US-11-120-338-22	Sequence 22, Appl
735	23	74.2	419	7	US-11-113-302-53	Sequence 23, Appl	808	23	74.2	451	7	US-11-120-338-25	Sequence 25, Appl
736	23	74.2	420	6	US-10-131-826A-290	Sequence 290, App	809	23	74.2	451	7	US-11-128-900-70	Sequence 70, Appl
737	23	74.2	421	6	US-10-763-712A-2	Sequence 2, Appl1	810	23	74.2	451	7	US-11-158-505-33	Sequence 33, Appl
738	23	74.2	421	6	US-10-763-712A-7	Sequence 7, Appl1	811	23	74.2	451	7	US-11-124-620-5	Sequence 5, Appl1
739	23	74.2	421	6	US-10-763-712A-13	Sequence 13, Appl	812	23	74.2	451	7	US-11-124-620-7	Sequence 7, Appl1
740	23	74.2	421	6	US-10-763-712A-15	Sequence 15, Appl	813	23	74.2	451	7	US-11-143-027-72	Sequence 22, Appl
741	23	74.2	421	6	US-10-763-712A-41	Sequence 41, Appl	814	23	74.2	452	7	US-11-016-503-6	Sequence 6, Appl1
742	23	74.2	421	6	US-10-763-712A-103	Sequence 103, App	815	23	74.2	452	7	US-11-120-338-15	Sequence 15, Appl
743	23	74.2	422	7	US-10-453-372-220	Sequence 220, App	816	23	74.2	452	7	US-11-120-338-15	Sequence 15, Appl
744	23	74.2	422	7	US-11-080-248-4	Sequence 4, Appl1	817	23	74.2	452	7	US-11-107-028-37	Sequence 37, Appl
745	23	74.2	422	7	US-11-029-003-10	Sequence 10, Appl	818	23	74.2	452	7	US-11-107-028-32	Sequence 32, Appl
746	23	74.2	427	6	US-10-513-639-20	Sequence 20, Appl	819	23	74.2	452	7	US-11-107-028-43	Sequence 43, Appl
747	23	74.2	427	7	US-11-182-946-5	Sequence 5, Appl1	820	23	74.2	452	7	US-11-107-028-45	Sequence 43, Appl
748	23	74.2	427	7	US-11-185-878-4	Sequence 4, Appl1	821	23	74.2	452	7	US-11-107-028-45	Sequence 45, Appl
749	23	74.2	428	7	US-11-029-003-24	Sequence 24, Appl	822	23	74.2	452	7	US-11-107-028-46	Sequence 46, Appl
750	23	74.2	428	7	US-11-072-512-3675	Sequence 3675, Ap	823	23	74.2	452	7	US-11-106-820-26	Sequence 26, Appl
751	23	74.2	430	7	US-11-016-503-17	Sequence 17, Appl	824	23	74.2	452	7	US-11-106-820-28	Sequence 28, Appl
752	23	74.2	430	7	US-11-029-003-22	Sequence 22, Appl	825	23	74.2	452	7	US-11-106-820-30	Sequence 30, Appl
753	23	74.2	430	7	US-11-042-814-2	Sequence 2, Appl1	826	23	74.2	452	7	US-11-106-820-45	Sequence 45, Appl
754	23	74.2	433	6	US-10-467-657-5876	Sequence 6876, Ap	827	23	74.2	452	7	US-11-143-077-14	Sequence 14, Appl
755	23	74.2	433	6	US-10-877-346-77	Sequence 77, Appl	828	23	74.2	452	7		

829	23	74.2	452	7	US-11-143-077-15	Sequence 15, Appl	902	23	74.2	470	7	US-11-144-222-49	Sequence 49, Appl
830	23	74.2	455	7	US-11-143-077-17	Sequence 17, Appl	903	23	74.2	470	7	US-11-086-289-18	Sequence 18, Appl
831	23	74.2	452	7	US-11-016-503-14	Sequence 14, Appl	904	23	74.2	470	7	US-11-121-438-35	Sequence 35, Appl
832	23	74.2	455	7	US-11-089-803-4	Sequence 4, Appl	905	23	74.2	470	7	US-11-182-343-45	Sequence 45, Appl
833	23	74.2	455	7	US-11-218-234-4	Sequence 4, Appl	906	23	74.2	470	7	US-11-182-343-46	Sequence 46, Appl
834	23	74.2	456	5	US-09-978-360A-523	Sequence 523, App	907	23	74.2	470	7	US-11-182-343-49	Sequence 49, Appl
835	23	74.2	456	6	US-10-763-712A-44	Sequence 44, Appl	908	23	74.2	470	7	US-11-041-095-22	Sequence 22, Appl
836	23	74.2	457	6	US-10-951-236-10	Sequence 10, Appl	909	23	74.2	470	7	US-11-072-512-3730	Sequence 3730, Ap
837	23	74.2	458	6	US-10-763-712A-32	Sequence 32, Appl	910	23	74.2	471	7	US-11-086-289-6	Sequence 6, Appl
838	23	74.2	458	7	US-11-016-503-12	Sequence 12, Appl	911	23	74.2	471	7	US-11-106-820-25	Sequence 25, Appl
839	23	74.2	458	7	US-11-016-503-16	Sequence 16, Appl	912	23	74.2	471	7	US-11-106-820-27	Sequence 27, Appl
840	23	74.2	458	7	US-11-089-803-2	Sequence 2, Appl	913	23	74.2	471	7	US-11-190-364-22	Sequence 23, Appl
841	23	74.2	458	7	US-11-089-803-6	Sequence 6, Appl	914	23	74.2	471	7	US-11-190-364-23	Sequence 23, Appl
842	23	74.2	458	7	US-11-149-738-2	Sequence 2, Appl	915	23	74.2	471	7	US-11-190-364-23	Sequence 23, Appl
843	23	74.2	458	7	US-11-155-269-2	Sequence 2, Appl	916	23	74.2	471	7	US-11-147-780-22	Sequence 22, Appl
844	23	74.2	458	7	US-11-193-746-2	Sequence 2, Appl	917	23	74.2	472	7	US-11-147-780-23	Sequence 23, Appl
845	23	74.2	458	7	US-11-218-234-2	Sequence 2, Appl	918	23	74.2	472	7	US-11-086-289-10	Sequence 10, Appl
846	23	74.2	458	7	US-11-218-234-6	Sequence 6, Appl	919	23	74.2	473	7	US-11-144-224-50	Sequence 50, Appl
847	23	74.2	459	6	US-10-949-720-390	Sequence 390, App	920	23	74.2	473	7	US-11-165-141-23	Sequence 23, Appl
848	23	74.2	460	6	US-10-763-712A-70	Sequence 70, Appl	921	23	74.2	473	7	US-11-144-222-50	Sequence 50, Appl
849	23	74.2	460	6	US-10-995-561-857	Sequence 857, App	922	23	74.2	473	7	US-11-182-343-50	Sequence 50, Appl
850	23	74.2	461	7	US-11-132-285-6	Sequence 6, Appl	923	23	74.2	474	6	US-10-763-712A-47	Sequence 47, Appl
851	23	74.2	461	7	US-11-182-946-4	Sequence 4, Appl	924	23	74.2	474	6	US-11-000-463-284	Sequence 284, App
852	23	74.2	461	7	US-11-183-205-32	Sequence 32, Appl	925	23	74.2	475	7	US-11-041-095-16	Sequence 16, Appl
853	23	74.2	462	7	US-11-016-503-8	Sequence 8, Appl	926	23	74.2	476	7	US-11-008-727-22	Sequence 22, Appl
854	23	74.2	462	7	US-11-177-648-9	Sequence 9, Appl	927	23	74.2	476	7	US-11-139-499-4	Sequence 4, Appl
855	23	74.2	462	7	US-11-177-648-26	Sequence 26, Appl	928	23	74.2	477	7	US-11-139-499-12	Sequence 12, Appl
856	23	74.2	462	7	US-11-177-648-27	Sequence 27, Appl	929	23	74.2	477	7	US-11-000-463-395	Sequence 395, App
857	23	74.2	462	7	US-11-177-648-28	Sequence 28, Appl	930	23	74.2	478	7	US-11-139-499-8	Sequence 8, Appl
858	23	74.2	462	7	US-11-177-648-29	Sequence 29, Appl	931	23	74.2	478	7	US-11-072-512-3812	Sequence 3812, Ap
859	23	74.2	462	7	US-11-177-648-30	Sequence 30, Appl	932	23	74.2	482	6	US-10-821-234-972	Sequence 972, App
860	23	74.2	462	7	US-11-177-648-31	Sequence 31, Appl	933	23	74.2	484	6	US-10-467-657-5472	Sequence 5472, Ap
861	23	74.2	462	7	US-11-177-648-32	Sequence 32, Appl	934	23	74.2	484	6	US-10-763-712A-12	Sequence 12, Appl
862	23	74.2	462	7	US-11-177-648-33	Sequence 33, Appl	935	23	74.2	487	7	US-11-147-047-50	Sequence 50, Appl
863	23	74.2	462	7	US-11-177-648-79	Sequence 79, Appl	936	23	74.2	487	7	US-11-072-512-2868	Sequence 2868, Ap
864	23	74.2	462	7	US-11-177-648-92	Sequence 92, Appl	937	23	74.2	487	7	US-11-072-512-3083	Sequence 3083, Ap
865	23	74.2	462	7	US-11-177-648-93	Sequence 93, Appl	938	23	74.2	488	6	US-10-821-234-1000	Sequence 1000, Ap
866	23	74.2	462	7	US-11-177-648-94	Sequence 94, Appl	939	23	74.2	489	6	US-10-835-475-11	Sequence 11, Appl
867	23	74.2	462	7	US-11-177-648-95	Sequence 95, Appl	940	23	74.2	489	7	US-11-072-512-2922	Sequence 2922, Ap
868	23	74.2	462	7	US-11-177-648-96	Sequence 96, Appl	941	23	74.2	489	7	US-11-072-512-3329	Sequence 3329, Ap
869	23	74.2	462	7	US-11-177-648-97	Sequence 97, Appl	942	23	74.2	490	6	US-10-763-712A-65	Sequence 65, Appl
870	23	74.2	462	7	US-11-177-648-98	Sequence 98, Appl	943	23	74.2	490	7	US-11-072-512-2640	Sequence 2640, Ap
871	23	74.2	463	6	US-10-821-234-1094	Sequence 1094, Ap	944	23	74.2	491	6	US-10-954-466-54	Sequence 54, Appl
872	23	74.2	463	7	US-11-128-900-1	Sequence 1, Appl	945	23	74.2	492	6	US-10-467-657-8422	Sequence 8422, Ap
873	23	74.2	463	7	US-11-128-900-4	Sequence 4, Appl	946	23	74.2	494	6	US-10-763-712A-71	Sequence 71, Appl
874	23	74.2	463	7	US-11-128-900-63	Sequence 63, Appl	947	23	74.2	494	6	US-10-763-712A-111	Sequence 111, App
875	23	74.2	463	7	US-11-128-900-64	Sequence 64, Appl	948	23	74.2	496	7	US-11-165-697-50	Sequence 50, Appl
876	23	74.2	463	7	US-11-128-900-68	Sequence 68, Appl	949	23	74.2	496	7	US-11-240-406-6	Sequence 6, Appl
877	23	74.2	464	6	US-10-763-712A-46	Sequence 46, Appl	950	23	74.2	498	7	US-11-072-512-2548	Sequence 2548, Ap
878	23	74.2	464	7	US-11-128-900-2	Sequence 2, Appl	951	23	74.2	502	7	US-11-054-281-140	Sequence 140, App
879	23	74.2	464	7	US-11-128-900-66	Sequence 66, Appl	952	23	74.2	504	6	US-10-999-789-2	Sequence 2, Appl
880	23	74.2	467	6	US-10-763-712A-19	Sequence 19, Appl	953	23	74.2	509	7	US-11-008-727-16	Sequence 16, Appl
881	23	74.2	467	7	US-11-158-505-5	Sequence 5, Appl	954	23	74.2	512	7	US-11-072-512-2978	Sequence 2978, Ap
882	23	74.2	467	7	US-11-158-505-7	Sequence 7, Appl	955	23	74.2	514	6	US-10-835-475-2	Sequence 2, Appl
883	23	74.2	467	7	US-11-158-505-13	Sequence 13, Appl	956	23	74.2	515	6	US-10-821-234-1111	Sequence 1211, Ap
884	23	74.2	467	7	US-11-158-505-15	Sequence 15, Appl	957	23	74.2	515	6	US-10-954-466-33	Sequence 33, Appl
885	23	74.2	467	7	US-11-158-505-21	Sequence 21, Appl	958	23	74.2	516	6	US-10-954-466-32	Sequence 32, Appl
886	23	74.2	467	7	US-11-158-505-23	Sequence 23, Appl	959	23	74.2	517	6	US-10-954-466-16	Sequence 16, Appl
887	23	74.2	467	7	US-11-158-505-29	Sequence 29, Appl	960	23	74.2	518	6	US-10-954-466-31	Sequence 31, Appl
888	23	74.2	467	7	US-11-158-505-31	Sequence 31, Appl	961	23	74.2	519	6	US-10-954-466-30	Sequence 30, Appl
889	23	74.2	467	7	US-11-158-505-72	Sequence 72, Appl	962	23	74.2	519	7	US-11-033-039-442	Sequence 442, App
890	23	74.2	467	7	US-11-182-908-18	Sequence 18, Appl	963	23	74.2	520	6	US-10-467-657-1992	Sequence 1992, Ap
891	23	74.2	468	6	US-10-763-712A-3	Sequence 3, Appl	964	23	74.2	520	6	US-10-954-466-13	Sequence 13, Appl
892	23	74.2	468	6	US-10-763-712A-20	Sequence 20, Appl	965	23	74.2	523	6	US-10-453-372-1006	Sequence 1006, Ap
893	23	74.2	468	6	US-10-763-712A-100	Sequence 100, App	966	23	74.2	523	6	US-10-453-372-1008	Sequence 1008, Ap
894	23	74.2	468	7	US-11-086-289-14	Sequence 14, Appl	967	23	74.2	523	7	US-11-072-512-2046	Sequence 2046, Ap
895	23	74.2	468	7	US-11-086-289-22	Sequence 22, Appl	968	23	74.2	524	7	US-11-041-095-58	Sequence 58, Appl
896	23	74.2	470	7	US-11-144-248-45	Sequence 45, Appl	969	23	74.2	525	7	US-11-102-120-13	Sequence 13, Appl
897	23	74.2	470	7	US-11-144-248-46	Sequence 46, Appl	970	23	74.2	526	7	US-11-041-095-10	Sequence 10, Appl
898	23	74.2	470	7	US-11-144-248-49	Sequence 49, Appl	971	23	74.2	526	7	US-11-072-512-3582	Sequence 3582, Ap
899	23	74.2	470	7	US-11-008-727-20	Sequence 20, Appl	972	23	74.2	528	7	US-11-024-955-343	Sequence 343, Ap
900	23	74.2	470	7	US-11-144-222-45	Sequence 45, Appl	973	23	74.2	530	6	US-10-995-805-4	Sequence 4, Appl
901	23	74.2	470	7	US-11-144-222-46	Sequence 46, Appl	974	23	74.2	530	7	US-11-183-136-44	Sequence 44, Appl

```
975      23      74.2      530 7 US-11-098-686-11263      Sequence 11263, A
976      23      74.2      530 7 US-11-124-367A-314      Sequence 314, App
977      23      74.2      531 7 US-11-008-727-18      Sequence 18, Appl
978      23      74.2      534 7 US-11-077-386-25      Sequence 25, Appl
979      23      74.2      539 7 US-11-183-136-38      Sequence 38, Appl
980      23      74.2      541 7 US-11-072-512-2161      Sequence 2161, Ap
981      23      74.2      542 7 US-11-098-686-11311      Sequence 11311, A
982      23      74.2      544 6 US-10-980-888-40      Sequence 40, Appl
983      23      74.2      545 6 US-10-453-372-222      Sequence 222, App
984      23      74.2      548 7 US-11-022-289-3      Sequence 3, Appl1
985      23      74.2      551 7 US-11-022-289-7      Sequence 7, Appl1
986      23      74.2      551 7 US-11-022-289-8      Sequence 8, Appl1
987      23      74.2      552 6 US-10-453-372-234      Sequence 234, Appl
988      23      74.2      552 6 US-10-453-372-236      Sequence 236, App
989      23      74.2      552 6 US-10-453-372-238      Sequence 238, App
990      23      74.2      552 6 US-10-453-372-240      Sequence 240, App
991      23      74.2      552 6 US-10-453-372-242      Sequence 242, App
992      23      74.2      552 6 US-10-453-372-244      Sequence 244, App
993      23      74.2      552 6 US-10-453-372-246      Sequence 246, App
994      23      74.2      552 6 US-10-453-372-248      Sequence 248, App
995      23      74.2      552 7 US-10-453-372-250      Sequence 250, App
996      23      74.2      552 7 US-11-072-512-3426      Sequence 3426, Ap
997      23      74.2      553 7 US-11-103-957-43      Sequence 43, Appl
998      23      74.2      553 7 US-11-018-868-30      Sequence 30, Appl
999      23      74.2      554 6 US-10-763-712A-33      Sequence 33, Appl
1000     23      74.2      555 6 US-10-763-712A-30      Sequence 30, Appl
```

ALIGNMENTS

```
RESULT 1
US-11-090-916-1
; Sequence 1, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-11-090-916-1
```

```
Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
Db      1 CGPC 4
```

RESULT 2

```
US-11-144-301A-8
; Sequence 8, Application US/11144301A
; Publication No. US20050288227A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Paul A.
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-144-301A-8
```

```
Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
Db      1 CGPC 4
```

```
RESULT 3
US-11-223-405-1
; Sequence 1, Application US/11223405
; Publication No. US20060009526A1
; GENERAL INFORMATION:
; APPLICANT: Richon, Victoria M.
; APPLICANT: Marks, Paul A.
; APPLICANT: Rifkind, Richard A.
; APPLICANT: Butler, Lisa M.
; TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
; FILE REFERENCE: 3254.1005-001
; CURRENT APPLICATION NUMBER: US/11/223,405
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: U.S. 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-223-405-1
```

```
Query Match      100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
Db      1 CGPC 4
```

```
RESULT 4
US-11-223-547-1
; Sequence 1, Application US/11223547
; Publication No. US20060009527A1
```



```
/ GENERAL INFORMATION:
/ APPLICANT: Richon, Victoria M.
/ APPLICANT: Marks, Paul A.
/ APPLICANT: Riekind, Richard A.
/ APPLICANT: Butler, Lisa M.
/ TITLE OF INVENTION: Method of Treating TRX Mediated Diseases
/ FILE REFERENCE: 3254.1005-001
/ CURRENT APPLICATION NUMBER: US/11/223,547
/ PRIOR FILING DATE: 2005-09-09
/ PRIOR APPLICATION NUMBER: US/10/369,094
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: U.S. 60/357,383
/ PRIOR FILING DATE: 2002-02-15
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-11-223-547-1
```

```
Query Match          100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       1 CGPC 4
```

```
RESULT 5
US-11-058-926-2
/ Sequence 2, Application US/11058926
/ Publication No. US20060030022A1
/ GENERAL INFORMATION:
/ APPLICANT: BECKWITH, JONATHAN
/ APPLICANT: ASLUND, FREDRIK
/ APPLICANT: BESETTE, PAUL H.
/ APPLICANT: GEORGIOU, GEORGE
/ APPLICANT: RITZ, DANIEL
/ APPLICANT: LIM, JACKIE EUN-AH
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCTION OF DISULFIDE
/ FILE REFERENCE: HMV-052.01
/ CURRENT APPLICATION NUMBER: US/11/058,926
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/679,705
/ PRIOR FILING DATE: 2000-10-05
/ PRIOR APPLICATION NUMBER: 60/157,770
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/163,939
/ PRIOR FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/166,044
/ PRIOR FILING DATE: 1999-11-17
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-058-926-2
```

```
Query Match          100.0%; Score 31; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       1 CGPC 4
```

```
RESULT 6
US-11-090-916-2
/ Sequence 2, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Rees
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 2
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide motif
/ NAME/KEY: misc feature
/ LOCATION: (1)..(6)
/ OTHER INFORMATION: Xaa = any amino acid
US-11-090-916-2
```

```
Query Match          100.0%; Score 31; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       2 CGPC 5
```

```
RESULT 7
US-11-090-916-3
/ Sequence 3, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Rees
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 3
/ LENGTH: 6
/ TYPE: PRT
```

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide motif
US-11-090-916-3

Query Match 100.0%; Score 31; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 2 CGPC 5

RESULT 8
US-11-131-744-2
Sequence 2, Application US/11131744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHOD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 2
LENGTH: 75
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-2

Query Match 100.0%; Score 31; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 33 CGPC 36

RESULT 9
US-10-467-657-5372
Sequence 5372, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZGA Mariagrazia
APPLICANT: MISIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04
SEQ ID NO 5372
LENGTH: 84
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5372

Query Match 100.0%; Score 31; DB 6; Length 84;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 10
US-11-131-744-1
Sequence 1, Application US/11131744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHOD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 1
LENGTH: 91
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-1

Query Match 100.0%; Score 31; DB 7; Length 91;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 32 CGPC 35

RESULT 11
US-11-074-176-286
Sequence 286, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Kjaerhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAniff, Olivia

APPLICANT: Perill, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
PRIOR FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 286
LENGTH: 103
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-286

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 12

US-11-090-916-6
Sequence 6; Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6
LENGTH: 103
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-090-916-6

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 28 CGPC 31

RESULT 13

US-11-090-916-7
Sequence 7; Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof

FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 7
LENGTH: 103
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-11-090-916-7

Query Match 100.0%; Score 31; DB 7; Length 103;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 30 CGPC 33

RESULT 14

US-11-090-916-5
Sequence 5; Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5
LENGTH: 104
TYPE: PRT
ORGANISM: Porphyromonas gingivalis
US-11-090-916-5

Query Match 100.0%; Score 31; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 29 CGPC 32

RESULT 15

US-10-821-234-1371
Sequence 1371; Application US/10821234
Publication No. US20050255114A1

```
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andaman, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1371
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1371
```

```
Query Match          100.0%; Score 31; DB 6; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```
RESULT 16
US-11-090-916-8
; Sequence 8, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Gallus gallus
US-11-090-916-8
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```
RESULT 17
US-11-090-916-9
; Sequence 9, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
```

```
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Reese
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-090-916-9
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```
RESULT 18
US-11-090-916-10
; Sequence 10, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-090-916-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db       32 CGPC 35
```

```
RESULT 19
```

US-11-090-916-11
; Sequence 11, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-090-916-11

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 32 CGPC 35

RESULT 20
US-11-090-916-12
; Sequence 12, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-916-12

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5

DB 32 CGPC 35
|||||
RESULT 21
US-11-106-796-13
; Sequence 13, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SITOVSKI, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-13

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 32 CGPC 35

RESULT 22
US-11-144-301A-9
; Sequence 9, Application US/11144301A
; Publication No. US20050288227A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Paul A.
; APPLICANT: Johanna, Ungerechte
; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
; FILE REFERENCE: 28517-501 UTIL
; CURRENT APPLICATION NUMBER: US/11/144,301A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,089
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 10/369,094
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,383
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-301A-9

Query Match 100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||||
DB 32 CGPC 35

RESULT 23
US-11-144-301A-10
; Sequence 10, Application US/11144301A
; Publication No. US20050288227A1
; GENERAL INFORMATION:

```
/ APPLICANT: Marks, Paul A.
/ APPLICANT: Johanna, Understedt
/ TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
/ FILE REFERENCE: 28517-501 UTIL
/ CURRENT APPLICATION NUMBER: US/11/144,301A
/ PRIOR FILING DATE: 2005-06-03
/ PRIOR APPLICATION NUMBER: US 60/577,089
/ PRIOR FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: US 10/369,094
/ PRIOR FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: US 60/357,383
/ PRIOR FILING DATE: 2002-02-15
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 10
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-144-301A-10
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

```
RESULT 24
US-11-032-773-943
/ Sequence 943, Application US/11032773
/ Publication No. US20060018911A1
/ GENERAL INFORMATION:
/ APPLICANT: Ault-Riche, Dana
/ APPLICANT: Levy, Ronald
/ TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
/ FILE REFERENCE: 17102-013001 / 1762
/ CURRENT APPLICATION NUMBER: US/11/032,773
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 60/536,184
/ PRIOR FILING DATE: 2004-01-12
/ PRIOR APPLICATION NUMBER: 60/557,591
/ PRIOR FILING DATE: 2004-03-29
/ NUMBER OF SEQ ID NOS: 958
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 943
/ LENGTH: 105
/ TYPE: PRT
/ ORGANISM: Mus musculus
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: Genbank BAA04881
/ DATABASE ENTRY DATE: 2002-12-25
US-11-032-773-943
```

```
Query Match          100.0%; Score 31; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

```
RESULT 25
US-10-689-742-19
/ Sequence 19, Application US/10689742
/ Publication No. US20050250180A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M
/ APPLICANT: Lavallee, Edward R
/ APPLICANT: Racie, Lisa A
```

```
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Spaulding, Vikki
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: 00766.000091.10
/ CURRENT APPLICATION NUMBER: US/10/689,742
/ CURRENT FILING DATE: 2003-10-22
/ PRIOR APPLICATION NUMBER: 09/746,783
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 231
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 19
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-689-742-19
```

```
Query Match          100.0%; Score 31; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      32 CGPC 35
```

```
RESULT 26
US-11-098-686-10612
/ Sequence 10612, Application US/11098686
/ Publication No. US20060024696A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ FILE REFERENCE: 09531-128001
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10612
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Lawsonia intracellularis
US-11-098-686-10612
```

```
Query Match          100.0%; Score 31; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPC 5
        ||||
Db      30 CGPC 33
```

```
RESULT 27
US-11-090-916-4
/ Sequence 4, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ TITLE OF INVENTION: Muscolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
```

PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/550,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 109
TYPE: PRT
ORGANISM: Pseudomonas syringae
US-11-090-916-4

Query Match 100.0%; Score 31; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 34 CGPC 37

RESULT 28
US-11-072-512-3199

Sequence 3199, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHITO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOTYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3199
LENGTH: 113
TYPE: PRT
ORGANISM: Homo sapiens
US-11-072-512-3199

Query Match 100.0%; Score 31; DB 7; Length 113;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 37 CGPC 40

RESULT 29
US-11-195-459-12

Sequence 12, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Meeley, Robert
APPLICANT: Hankke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PR
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 122
TYPE: PRT
ORGANISM: Zea mays
US-11-195-459-12

Query Match 100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 40 CGPC 43

RESULT 30
US-11-195-459-16

Sequence 16, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Meeley, Robert
APPLICANT: Hankke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PR
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 122
TYPE: PRT
ORGANISM: Hordeum vulgare
US-11-195-459-16

Query Match 100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
DB 46 CGPC 49

RESULT 31
US-11-195-459-19
; Sequence 19, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Mealey, Robert
; APPLICANT: Hanke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; PRIOR FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
US-11-195-459-19

Query Match 100.0%; Score 31; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 40 CGPC 43

RESULT 32
US-11-195-459-10
; Sequence 10, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Mealey, Robert
; APPLICANT: Hanke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,703
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Zea mays
US-11-195-459-10

Query Match 100.0%; Score 31; DB 7; Length 123;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 41 CGPC 44

RESULT 33
US-10-995-561-703
; Sequence 703, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CI001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 703
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-703

Query Match 100.0%; Score 31; DB 6; Length 126;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 63 CGPC 66

RESULT 34
US-11-106-796-10
; Sequence 10, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UVM0:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-10

Query Match 100.0%; Score 31; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 35
US-11-106-796-11
; Sequence 11, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY


```

; FILE REFERENCE: UWMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-796-11

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 32 CGPC 35

RESULT 36
US-11-106-796-12
; Sequence 12, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 127
; TYPE: PRT
; ORGANISM: RAT
US-11-106-796-12

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 127;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 32 CGPC 35

RESULT 37
US-10-467-657-4354
; Sequence 4354, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMin99, version 1.04
; SEQ ID NO 4354
; LENGTH: 129
; TYPE: PRT
```

```

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4354

Query Match
Best Local Similarity 100.0%; Score 31; DB 6; Length 129;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 53 CGPC 56

RESULT 38
US-11-072-512-2145
; Sequence 2145, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2145
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2145

Query Match
Best Local Similarity 100.0%; Score 31; DB 7; Length 129;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
   ||||
Db 74 CGPC 77

RESULT 39
US-11-090-916-13
; Sequence 13, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
```

PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13
LENGTH: 134
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-11-090-916-13

Query Match 100.0%; Score 31; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 60 CGPC 63

RESULT 40
US-11-195-459-8
Sequence 8, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Mealey, Robert
APPLICANT: Hancke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO

FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 134
TYPE: PRT
ORGANISM: Zea mays
US-11-195-459-8

Query Match 100.0%; Score 31; DB 7; Length 134;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 55 CGPC 58

RESULT 41
US-09-978-360A-641
Sequence 641, Application US/09978360A
Publication No. US2006009633A9
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste
APPLICANT: Duciery, Aymeric
APPLICANT: Bougueterec, Lydie
APPLICANT: Jobert, Severin
APPLICANT: Clusel, Catherine

TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56, USA, CIP
CURRENT APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 60/099,273
PRIOR FILING DATE: -09-04
PRIOR APPLICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: US 09/215,435
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: PCT/IB98/02122
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: US 09/247,155
PRIOR FILING DATE: 1999-02-09
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
SEQ ID NO 641
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -41...-1
US-09-978-360A-641

Query Match 100.0%; Score 31; DB 5; Length 143;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 133 CGPC 136

RESULT 42
US-11-090-916-14
Sequence 14, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Biastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 14
LENGTH: 167
TYPE: PRT
ORGANISM: Zea mays

US-11-090-916-14

Query Match 100.0%; Score 31; DB 7; Length 167;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 89 CGPC 92

RESULT 43

US-11-090-916-15

; Sequence 15, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: Lee, Rees
; APPLICANT: del Val, Greg
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-090-916-15

Query Match 100.0%; Score 31; DB 7; Length 172;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 95 CGPC 98

RESULT 44

US-11-131-744-3

; Sequence 3, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADRCHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26

; PRIOR APPLICATION NUMBER: 60/621,686
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-3

Query Match 100.0%; Score 31; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 32 CGPC 35

RESULT 45

US-10-467-962B-6

; Sequence 6, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000 857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 6
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-6

Query Match 100.0%; Score 31; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
Db 106 CGPC 109

RESULT 46

US-10-995-561-643

; Sequence 643, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-643

Query Match 100.0%; Score 31; DB 6; Length 189;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
143 CGPC 146

RESULT 47
US-10-995-561-642

; Sequence 642, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: C1001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-642

Query Match 100.0%; Score 31; DB 6; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
143 CGPC 146

RESULT 48
US-11-064-774A-2

; Sequence 2, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Alitalia et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; FILE REFERENCE: 28967/35977B2
; CURRENT APPLICATION NUMBER: US/11/064,774A
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
; SOFTWARE: Patentn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-774A-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
143 CGPC 146

RESULT 49
US-11-075-400-2
; Sequence 2, Application US/11075400
; Publication No. US20050282233A1
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, et al.
; TITLE OF INVENTION: MULTIVALENT ANTIBODY MATERIALS AND METHODS FORVEGF/PDGF FAMILY OF
; FILE REFERENCE: 28967/39820B
; CURRENT APPLICATION NUMBER: US/11/075,400
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,511
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/586,662
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentn version 3.3
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-400-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
143 CGPC 146

RESULT 50
US-11-226-005-4

; Sequence 4, Application US/11226005
; Publication No. US20060014252A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D. et al.
; TITLE OF INVENTION: FLK-1 Binding Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/226,005
; FILING DATE: 14-Sep-2005
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/743,868
; FILING DATE: 05-NOV-1996
; APPLICATION NUMBER: 08/554,374
; FILING DATE: 08-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2837
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEetical: NO
IMMEDIATE SOURCE:
CLONE: Hu VEGF
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-226-005-4

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 51
US-11-129-076-9
; Sequence 9, Application US/11129076
; Publication No. US20060019891A1
; GENERAL INFORMATION:
; APPLICANT: Edelman, Jay A.
; APPLICANT: Kaymarden, Munirva
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Protection of Cardiac Myocardium
; FILE REFERENCE: 1676.009US
; CURRENT APPLICATION NUMBER: US/11/129,076
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-076-9

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 52
US-11-145-494-2
; Sequence 2, Application US/11145494
; Publication No. US20060024785A1
; GENERAL INFORMATION:
; APPLICANT: Keyt, Bruce A.
; APPLICANT: Nguyen, Francis H.
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING VARIANTS OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: CELL GROWTH FACTOR
; FILE REFERENCE: A-62326-2
; CURRENT APPLICATION NUMBER: US/11/145,494
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US/09/346,069
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/567,200
; PRIOR FILING DATE: 1995-12-05
; PRIOR APPLICATION NUMBER: 60/002,827
; PRIOR FILING DATE: 1995-08-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Bovine
US-11-145-494-2

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 53
US-11-075-047A-81
; Sequence 81, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patent version 3.2
; SEQ ID NO 81
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-81

Query Match 100.0%; Score 31; DB 7; Length 191;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 143 CGPC 146

RESULT 54
US-11-098-686-11017
; Sequence 11017, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11017
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-11017

Query Match 100.0%; Score 31; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
|||
Db 10 CGPC 13

RESULT 55
US-10-467-657-8494
; Sequence 8494, Application US/10467657

```
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CITRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8494
/ LENGTH: 209
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-8494

Query Match          100.0%; Score 31; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      102 CGPC 105

RESULT 56
US-10-995-561-640
/ Sequence 640, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 640
/ LENGTH: 209
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-640

Query Match          100.0%; Score 31; DB 6; Length 209;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      161 CGPC 164

RESULT 57
US-10-995-561-645
/ Sequence 645, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
/ SEQ ID NO 645
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-645

Query Match          100.0%; Score 31; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      167 CGPC 170

RESULT 58
US-10-995-561-646
/ Sequence 646, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 646
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-646

Query Match          100.0%; Score 31; DB 6; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      167 CGPC 170

RESULT 59
US-11-149-462-3
/ Sequence 3, Application US/11149462
/ Publication No. US20060002978A1
/ GENERAL INFORMATION:
/ APPLICANT: Shea, Lonnie D.
/ APPLICANT: Shea, Lonnie L.
/ APPLICANT: Whitteley, Kevin
/ APPLICANT: Yang, Yang
/ APPLICANT: Rives, Christopher
/ APPLICANT: Rovedo, Mark
/ APPLICANT: Iskandar, Bernans
/ TITLE OF INVENTION: Biodegradable Scaffolds and Uses Thereof
/ FILE REFERENCE: 1720-1-011N
/ CURRENT APPLICATION NUMBER: US/11/149,462
/ CURRENT FILING DATE: 2005-06-09
/ PRIOR APPLICATION NUMBER: 60/578,785
/ PRIOR FILING DATE: 2004-06-10
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-149-462-3

Query Match          100.0%; Score 31; DB 7; Length 215;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 CGPC 5
Db 167 CGPC 170

RESULT 60

US-11-106-399-8
; Sequence 8, Application US/11106399
; Publication No. US2006002892A1
; GENERAL INFORMATION:
; APPLICANT: MATHEW, FORUNELLOOR A.
; APPLICANT: BOLES, KENT S.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/11/106,399
; CURRENT FILING DATE: 2005-04-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-399-8

Query Match 100.0%; Score 31; DB 7; Length 216;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 96 CGPC 99

RESULT 61

US-11-072-512-3343
; Sequence 3343, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOMYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3343
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3343

Query Match 100.0%; Score 31; DB 7; Length 224;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 28 CGPC 31

RESULT 62

US-10-995-561-641
; Sequence 641, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 641
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-641

Query Match 100.0%; Score 31; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 184 CGPC 187

RESULT 63

US-10-995-561-644
; Sequence 644, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 644
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-644

Query Match 100.0%; Score 31; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGPC 5
Db 184 CGPC 187

RESULT 64

US-11-153-880-7
; Sequence 7, Application US/11153880
; Publication No. US20050256050A1
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN

```
; APPLICANT: ROSEN, CRAIG A.
; APPLICANT: CAO, LIANG
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
; STREET: 1100 NEW YORK AVENUE
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/153,880
; FILING DATE: 16-Jun-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/219,442
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/999,811
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MARKOWICZ, KAREN R.
; REGISTRATION NUMBER: 36/351
; REFERENCE/DOCKET NUMBER: 1488.1000004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2600
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: Not Relevant
; MOLECULE TYPE: protein
; US-11-153-880-7

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 65
US-11-064-774A-147
; Sequence 147, Application US/11064774A
; Publication No. US20050267024A1
; GENERAL INFORMATION:
; APPLICANT: Aitala et al.
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR ENDOTHELIAL GROWTH
; FILE REFERENCE: 28967/35977B2
; CURRENT APPLICATION NUMBER: US/11/064,774A
; FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 09/795,006
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,311
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 1212
```

```
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 147
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-064-774A-147

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 66
US-11-211-724-5
; Sequence 5, Application US/11211724
; Publication No. US20050287143A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Vascular Endothelial Growth Factor 2
; FILE REFERENCE: PF112P1
; CURRENT APPLICATION NUMBER: US/11/211,724
; FILING DATE: 2005-08-26
; PRIOR APPLICATION NUMBER: US/08/465,968
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/207,550
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-211-724-5

Query Match          100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CGPC 5
Db      184 CGPC 187

RESULT 67
US-11-233-119-7
; Sequence 7, Application US/11233119
; Publication No. US20060025331A1
; GENERAL INFORMATION:
; APPLICANT: HU, JING-SHAN et al.
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR 2
; FILE REFERENCE: PF112P4D1
; CURRENT APPLICATION NUMBER: US/11/233,119
; FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: 09/107,997
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: 09/042,105
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/999,811
; PRIOR FILING DATE: 1997-12-24
; PRIOR APPLICATION NUMBER: 08/465,968
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/207,550
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: homo sapiens
```


US-11-233-119-7

Query Match 100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 184 CGPC 187

RESULT 68

US-11-075-047A-91
; Sequence 91, Application US/11075047A
; Publication No. US20060030000A1
; GENERAL INFORMATION:
; APPLICANT: ALITALO, et al.
; TITLE OF INVENTION: GROWTH FACTOR BINDING CONSTRUCTS MATERIALS AND METHODS
; FILE REFERENCE: 28967/39700A
; CURRENT APPLICATION NUMBER: US/11/075,047A
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/550,907
; PRIOR FILING DATE: 2004-03-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-075-047A-91

Query Match 100.0%; Score 31; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 184 CGPC 187

RESULT 69
US-11-131-744-6
; Sequence 6, Application US/11131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIYUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: protein sequence
US-11-131-744-6

Query Match 100.0%; Score 31; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 32 CGPC 35

RESULT 70
US-11-186-284-85
; Sequence 85, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-85

Query Match 100.0%; Score 31; DB 7; Length 282;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPC 5
1111
DB 32 CGPC 35

Search completed: February 23, 2006, 00:48:08
Job time : 16.5 secs

This Page Blank (usg09)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:31:07 : Search time 142 Seconds
(without alignments)
18.565 Million cell updates/sec

Title: US-10-660-118a-3
Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq.21.*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	6	1 AAP71087	Sequence
2	47	100.0	6	5 ABP54936	Active si
3	47	100.0	6	6 ADA08451	Mammalian
4	47	100.0	6	8 ADM32929	Amino aci
5	47	100.0	6	8 ADP87509	Thioredox
6	47	100.0	6	8 ADP67423	Thioredox
7	47	100.0	6	8 ADP97008	Thioredox
8	47	100.0	12	2 AAM45003	Immunomod
9	47	100.0	12	2 AAY09429	Immunomod
10	47	100.0	52	4 AAU08670	Thioredox
11	47	100.0	80	2 AAR42822	RECEP 84.
12	47	100.0	84	2 AAR42821	RECEP 84.
13	47	100.0	84	7 ADJ68506	Human hea
14	47	100.0	91	5 ABP60794	Human hea
15	47	100.0	95	4 AAB49948	Thiocapsa
16	47	100.0	102	5 ABP60779	A. oryzae
17	47	100.0	102	5 ABP60755	Mycoplasma
18	47	100.0	102	5 ABP60756	Mytilus
19	47	100.0	102	5 ABP60753	Chlamydia
20	47	100.0	102	5 ABP60777	Chlamydia
21	47	100.0	102	6 ADB09186	Mycoplasma
22	47	100.0	103	5 ABP60747	Bacillus
23	47	100.0	103	5 ABG93246	C. albica
24	47	100.0	103	5 ABG93156	S. cerevi

25	47	100.0	103	5 ABG93328	Abg93328 C. albica
26	47	100.0	103	5 ABP73948	Abp73948 Candida a
27	47	100.0	103	6 ABR41607	Abri41607 Human DIT
28	47	100.0	103	8 ADK90669	Adk90669 Baker's Y
29	47	100.0	103	8 ADM32933	Adm32933 Amino aci
30	47	100.0	104	2 AAR42820	Aar42820 RECEP 104
31	47	100.0	104	2 AAR47855	Aar47855 Human ADF
32	47	100.0	104	2 AAR72389	Aar72389 Recombina
33	47	100.0	104	5 AAG80708	Aag80708 S. cerevi
34	47	100.0	104	5 ABP60927	Abp60927 Staphyloc
35	47	100.0	104	5 ABP60803	Abp60803 Homo septi
36	47	100.0	104	5 ABP60797	Abp60797 Bos tauru
37	47	100.0	104	5 ABP60812	Abp60812 Ovis arie
38	47	100.0	104	5 ABP60805	Abp60805 Mus muscu
39	47	100.0	104	5 ABP60809	Abp60809 Oryctolag
40	47	100.0	104	5 ABP60810	Abp60810 Rattus no
41	47	100.0	104	5 ABP60801	Abp60801 Gallus ga
42	47	100.0	104	5 ABG93115	Abg93115 S. cerevi
43	47	100.0	104	5 ADK90667	Adk90667 Baker's Y
44	47	100.0	104	8 ADO59801	Ado59801 B. subtil
45	47	100.0	104	8 ADS88157	Ads88157 Human pro
46	47	100.0	105	1 AAP92141	Aap92141 Recombina
47	47	100.0	105	2 AAR42819	Aar42819 RECEP/Chio
48	47	100.0	105	2 AAR37700	Aar37700 ADF. 11/1
49	47	100.0	105	2 AAR47856	Aar47856 Human ADF
50	47	100.0	105	2 AAR72390	Aar72390 Recombina
51	47	100.0	105	2 AAM69567	Aam69567 Human thl
52	47	100.0	105	2 AAY25908	Aay25908 Human thl
53	47	100.0	105	3 AAG03956	Aag03956 Human sec
54	47	100.0	105	3 ABP60700	Abp60700 Human thl
55	47	100.0	105	5 ABP60757	Abp60757 Corynebac
56	47	100.0	105	5 ABG93363	Abg93363 Human Bax
57	47	100.0	105	5 ABP07225	Abp07225 Human p53
58	47	100.0	105	6 ABR92158	Abri92158 Human cer
59	47	100.0	105	7 ADP67269	Adp67269 Thioredox
60	47	100.0	105	7 ADF30728	Adf30728 Rat angio
61	47	100.0	105	7 ADJ70213	Adj70213 Human hea
62	47	100.0	105	7 ADJ47593	Adj47593 Wild-type
63	47	100.0	105	8 ADI82895	Adi82895 Human PRO
64	47	100.0	105	8 ADM32938	Adm32938 Amino aci
65	47	100.0	105	8 ADM32935	Adm32935 Amino aci
66	47	100.0	105	8 ADM32936	Adm32936 Amino aci
67	47	100.0	105	8 ADM32937	Adm32937 Amino aci
68	47	100.0	105	8 ADM32934	Adm32934 Amino aci
69	47	100.0	105	8 ADP19655	Adp19655 Human PRO
70	47	100.0	105	8 ADP54775	Adp54775 Human PRO
71	47	100.0	105	8 ADR49671	Adr49671 Murine th
72	47	100.0	105	8 ADP24148	Adp24148 PRO polyP
73	47	100.0	105	8 ADP08493	Adp08493 Wild-type
74	47	100.0	105	8 ADU06404	Adu06404 Novel bto
75	47	100.0	105	8 ADY19738	Ady19738 PRO polyP
76	47	100.0	105	9 ADY16038	Ady16038 PRO polyP
77	47	100.0	105	9 ADW97622	Adw97622 Human thl
78	47	100.0	105	9 AEB30735	Aeb30735 Therapeut
79	47	100.0	105	4 ABB60229	Abb60229 Drosophill
80	47	100.0	106	5 AAO22592	Aao22592 106-mer H
81	47	100.0	106	5 ABP60783	Abp60783 Penicilli
82	47	100.0	106	5 ABP60827	Abp60827 Manduca s
83	47	100.0	106	5 ABP60788	Abp60788 Streptomy
84	47	100.0	106	5 ABP60774	Abp60774 Helicobac
85	47	100.0	106	5 ABP60478	Abp60478 Drosophill
86	47	100.0	107	4 ABP60802	Abp60802 Drosophill
87	47	100.0	107	5 ABP60772	Abp60772 Haemophill
88	47	100.0	107	5 ABP60760	Abp60760 Chromatiu
89	47	100.0	107	6 ABM71327	Abm71327 Staphyloc
90	47	100.0	108	5 ABG70953	Abg70953 Escherich
91	47	100.0	108	5 ABG70952	Abg70952 Escherich
92	47	100.0	108	5 ABP60784	Abp60784 Pseudomon
93	47	100.0	108	5 ABP60768	Abp60768 Escherich
94	47	100.0	108	5 ABP60793	Abp60793 Thiobacil
95	47	100.0	108	7 ABM73822	Abm73822 DNA clone
96	47	100.0	108	7 AAR15646	Aar15646 Thioredox
97	47	100.0	109	2	

98	47	100.0	109	2	AAR75767	Aar75767	Hls-patch	171	47	100.0	166	2	AAW59886	Aaw59886	Amino aci
99	47	100.0	109	2	AAR75769	Aar75769	E. coli t	172	47	100.0	166	2	AAW49006	Aaw49006	Human thi
100	47	100.0	109	2	AAR75768	Aar75768	Histidine	173	47	100.0	166	5	ABP41978	Abp41978	Human ova
101	47	100.0	109	2	AAI25383	Aay25383	Plasmid p	174	47	100.0	166	5	ABP60804	Abp60804	Homo sapi
102	47	100.0	109	2	AAI02639	Aay02639	Thioredox	175	47	100.0	166	5	ABP60798	Abp60798	Bos tauri
103	47	100.0	109	3	AAAB3553	Aab23553	Thioredox	176	47	100.0	166	5	ABP60807	Abp60807	Mus muscu
104	47	100.0	109	5	ABBI79749	Aab79749	Thioredox	177	47	100.0	166	7	ADBE2952	Aade2952	Rat prote
105	47	100.0	109	5	ABP66968	Abp66968	Escherich	178	47	100.0	167	4	AAAB85253	Aab85253	Thioredox
106	47	100.0	109	5	ABP60744	Abp60744	Aspergill	179	47	100.0	167	4	AAAB85254	Aab85254	Thioredox
107	47	100.0	109	6	ABJ26015	Abj26015	Aspergill	180	47	100.0	170	3	AAAG09381	Aag09381	Arabidops
108	47	100.0	109	6	ABJ25415	Abj25415	Aspergill	181	47	100.0	170	3	AAAB75114	Aab75114	Arabidops
109	47	100.0	109	6	ADOS9277	Ados9277	E. coli t	182	47	100.0	170	8	AD033544	Ado33544	Thioredox
109	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	183	47	100.0	170	8	AD033539	Ado33539	Thioredox
110	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	184	47	100.0	170	8	AD266909	Adz66909	Tx-DP-TM
111	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	185	47	100.0	170	9	AD266915	Adz66915	Tx-DP-TM
112	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	186	47	100.0	170	9	AD266915	Adz66915	Tx-DP-TM
113	47	100.0	109	8	ADJ57878	Adj57878	E. coli t	187	47	100.0	170	9	AD266915	Adz66915	Tx-DP-TM
114	47	100.0	109	9	ADJ57878	Adj57878	E. coli t	188	47	100.0	170	9	AD266915	Adz66915	Tx-DP-TM
115	47	100.0	109	9	ADJ57878	Adj57878	E. coli t	189	47	100.0	171	3	AAAG27357	Aag27357	Arabidops
116	47	100.0	111	5	ABP39014	Abp39014	Staphyloc	190	47	100.0	171	3	AAAG27358	Aag27358	Arabidops
117	47	100.0	111	5	ABP39014	Abp39014	Staphyloc	191	47	100.0	172	1	AAAP94809	Aap94809	Human int
118	47	100.0	111	8	ADSO6336	Adso6336	Staphyloc	192	47	100.0	173	7	ABMB6658	Abm6658	Rice abio
119	47	100.0	111	8	ADSO6336	Adso6336	Staphyloc	193	47	100.0	177	3	ADCI4129	Adci4129	Chimeric
120	47	100.0	112	5	ABP60738	Abp60738	Chlamydom	194	47	100.0	177	5	ABP60714	Abp60714	Brassicic
121	47	100.0	112	5	ABP60780	Abp60780	Mycobacte	195	47	100.0	178	3	AAAG19366	Aag19366	Arabidops
122	47	100.0	115	5	ABP60781	Abp60781	Mycobacte	196	47	100.0	178	5	ABP60703	Abp60703	Arabidops
123	47	100.0	115	5	ABP60799	Abp60799	Caenorhab	197	47	100.0	178	8	ADN74765	Adn74765	Thale cre
124	47	100.0	116	7	ABMB6532	Abmb6532	Mouse pro	198	47	100.0	179	3	AAAG30359	Aag30359	Arabidops
125	47	100.0	117	5	ABP60743	Abp60743	Borrelia	199	47	100.0	179	5	ABP60710	Abp60710	Arabidops
126	47	100.0	118	5	ABP60733	Abp60733	Nicotiana	200	47	100.0	179	7	ADG46659	Adg46659	Arabidops
127	47	100.0	120	7	ADP70794	Adp70794	Minicell	201	47	100.0	181	3	AAAG09380	Aag09380	Arabidops
128	47	100.0	120	7	ADP70792	Adp70792	Minicell	202	47	100.0	181	5	ABP60719	Abp60719	Spinacia
129	47	100.0	120	7	ADP70791	Adp70791	Minicell	203	47	100.0	182	3	AAAG52357	Aag52357	Arabidops
130	47	100.0	120	7	ADP70793	Adp70793	Minicell	204	47	100.0	182	3	AAAG27356	Aag27356	Arabidops
131	47	100.0	122	7	ADP70792	Adp70792	Bacterial	205	47	100.0	182	5	ABP60707	Abp60707	Pisum sat
132	47	100.0	124	4	AAAG93165	Aag93165	C. glutami	206	47	100.0	182	5	ABP60705	Abp60705	Brassicic
133	47	100.0	124	7	ADDI3226	Addi3226	C. glutami	207	47	100.0	182	8	ADN74793	Adn74793	Thale cre
134	47	100.0	124	7	ABO61500	Abob61500	Klebsiell	208	47	100.0	183	8	ADY72703	Ady72703	Conoc
135	47	100.0	125	7	ABMB6533	Abmb6533	Human pro	209	47	100.0	184	3	AAAG38661	Aag38661	Arabidops
136	47	100.0	127	4	ABGI8304	Abgi8304	Novel hum	210	47	100.0	185	5	ABP60704	Abp60704	Arabidops
137	47	100.0	127	4	ABP60782	Abp60782	Neurospor	211	47	100.0	185	6	ABU01415	Abu01415	S. pneumo
138	47	100.0	129	6	ABP78912	Abp78912	N. gonorr	212	47	100.0	185	8	ADK48707	Adk48707	Streptoco
139	47	100.0	129	6	ABD69961	Abd69961	C. neofor	213	47	100.0	185	8	ADT56788	Adt56788	Plant pol
140	47	100.0	130	5	ABP60787	Abp60787	Rickettsi	214	47	100.0	185	8	ADT56140	Adt56140	Plant pol
141	47	100.0	132	7	ADCC3012	Adcc3012	Human nov	215	47	100.0	186	3	AAAG1897	Aag1897	Arabidops
142	47	100.0	133	7	ADP70773	Adp70773	Minicell	216	47	100.0	186	5	ABP60711	Abp60711	Arabidops
143	47	100.0	134	3	ADCI4128	Adci4128	Human thi	217	47	100.0	187	7	ABMB90060	Abm90060	Rice abio
144	47	100.0	137	2	AAW55082	Aaw55082	Streptoco	218	47	100.0	187	7	ABMB90236	Abm90236	Rice abio
145	47	100.0	137	5	ABP54576	Abp54576	S. pneumo	219	47	100.0	190	5	ABP60708	Abp60708	Spinacia
146	47	100.0	137	7	ADCA5121	Adca5121	S. pneumo	220	47	100.0	191	5	ABP60706	Abp60706	Meembrya
147	47	100.0	140	3	AAAG09942	Aag09942	Arabidops	221	47	100.0	191	6	ABP81583	Abp81583	Streptoco
148	47	100.0	140	3	AAAG37258	Aag37258	Arabidops	222	47	100.0	194	8	ADRB6469	Adrb6469	Novel S.
149	47	100.0	140	3	AAAG37257	Aag37257	Arabidops	223	47	100.0	194	9	AAE60339	Aae60339	Streptoco
150	47	100.0	140	3	AAAG38662	Aag38662	Arabidops	224	47	100.0	196	8	ADH89354	Adh89354	Colias eu
151	47	100.0	140	3	AAAG10594	Aag10594	Arabidops	225	47	100.0	206	8	ADRB9864	Adrb9864	Fusio pr
152	47	100.0	140	5	ABP60814	Abp60814	Arabidops	226	47	100.0	209	2	AAAR31931	Aar31931	Human TC-
153	47	100.0	145	5	ABP60759	Abp60759	Corynebac	227	47	100.0	209	5	ABBI79754	Abb79754	Thioredox
154	47	100.0	145	6	ADAA34073	Adaa34073	Acinetoba	228	47	100.0	210	4	AAAB05136	Aab05136	Human T c
155	47	100.0	147	3	AAAG30361	Aag30361	Arabidops	229	47	100.0	222	8	ADY94028	Ady94028	Plant ful
156	47	100.0	152	3	AAAG41898	Aag41898	Arabidops	230	47	100.0	222	4	ABG29563	Abg29563	Novel hum
157	47	100.0	154	7	ADP70797	Adp70797	pMPX-91 M	231	47	100.0	232	8	ADP49017	Adp49017	HTLV-II g
158	47	100.0	154	7	ADP70798	Adp70798	pMPX-96 M	232	47	100.0	232	8	ADP49016	Adp49016	HTLV-I gp
159	47	100.0	154	7	ADP70795	Adp70795	pMPX-80 M	233	47	100.0	233	7	ADMO4124	Admo4124	Human pro
160	47	100.0	154	7	ADP70796	Adp70796	pMPX-81 M	234	47	100.0	235	2	AAW26620	Aaw26620	Thioredox
161	47	100.0	155	5	ABBI97761	Abbi97761	Human sec	235	47	100.0	235	8	ADII19301	Adi19301	Ag2/PRA1-
162	47	100.0	159	5	ABBI97752	Abbi97752	Thioredox	236	47	100.0	236	9	ADMA47875	Adm47875	Respirato
163	47	100.0	161	8	AD033540	Ado33540	Thioredox	237	47	100.0	274	9	ADMA47873	Adm47873	Respirato
164	47	100.0	161	9	ADZ66921	Adz66921	Tix-DP-TM	238	47	100.0	281	4	AAAB49947	Aab49947	A. Oryzae
165	47	100.0	161	9	ADZ66918	Adz66918	Tix-DP-TM	239	47	100.0	283	9	ADMA47881	Adm47881	Respirato
166	47	100.0	164	5	AAAG30360	Aag30360	Arabidops	240	47	100.0	283	9	ADMA47877	Adm47877	Respirato
167	47	100.0	164	5	ADII19317	Adi19317	Human ova	241	47	100.0	283	9	ADMA47883	Adm47883	Respirato
168	47	100.0	165	8	ADJ47601	Adj47601	Wild-type	242	47	100.0	284	5	ABP60840	Abp60840	Caenorhab
169	47	100.0	166	8	AAW59885	Aaw59885	Amino aci	243	47	100.0					

244	47	100.0	287	4	ABB61581	Abp61581 Drosophil	317	47	100.0	591	7	ADB67536	Adp67536 Human WT1
245	47	100.0	287	5	ABP60841	Abp60841 Drosophil	318	47	100.0	591	7	ADJ80769	Adj80769 Wilm's tu
246	47	100.0	290	5	ABP60837	Abp60837 Schistos	319	47	100.0	591	8	ADJ83689	Adj83689 Human WT1
247	47	100.0	296	2	AAR26213	Aar26213 Fusion pr	320	47	100.0	591	8	ADL57577	Adl57577 Human Ttx
248	47	100.0	296	2	AAR26051	Aar26051 Thioiodex	321	47	100.0	591	8	ADN09132	Adn09132 Human Ttx
249	47	100.0	296	2	AAR45916	Aar45916 E.coli th	322	47	100.0	602	8	ADM30972	Adm30972 Human Ttx
250	47	100.0	296	2	AAR50177	Aar50177 Thioiodex	323	47	100.0	602	8	ADM30974	Adm30974 Human Ttx
251	47	100.0	296	2	AAR57672	Aar57672 Thioiodex	324	47	100.0	602	8	ADM30970	Adm30970 Human Ttx
252	47	100.0	296	2	AAR76812	Aar76812 Thioiodex	325	47	100.0	602	8	ADM30976	Adm30976 Human Ttx
253	47	100.0	323	6	AAO20598	Aao20598 Thioiodex	326	47	100.0	710	5	AAM50661	Aam50661 Human Ttx
254	47	100.0	323	7	ADD26516	Add26516 Human thl	327	47	100.0	824	5	AAM48247	Aam48247 Thioiodex
255	47	100.0	330	8	ADM30905	Adm30905 Human thl	328	47	100.0	824	7	ADC29712	Adc29712 A. thalia
256	47	100.0	330	5	ABP53264	Abp53264 Human MND	329	47	100.0	858	7	ADG75020	Adg75020 Human her
257	47	100.0	330	7	ADC31343	Adc31343 Human nov	330	47	100.0	858	7	ADP70776	Adp70776 H1E(1-37
258	47	100.0	333	8	ADR86123	Adr86123 Aspergill	331	47	100.0	1285	2	AAM47000	Aam47000 HIS tagge
259	47	100.0	342	5	ABG33381	Abg33381 Human Ttx	332	44	93.6	19	5	AAE23038	Aae23038 Human thl
260	47	100.0	342	7	ADB67534	Adb67534 Human WT1	333	44	93.6	71	4	AU023152	Au023152 Novel hum
261	47	100.0	342	7	ADJ80767	Adj80767 Wilm's tu	334	44	93.6	71	4	AAM84127	Aam84127 Human lmm
262	47	100.0	342	8	ADJ83687	Adj83687 Human WT1	335	44	93.6	71	4	AAU087497	Aau087497 Novel cen
263	47	100.0	342	8	ADL57575	Adl57575 Human Ttx	336	44	93.6	88	5	ADL54812	Adl54812 Novel hum
264	47	100.0	342	8	ADO09130	Ado09130 Human Ttx	337	44	93.6	88	5	ABP60767	Abp60767 Dicyoste
265	47	100.0	355	6	ABR54578	Abz54578 Prostate	338	44	93.6	88	5	ABP60766	Abp60766 Dicyoste
266	47	100.0	355	7	ADB14461	Adb14461 Fusion co	339	44	93.6	89	3	AAG44849	Aag44849 Zea maye
267	47	100.0	355	7	ADG26984	Adg26984 Human pro	340	44	93.6	102	2	AAZ35279	Aaz35279 Chlamydia
268	47	100.0	366	9	ADY61037	Ady61037 Abioticic s	341	44	93.6	102	5	ABP60754	Abp60754 Chlamydia
269	47	100.0	374	6	ABP72770	Abp72770 Thioiodex	342	44	93.6	102	5	AAB60723	Aab60723 Cyanidios
270	47	100.0	402	5	ABG67256	Abg67256 Polychoa	343	44	93.6	102	5	AU0949439	Au0949439 Chlamydo
271	47	100.0	407	5	ABG67270	Abg67270 Polychoa	344	44	93.6	103	5	ABP60775	Abp60775 Listeria
272	47	100.0	407	5	ABG67267	Abg67267 Polychoa	345	44	93.6	103	5	ABP60775	Abp60775 Listeria
273	47	100.0	408	2	AAW84315	Aaw84315 TrxA-rab	346	44	93.6	103	8	ADM32932	Adm32932 Amino aci
274	47	100.0	410	5	ABG33382	Abg33382 Human Ttx	347	44	93.6	104	5	ABP30470	Abp30470 Streptoco
275	47	100.0	410	7	ADB67535	Adb67535 Human WT1	348	44	93.6	104	5	ABBS4990	Abbs4990 Lactococo
276	47	100.0	410	7	ADJ80768	Adj80768 Wilm's tu	349	44	93.6	104	5	ABP60785	Abp60785 Rhodospir
277	47	100.0	410	8	ADJ83688	Adj83688 Human WT1	350	44	93.6	104	6	ABU02257	Abu02257 S. pneumo
278	47	100.0	410	8	ADL57576	Adl57576 Human Ttx	351	44	93.6	104	6	ABP81634	Abp81634 Streptoco
279	47	100.0	421	8	ADO09131	Ado09131 Human Ttx	352	44	93.6	104	8	ADK46563	Adk46563 Streptoco
280	47	100.0	421	5	AAAS0663	Aaas0663 Thioiodex	353	44	93.6	104	8	ADM32931	Adm32931 Amino aci
281	47	100.0	437	8	ADM30966	Adm30966 Human Ttx	354	44	93.6	104	8	ADY82057	Ady82057 Streptoco
282	47	100.0	438	8	ADM30964	Adm30964 Human Ttx	355	44	93.6	105	5	ABP60765	Abp60765 Dicyoste
283	47	100.0	438	8	ADM30968	Adm30968 Human Ttx	356	44	93.6	105	5	ABP60786	Abp60786 Rhodobact
284	47	100.0	438	8	ADM30962	Adm30962 Human Ttx	357	44	93.6	105	5	ABP60745	Abp60745 A.licyclob
285	47	100.0	447	8	ADU02345	Adu02345 Novel hum	358	44	93.6	105	8	ADOS5473	Ados5473 D. discob
286	47	100.0	458	5	ABP60865	Abp60865 Mycobacte	359	44	93.6	106	5	ABP60791	Abp60791 Synechocy
287	47	100.0	458	5	ABP60778	Abp60778 Mycobacte	360	44	93.6	106	5	ABP60721	Abp60721 Anacystis
288	47	100.0	458	5	ABP60634	Abp60634 Mycobacte	361	44	93.6	106	5	ABP60709	Abp60709 Anabaena
289	47	100.0	458	5	ABP60702	Abp60702 Mycobacte	362	44	93.6	106	5	ABP60764	Abp60764 Coprinus
290	47	100.0	458	6	AAO20628	Aao20628 Thioiodex	363	44	93.6	107	5	ABP60725	Abp60725 Porphyra
291	47	100.0	458	6	AAO20619	Aao20619 Thioiodex	364	44	93.6	107	5	ABP60790	Abp60790 Cyanidium
292	47	100.0	458	7	ADD26554	Add26554 M. leprae	365	44	93.6	107	5	ABP60722	Abp60722 Cyanidium
293	47	100.0	458	8	ADM30944	Adm30944 M. leprae	366	44	93.6	107	5	ABP60726	Abp60726 Porphyra
294	47	100.0	467	3	AAZ79067	Aaz79067 Murine se	367	44	93.6	108	9	ABE42151	Aeb42151 L. pneumo
295	47	100.0	467	3	AAZ85150	Aaz85150 Mouse sec	368	44	93.6	109	2	AAZ93015	Aaz93015 Thioiodex
296	47	100.0	467	9	ADM00726	Adm00726 Amino aci	369	44	93.6	109	5	ABP60792	Abp60792 Synechocy
297	47	100.0	485	7	ADP70799	Adp70799 Minicell	370	44	93.6	109	5	ABP60724	Abp60724 Griffliths
298	47	100.0	485	7	ADP70800	Adp70800 Minicell	371	44	93.6	109	5	ABP60836	Abp60836 Synechocy
299	47	100.0	485	7	ADP70802	Adp70802 Minicell	372	44	93.6	110	5	ABP60789	Abp60789 Streptococ
300	47	100.0	485	7	ADP70801	Adp70801 Minicell	373	44	93.6	110	8	ADY88658	Ady88658 Streptoco
301	47	100.0	499	9	AEA51601	Aea51601 RTV VP7 a	374	44	93.6	110	8	ADY79911	Ady79911 Streptoco
302	47	100.0	500	2	AAZ90303	Aaz90303 Thioiodex	375	44	93.6	111	7	ADM80195	Adm80195 Human NOV
303	47	100.0	513	3	ABP60691	Abp60691 Phaseolin	376	44	93.6	111	9	ABE39008	Aeb39008 L. pneumo
304	47	100.0	516	6	ABG71115	Abg71115 Human Pet	377	44	93.6	112	5	ABG60236	Abg60236 Human Thl
305	47	100.0	518	6	ABG71114	Abg71114 Human Pet	378	44	93.6	112	5	AAU91276	Aau91276 Human NOV
306	47	100.0	522	5	AAAS0660	Aaas0660 Thioiodex	379	44	93.6	112	5	AAU78664	Aau78664 Human NOV
307	47	100.0	530	5	AAAS0662	Aaas0662 Thioiodex	380	44	93.6	112	7	ADC97112	Adc97112 E. faeciu
308	47	100.0	536	6	ADP70777	Adp70777 P. faalcp	381	44	93.6	114	3	AAAG08114	Aag808114 Arabidops
309	47	100.0	546	6	ABP71271	Abp71271 P. faalcp	382	44	93.6	114	3	AAAG54021	Aag54021 Arabidops
310	47	100.0	551	7	ADM65518	Adm65518 PERT-Tx42	383	44	93.6	114	5	ABP60696	Abp60696 Arabidops
311	47	100.0	551	4	AAAB85251	Aaab85251 Plant thl	384	44	93.6	114	5	ABP60680	Abp60680 Phaseolin
312	47	100.0	551	4	AAAB85252	Aaab85252 Plant thl	385	44	93.6	114	5	ABP60727	Abp60727 Arabidops
313	47	100.0	572	9	AAAD26575	Aaad26575 Human syn	386	44	93.6	114	7	ABG32916	Abg32916 Arabidops
314	47	100.0	580	7	ABO74197	Ab074197 Pseudomon	387	44	93.6	114	8	ADR94295	Adr94295 Novel S.
315	47	100.0	591	5	ABG33383	Abg33383 Human Ttx	388	44	93.6	114	8	ADR94295	Adr94295 Novel S.
316	47	100.0	591	5	ABG33383	Abg33383 Human Ttx	389	44	93.6	114	9	AEA58165	Aea58165 Streptoco

390	44	93.6	115	3	AAg12953	AAg12953	Arabidops	463	44	93.6	152	3	AAg26778	AAg26778	Zea mays
391	44	93.6	115	3	AAg45020	AAg45020	Zea mays	464	44	93.6	152	8	ADY06632	ADY06632	Plant ful
392	44	93.6	116	5	ABP60739	ABP60739	Pagopyrum	465	44	93.6	153	8	ADY87889	ADY87889	Plant ful
393	44	93.6	118	3	AAy70480	AAy70480	Catalpa s	466	44	93.6	159	3	AAg36125	AAg36125	Arabidops
394	44	93.6	118	5	AAy70483	AAy70483	Vernonia	467	44	93.6	160	5	ABP60832	ABP60832	Neisseria
395	44	93.6	118	5	ABP27942	ABP27942	Streptoco	468	44	93.6	160	7	ABO65111	ABO65111	Klebsiell
396	44	93.6	118	5	ABP27941	ABP27941	Streptoco	469	44	93.6	163	8	ADY89993	ADY89993	Plant ful
397	44	93.6	118	5	ABP60742	ABP60742	Ricinus c	470	44	93.6	163	8	ADY72134	ADY72134	Plant ful
398	44	93.6	119	5	ABP60826	ABP60826	Secale ce	471	44	93.6	167	8	ADY80716	ADY80716	Zea mays
399	44	93.6	120	5	AAy70481	AAy70481	Glycine m	472	44	93.6	167	8	ADM32940	ADM32940	Amino aci
400	44	93.6	120	2	AAy70481	AAy70481	Protein f	473	44	93.6	168	3	AAg20217	AAg20217	Arabidops
401	44	93.6	122	2	AAy70481	AAy70481	Protein f	474	44	93.6	169	4	AAg83359	AAg83359	P patens
402	44	93.6	122	3	AAy70479	AAy70479	Arabidops	475	44	93.6	169	4	AAg80909	AAg80909	Co-fact
403	44	93.6	122	3	AAy70479	AAy70479	Arabidops	476	44	93.6	169	5	ABP60682	ABP60682	Phaseolin
404	44	93.6	122	3	AAy70479	AAy70479	Arabidops	477	44	93.6	172	5	ABP60718	ABP60718	Pisum sat
405	44	93.6	122	5	ABP60740	ABP60740	Rice thio	478	44	93.6	172	5	ABP60717	ABP60717	Oryza sat
406	44	93.6	122	7	AAE39220	AAE39220	Oryza sat	479	44	93.6	172	7	ABM87854	ABM87854	Rice abio
407	44	93.6	122	7	AAE39220	AAE39220	Barley th	480	44	93.6	172	8	ADM32941	ADM32941	Amino aci
408	44	93.6	122	7	AAE39223	AAE39223	Barley H-	481	44	93.6	173	3	AAg45018	AAg45018	Zea mays
409	44	93.6	122	7	ADOS9272	ADOS9272	Rice thio	482	44	93.6	173	5	ABP60712	ABP60712	Arabidops
410	44	93.6	123	3	AAy70482	AAy70482	Glycine m	483	44	93.6	175	5	ABP60720	ABP60720	Triticum
411	44	93.6	123	3	AAy70482	AAy70482	Zea mays	484	44	93.6	175	5	ABP60817	ABP60817	Arabidops
412	44	93.6	123	4	AAy70482	AAy70482	Wheat Tat	485	44	93.6	175	8	ADY88193	ADY88193	Arabidops
413	44	93.6	123	5	ABP65992	ABP65992	Blifidbac	486	44	93.6	177	8	ADY90870	ADY90870	Brevibaci
414	44	93.6	124	5	ABP78905	ABP78905	C. glutam	487	44	93.6	179	8	ADY06451	ADY06451	Plant ful
415	44	93.6	125	3	AAy70482	AAy70482	Arabidops	488	44	93.6	179	8	ADY10996	ADY10996	Plant ful
416	44	93.6	125	5	ABP60741	ABP60741	Picea mar	489	44	93.6	180	8	ADY78704	ADY78704	Plant ful
417	44	93.6	125	7	ADOS9273	ADOS9273	Wheat thi	490	44	93.6	180	8	ADY89807	ADY89807	Plant ful
418	44	93.6	125	5	ABM95048	ABM95048	M. xanthu	491	44	93.6	180	8	ADY10998	ADY10998	Plant ful
419	44	93.6	126	5	ABP60743	ABP60743	Triticum	492	44	93.6	182	8	ADY11259	ADY11259	Plant ful
420	44	93.6	126	5	ABP60730	ABP60730	Nicotiana	493	44	93.6	183	3	ABM95783	ABM95783	M. xanthu
421	44	93.6	126	7	ADOS9275	ADOS9275	Tobacco t	494	44	93.6	185	4	AAg80918	AAg80918	Thioredux
422	44	93.6	127	2	AAy70482	AAy70482	Soft whea	495	44	93.6	193	3	AAg37884	AAg37884	Arabidops
423	44	93.6	127	3	AAy70482	AAy70482	Wheat thi	496	44	93.6	193	5	AAg60713	AAg60713	Arabidops
424	44	93.6	127	3	AAy70482	AAy70482	Arabidops	497	44	93.6	194	3	AAg24095	AAg24095	Arabidops
425	44	93.6	127	3	AAy70482	AAy70482	Arabidops	498	44	93.6	194	3	AAg32511	AAg32511	Arabidops
426	44	93.6	130	2	AAy70482	AAy70482	Hard whea	499	44	93.6	194	3	AAg47218	AAg47218	Arabidops
427	44	93.6	130	3	AAy70482	AAy70482	Wheat thi	500	44	93.6	197	8	ADY67695	ADY67695	Novel hum
428	44	93.6	131	4	AAy70482	AAy70482	P. patens	501	44	93.6	203	3	AAy70482	AAy70482	Arabidops
429	44	93.6	131	4	AAy70482	AAy70482	Co-factor	502	44	93.6	204	8	ADY77747	ADY77747	Plant ful
430	44	93.6	131	5	ABP60844	ABP60844	Phalaris	503	44	93.6	209	6	ABP80992	ABP80992	N. gonorr
431	44	93.6	131	5	ABP60821	ABP60821	Hordeum b	504	44	93.6	216	8	ADY10550	ADY10550	Plant ful
432	44	93.6	131	5	ABP60822	ABP60822	Oryza sat	505	44	93.6	217	3	AAy70482	AAy70482	Arabidops
433	44	93.6	131	5	ABP60823	ABP60823	Secale ce	506	44	93.6	217	3	AAy70482	AAy70482	Arabidops
434	44	93.6	131	5	ABP60825	ABP60825	DNA clone	507	44	93.6	222	5	ABP60683	ABP60683	Phaseolin
435	44	93.6	131	7	ABM74315	ABM74315	Arabidops	508	44	93.6	228	3	AAy70482	AAy70482	Arabidops
436	44	93.6	133	5	AAy70482	AAy70482	Arabidops	509	44	93.6	228	8	ADY54556	ADY54556	Human PRO
437	44	93.6	133	5	AAy70482	AAy70482	Arabidops	510	44	93.6	268	9	ADY15510	ADY15510	PRO polyp
438	44	93.6	133	8	ADY06180	ADY06180	Plant ful	511	44	93.6	268	9	ADY15512	ADY15512	PRO polyp
439	44	93.6	134	3	AAy70482	AAy70482	Amino aci	512	44	93.6	268	9	AAy70482	AAy70482	Arabidops
440	44	93.6	134	3	AAy70482	AAy70482	Amino aci	513	44	93.6	284	3	AAy70482	AAy70482	Arabidops
441	44	93.6	136	8	ADY06635	ADY06635	Plant ful	514	44	93.6	284	5	ABG32919	ABG32919	Thioredux
442	44	93.6	137	8	ADY09660	ADY09660	Plant ful	515	44	93.6	287	5	ABG32917	ABG32917	Oleostri-t
443	44	93.6	137	8	ADY09660	ADY09660	Plant ful	516	44	93.6	306	3	AAy70482	AAy70482	Arabidops
444	44	93.6	137	8	ADY09660	ADY09660	Plant ful	517	44	93.6	306	3	AAy70482	AAy70482	Arabidops
445	44	93.6	137	8	ADY09660	ADY09660	Plant ful	518	44	93.6	306	3	AAy70482	AAy70482	Arabidops
446	44	93.6	137	8	ADY09660	ADY09660	Plant ful	519	44	93.6	306	3	AAy70482	AAy70482	Arabidops
447	44	93.6	139	5	ABP60710	ABP60710	Escherich	520	44	93.6	306	3	AAy70482	AAy70482	Arabidops
448	44	93.6	139	5	ABP60710	ABP60710	Escherich	521	44	93.6	379	3	AAy70482	AAy70482	Arabidops
449	44	93.6	139	5	ABP60710	ABP60710	Escherich	522	44	93.6	380	3	AAy70482	AAy70482	Arabidops
450	44	93.6	140	5	ABP60715	ABP60715	Chlamydom	523	44	93.6	380	3	AAy70482	AAy70482	Arabidops
451	44	93.6	140	8	ADY04782	ADY04782	Plant ful	524	44	93.6	380	3	AAy70482	AAy70482	Arabidops
452	44	93.6	141	8	ADY04782	ADY04782	Plant ful	525	44	93.6	399	3	AAy70482	AAy70482	Arabidops
453	44	93.6	141	8	ADY04782	ADY04782	Plant ful	526	44	93.6	399	3	AAy70482	AAy70482	Arabidops
454	44	93.6	141	8	ADY04782	ADY04782	Plant ful	527	44	93.6	445	8	ADY04782	ADY04782	Plant ful
455	44	93.6	141	8	ADY04782	ADY04782	Plant ful	528	44	93.6	446	8	ADY04782	ADY04782	Plant ful
456	44	93.6	144	3	AAy70482	AAy70482	Arabidops	529	44	93.6	446	8	ADY04782	ADY04782	Plant ful
457	44	93.6	144	3	AAy70482	AAy70482	Arabidops	530	44	93.6	447	8	ADY04782	ADY04782	Plant ful
458	44	93.6	144	8	ADY09659	ADY09659	Plant ful	531	44	93.6	469	7	ADY09659	ADY09659	Plant ful
459	44	93.6	149	8	ADY09659	ADY09659	Plant ful	532	44	93.6	471	7	ADY09659	ADY09659	Plant ful
460	44	93.6	150	8	ADY09659	ADY09659	Plant ful	533	44	93.6	483	7	ADY09659	ADY09659	Plant ful
461	44	93.6	151	3	AAy70482	AAy70482	Zea mays	534	44	93.6	486	5	AAE23036	AAE23036	Human Tcf
462	44	93.6	151	8	ADY09659	ADY09659	Brevibaci	535	44	93.6	511	2	AAy70482	AAy70482	Human Tcf

536	44	93.6	511	4	AA72784	AA72784	Transcrip	609	43	91.5	747	6	ADA2498	ADA2498	Novel hum
537	44	93.6	518	7	ABP60693	ABP60693	Promoter-	610	43	91.5	747	6	ADB18875	ADB18875	Novel hum
538	44	93.6	553	5	ADM05890	ADM05890	Human pro	611	43	91.5	747	6	ADA94090	ADA94090	Human pro
539	44	93.6	553	9	AEA20430	AEA20430	Novel hum	612	43	91.5	747	6	ADB19986	ADB19986	Novel hum
540	44	93.6	588	2	AD69101	AD69101	Human hea	613	43	91.5	747	6	ADB13298	ADB13298	Human pro
541	44	93.6	596	2	AAW76820	AAW76820	Human Tcf	614	43	91.5	747	6	ABO43361	ABO43361	Novel hum
542	44	93.6	596	2	AAZ28991	AAZ28991	Human Tcf	615	43	91.5	747	6	ABO19715	ABO19715	Novel hum
543	44	93.6	596	3	AA70303	AA70303	Human Tcf	616	43	91.5	747	6	ADA12659	ADA12659	Human sec
544	44	93.6	596	4	AA72781	AA72781	Human Tcf	617	43	91.5	747	6	ADA74552	ADA74552	Human pro
545	44	93.6	596	7	AD880717	AD880717	Microsate	618	43	91.5	747	6	ADB24785	ADB24785	Human pro
546	44	93.6	596	8	AD028615	AD028615	Human TCF	619	43	91.5	747	6	ADA82309	ADA82309	Human pro
547	44	93.6	596	9	ADX05781	ADX05781	Cyclin-de	620	43	91.5	747	6	ADA75272	ADA75272	Human pro
548	44	93.6	596	9	ADZ70379	ADZ70379	Human pro	621	43	91.5	747	6	ADA85350	ADA85350	Novel hum
549	44	93.6	596	9	AEBS6496	AEBS6496	Radiochem	622	43	91.5	747	6	ADA84798	ADA84798	Human pro
550	44	93.6	602	8	AD017203	AD017203	Human sof	623	43	91.5	747	6	ADB30054	ADB30054	Human pro
551	44	93.6	678	8	ADX97589	ADX97589	Pancreati	624	43	91.5	747	6	ADA80582	ADA80582	Human pro
552	43	91.5	105	5	ABPE0835	ABPE0835	Synechocy	625	43	91.5	747	6	ADA75824	ADA75824	Human pro
553	43	91.5	105	5	ABPE0769	ABPE0769	Synechocy	626	43	91.5	747	6	ADA47049	ADA47049	Human pro
554	43	91.5	110	5	ABPE0728	ABPE0728	Anabaena	627	43	91.5	747	6	ADB25345	ADB25345	Human pro
555	43	91.5	126	8	AD039499	AD039499	Human myo	628	43	91.5	747	6	ADA93521	ADA93521	Human pro
556	43	91.5	147	6	ABMS2316	ABMS2316	Propionib	629	43	91.5	747	6	ADB26871	ADB26871	Human pro
557	43	91.5	147	6	ABMS2316	ABMS2316	Propionib	630	43	91.5	747	6	ADB31158	ADB31158	Human pro
558	43	91.5	151	5	ABPE0819	ABPE0819	Arabi-dops	631	43	91.5	747	6	ADA61086	ADA61086	Human pro
559	43	91.5	177	8	ADX71846	ADX71846	Plant ful	632	43	91.5	747	6	ADB24233	ADB24233	Human pro
560	43	91.5	277	4	AAW93406	AAW93406	Human pol	633	43	91.5	747	6	ADA96562	ADA96562	Human pro
561	43	91.5	277	5	ABP43696	ABP43696	Human ISO	634	43	91.5	747	6	ADA81134	ADA81134	Human pro
562	43	91.5	327	8	ADL30979	ADL30979	Human pro	635	43	91.5	747	6	ADA96010	ADA96010	Human pro
563	43	91.5	327	5	ABP73990	ABP73990	Candida a	636	43	91.5	747	6	ADB26319	ADB26319	Human pro
564	43	91.5	446	3	AAZ24650	AAZ24650	Arabi-dops	637	43	91.5	747	6	ADB21804	ADB21804	Novel hum
565	43	91.5	459	4	ABG18066	ABG18066	Novel hum	638	43	91.5	747	6	ABO19606	ABO19606	Novel hum
566	43	91.5	470	3	AAZ24649	AAZ24649	Arabi-dops	639	43	91.5	747	6	ADA77583	ADA77583	Human pro
567	43	91.5	512	7	ADM65853	ADM65853	Tyrosine	640	43	91.5	747	7	ADB18323	ADB18323	Human pro
568	43	91.5	578	3	AAZ24898	AAZ24898	Arabi-dops	641	43	91.5	747	7	ADA87006	ADA87006	Novel hum
569	43	91.5	601	3	AAZ24898	AAZ24898	Arabi-dops	642	43	91.5	747	7	ADA88109	ADA88109	Novel hum
570	43	91.5	612	4	AAZ24898	AAZ24898	Arabi-dops	643	43	91.5	747	7	ADA86497	ADA86497	Novel hum
571	43	91.5	644	3	AAZ24898	AAZ24898	Arabi-dops	644	43	91.5	747	7	ADA828527	ADA828527	Human pro
572	43	91.5	706	4	ABZ66693	ABZ66693	Drosophil	645	43	91.5	747	7	ADB29079	ADB29079	Human pro
573	43	91.5	747	2	AAZ41758	AAZ41758	Human pro	646	43	91.5	747	7	ADA77031	ADA77031	Human pro
574	43	91.5	747	3	AAZ44314	AAZ44314	Human pro	647	43	91.5	747	7	ADA88661	ADA88661	Novel hum
575	43	91.5	747	4	AAZ12384	AAZ12384	Human pro	648	43	91.5	747	7	ADA97666	ADA97666	Human pro
576	43	91.5	747	5	ABZ84873	ABZ84873	Human pro	649	43	91.5	747	7	ADB27423	ADB27423	Human pro
577	43	91.5	747	5	AAZ20464	AAZ20464	Human tum	650	43	91.5	747	7	ADB22356	ADB22356	Novel hum
578	43	91.5	747	5	ABZ95479	ABZ95479	Human ang	651	43	91.5	747	7	ADA67047	ADA67047	Human pro
579	43	91.5	747	6	ABO17828	ABO17828	Novel hum	652	43	91.5	747	7	ADA22908	ADA22908	Human pro
580	43	91.5	747	6	ABO25260	ABO25260	Novel hum	653	43	91.5	747	7	ADB23681	ADB23681	Human pro
581	43	91.5	747	6	ABO81082	ABO81082	Human pro	654	43	91.5	747	7	ADB24203	ADB24203	Human pro
582	43	91.5	747	6	ABU72266	ABU72266	Novel hum	655	43	91.5	747	7	ADB15466	ADB15466	Human pro
583	43	91.5	747	6	ABU6782	ABU6782	Human pro	656	43	91.5	747	7	ADB38718	ADB38718	Novel hum
584	43	91.5	747	6	ABU84946	ABU84946	Human sec	657	43	91.5	747	7	ADB38166	ADB38166	Novel hum
585	43	91.5	747	6	ABU59863	ABU59863	Novel sec	658	43	91.5	747	7	ADB66638	ADB66638	Novel hum
586	43	91.5	747	6	ABU61144	ABU61144	Human pro	659	43	91.5	747	7	ADB89718	ADB89718	Human pro
587	43	91.5	747	6	ABO25053	ABO25053	Human sec	660	43	91.5	747	7	ADB90450	ADB90450	Human pro
588	43	91.5	747	6	ABU80413	ABU80413	Human sec	661	43	91.5	747	7	ADB39551	ADB39551	Novel hum
589	43	91.5	747	6	ABG75950	ABG75950	Human ant	662	43	91.5	747	7	ADB73965	ADB73965	Human pro
590	43	91.5	747	6	ABU67058	ABU67058	Human sec	663	43	91.5	747	7	ADB47174	ADB47174	Novel hum
591	43	91.5	747	6	ADA5945	ADA5945	Novel hum	664	43	91.5	747	7	ADB86781	ADB86781	Human pro
592	43	91.5	747	6	ADA76376	ADA76376	Human pro	665	43	91.5	747	7	ADB76681	ADB76681	Human pro
593	43	91.5	747	6	ADA19026	ADA19026	Human pro	666	43	91.5	747	7	ADB77386	ADB77386	Novel hum
594	43	91.5	747	6	ADA61649	ADA61649	Homo sapi	667	43	91.5	747	7	ADB34543	ADB34543	Human pro
595	43	91.5	747	6	ADB19434	ADB19434	Novel hum	668	43	91.5	747	7	ADB35647	ADB35647	Human pro
596	43	91.5	747	6	ADB27975	ADB27975	Human pro	669	43	91.5	747	7	ADB33391	ADB33391	Human pro
597	43	91.5	747	6	ADA86454	ADA86454	Novel hum	670	43	91.5	747	7	ADB35095	ADB35095	Human pro
598	43	91.5	747	6	ADA66018	ADA66018	Human pro	671	43	91.5	747	7	ADB36199	ADB36199	Human pro
599	43	91.5	747	6	ADA47804	ADA47804	Human pro	672	43	91.5	747	7	ADA66594	ADA66594	Novel hum
600	43	91.5	747	6	ADA67599	ADA67599	Human pro	673	43	91.5	747	7	ADA44107	ADA44107	Human sec
601	43	91.5	747	6	ADA30606	ADA30606	Human pro	674	43	91.5	747	7	ADA61867	ADA61867	Human sec
602	43	91.5	747	6	ADA85902	ADA85902	Novel hum	675	43	91.5	747	7	ADA63831	ADA63831	Human sec
603	43	91.5	747	6	ADA97114	ADA97114	Human pro	676	43	91.5	747	7	ADA66931	ADA66931	Human sec
604	43	91.5	747	6	ADA79418	ADA79418	Human pro	677	43	91.5	747	7	ADA69055	ADA69055	Human sec
605	43	91.5	747	6	ADA87557	ADA87557	Novel hum	678	43	91.5	747	7	ADA63115	ADA63115	Human sec
606	43	91.5	747	6	ADA816759	ADA816759	Human pro	679	43	91.5	747	7	ADA68180	ADA68180	Human sec
607	43	91.5	747	6	ADA91851	ADA91851	Novel hum	680	43	91.5	747	7	ADA41500	ADA41500	Human sec
608	43	91.5	747	6	ADA14914	ADA14914	Human pro	681	43	91.5	747	7	ADA67555	ADA67555	Human sec

682	43	91.5	747	7	AD62491	Human	sec	755	43	91.5	747	7	AD680616	Ad680616	Human	PRO
683	43	91.5	747	7	AD642124	Human	sec	756	43	91.5	747	7	AD653056	Ad653056	Human	sec
684	43	91.5	747	7	AD650467	Human	sec	757	43	91.5	747	7	AD660376	Ad660376	Human	sec
685	43	91.5	747	7	AD672014	Novel	hum	758	43	91.5	747	7	AD680064	Ad680064	Human	PRO
686	43	91.5	747	7	AD659993	Novel	hum	759	43	91.5	747	7	AD685356	Ad685356	Novel	hum
687	43	91.5	747	7	AD653000	Novel	hum	760	43	91.5	747	7	AD685908	Ad685908	Novel	hum
688	43	91.5	747	7	AD657354	Novel	hum	761	43	91.5	747	7	AD681136	Ad681136	Human	sec
689	43	91.5	747	7	AD656545	Novel	hum	762	43	91.5	747	7	AD616127	Ad616127	Novel	hum
690	43	91.5	747	7	AD651020	Novel	hum	763	43	91.5	747	7	AD650076	Ad650076	Novel	hum
691	43	91.5	747	7	AD655547	Human	PRO	764	43	91.5	747	7	AD616357	Ad616357	Novel	hum
692	43	91.5	747	7	AD654645	Novel	hum	765	43	91.5	747	7	AD681999	Ad681999	Novel	hum
693	43	91.5	747	7	AD653606	Novel	hum	766	43	91.5	747	7	AD681437	Ad681437	Novel	hum
694	43	91.5	747	7	AD659129	Novel	hum	767	43	91.5	747	7	AD682606	Ad682606	Novel	hum
695	43	91.5	747	7	AD656007	Novel	hum	768	43	91.5	747	7	AD616005	Ad616005	Novel	hum
696	43	91.5	747	7	AD658577	Novel	hum	769	43	91.5	747	7	AD616634	Ad616634	Novel	hum
697	43	91.5	747	7	AD603251	Novel	hum	770	43	91.5	747	7	AD615453	Ad615453	Novel	hum
698	43	91.5	747	7	AD690243	Novel	hum	771	43	91.5	747	7	AD614901	Ad614901	Novel	hum
699	43	91.5	747	7	AD669662	Human	PRO	772	43	91.5	747	8	AD681163	Ad681163	Novel	hum
700	43	91.5	747	7	AD648551	Human	PRO	773	43	91.5	747	8	AD676611	Ad676611	Human	PRO
701	43	91.5	747	7	AD610080	Human	PRO	774	43	91.5	747	8	AD687975	Ad687975	Human	PRO
702	43	91.5	747	7	AD604655	Novel	hum	775	43	91.5	747	8	AD686379	Ad686379	Human	PRO
703	43	91.5	747	7	AD680611	Novel	hum	776	43	91.5	747	8	AD675827	Ad675827	Human	PRO
704	43	91.5	747	7	AD611118	Human	PRO	777	43	91.5	747	8	AD684873	Ad684873	Human	sec
705	43	91.5	747	7	AD610403	Human	sec	778	43	91.5	747	8	AD681364	Ad681364	Human	sec
706	43	91.5	747	7	AD647999	Human	PRO	779	43	91.5	747	8	AD623403	Ad623403	Human	PRO
707	43	91.5	747	7	AD680059	Novel	hum	780	43	91.5	747	8	AD623955	Ad623955	Human	PRO
708	43	91.5	747	7	AD611363	Human	sec	781	43	91.5	747	8	AD624598	Ad624598	Human	PRO
709	43	91.5	747	7	AD609528	Human	PRO	782	43	91.5	747	8	AD687423	Ad687423	Human	PRO
710	43	91.5	747	7	AD641241	Novel	hum	783	43	91.5	747	8	AD689289	Ad689289	Human	PRO
711	43	91.5	747	7	AD652380	Human	PRO	784	43	91.5	747	8	AD681842	Ad681842	Human	PRO
712	43	91.5	747	7	AD653120	Human	PRO	785	43	91.5	747	8	AD688737	Ad688737	Human	PRO
713	43	91.5	747	7	AD653672	Novel	hum	786	43	91.5	747	8	AD689894	Ad689894	Human	sec
714	43	91.5	747	7	AD637156	Human	sec	787	43	91.5	747	8	AD661534	Ad661534	Human	sec
715	43	91.5	747	7	AD651828	Human	PRO	788	43	91.5	747	8	AD646026	Ad646026	Human	sec
716	43	91.5	747	7	AD602627	Human	PRO	789	43	91.5	747	8	AD646026	Ad646026	Human	sec
717	43	91.5	747	7	AD602061	Human	PRO	790	43	91.5	747	8	AD684757	Ad684757	Human	PRO
718	43	91.5	747	7	AD654243	Novel	hum	791	43	91.5	747	8	AD689168	Ad689168	Human	PRO
719	43	91.5	747	7	AD649493	Human	sec	792	43	91.5	747	8	AD689530	Ad689530	Human	PRO
720	43	91.5	747	7	AD692560	Human	PRO	793	43	91.5	747	8	AD689349	Ad689349	Human	PRO
721	43	91.5	747	7	AD691456	Human	PRO	794	43	91.5	747	8	AD624418	Ad624418	Human	sec
722	43	91.5	747	7	AD680470	Human	PRO	795	43	91.5	747	8	AD640850	Ad640850	Human	sec
723	43	91.5	747	7	AD632367	Novel	hum	796	43	91.5	747	8	AD623794	Ad623794	Human	sec
724	43	91.5	747	7	AD622299	Human	PRO	797	43	91.5	747	8	AD633777	Ad633777	Human	sec
725	43	91.5	747	7	AD679523	Human	PRO	798	43	91.5	747	8	AD635000	Ad635000	Human	PRO
726	43	91.5	747	7	AD635547	Human	sec	799	43	91.5	747	8	AD627244	Ad627244	Human	sec
727	43	91.5	747	7	AD616661	Human	sec	800	43	91.5	747	8	AD627880	Ad627880	Human	sec
728	43	91.5	747	7	AD617327	Human	sec	801	43	91.5	747	8	AD682315	Ad682315	Novel	hum
729	43	91.5	747	7	AD642059	Human	PRO	802	43	91.5	747	8	AD685066	Ad685066	Human	PRO
730	43	91.5	747	7	AD617876	Human	PRO	803	43	91.5	747	8	AD641474	Ad641474	Human	sec
731	43	91.5	747	7	AD692008	Human	PRO	804	43	91.5	747	8	AD633153	Ad633153	Human	sec
732	43	91.5	747	7	AD633471	Novel	hum	805	43	91.5	747	8	AD625519	Ad625519	Human	sec
733	43	91.5	747	7	AD634023	Novel	hum	806	43	91.5	747	8	AD626620	Ad626620	Human	sec
734	43	91.5	747	7	AD680075	Human	PRO	807	43	91.5	747	8	AD634409	Ad634409	Human	sec
735	43	91.5	747	7	AD693112	Human	PRO	808	43	91.5	747	8	AD646646	Ad646646	Human	sec
736	43	91.5	747	7	AD672634	Human	sec	809	43	91.5	747	8	AD689176	Ad689176	Novel	hum
737	43	91.5	747	7	AD619532	Human	PRO	810	43	91.5	747	8	AD630234	Ad630234	Human	PRO
738	43	91.5	747	7	AD618980	Human	PRO	811	43	91.5	747	8	AD622128	Ad622128	Novel	hum
739	43	91.5	747	7	AD643176	Human	PRO	812	43	91.5	747	8	AD620198	Ad620198	Human	PRO
740	43	91.5	747	7	AD695965	Human	PRO	813	43	91.5	747	8	AD6898104	Ad6898104	Human	PRO
741	43	91.5	747	7	AD622851	Human	PRO	814	43	91.5	747	8	AD624321	Ad624321	Novel	hum
742	43	91.5	747	7	AD678969	Human	PRO	815	43	91.5	747	8	AD698675	Ad698675	Human	PRO
743	43	91.5	747	7	AD632919	Novel	hum	816	43	91.5	747	8	AD630350	Ad630350	Human	PRO
744	43	91.5	747	7	AD642611	Human	PRO	817	43	91.5	747	8	AD699227	Ad699227	Human	PRO
745	43	91.5	747	7	AD617285	Human	sec	818	43	91.5	747	8	AD616812	Ad616812	Human	PRO
746	43	91.5	747	7	AD680627	Human	PRO	819	43	91.5	747	8	AD6305271	Ad6305271	Human	PRO
747	43	91.5	747	7	AD689655	Human	PRO	820	43	91.5	747	8	AD6919538	Ad6919538	Human	PRO
748	43	91.5	747	7	AD640939	Human	PRO	821	43	91.5	747	8	AD693375	Ad693375	Human	PRO
749	43	91.5	747	7	AD604738	Human	PRO	822	43	91.5	747	8	AD6308432	Ad6308432	Novel	hum
750	43	91.5	747	7	AD692867	Human	PRO	823	43	91.5	747	8	AD6915602	Ad6915602	Human	PRO
751	43	91.5	747	7	AD647299	Human	sec	824	43	91.5	747	8	AD697000	Ad697000	Human	PRO
752	43	91.5	747	7	AD621576	Novel	hum	825	43	91.5	747	8	AD6906185	Ad6906185	Human	PRO
753	43	91.5	747	7	AD623217	Novel	hum	826	43	91.5	747	8	AD623769	Ad623769	Novel	hum
754	43	91.5	747	7	AD697552	Human	PRO	827	43	91.5	747	8	AD6304058	Ad6304058	Human	PRO

828	43	91.5	747	8	ADG24959	Adg24959	Novel	hum	901	42	89.4	62	4	AAU58028	AAU58028	Propionib
829	43	91.5	747	8	ADG07256	Adg07256	Novel	hum	902	42	89.4	62	6	ABM62346	ABM62346	Propionib
830	43	91.5	747	8	ADG07808	Adg07808	Novel	hum	903	42	89.4	62	6	ABM54547	ABM54547	Propionib
831	43	91.5	747	8	ADG55303	Adg55303	Novel	hum	904	42	89.4	71	3	AAI12496	AAI12496	Zea may
832	43	91.5	747	8	ADG60967	Adg60967	Novel	hum	905	42	89.4	71	3	AAI60135	AAI60135	Zea may
833	43	91.5	747	8	ADG62071	Adg62071	Novel	hum	906	42	89.4	81	3	AAI12495	AAI12495	Zea may
834	43	91.5	747	8	ADG82272	Adg82272	Novel	hum	907	42	89.4	84	9	ADY66554	ADY66554	S. mansoni
835	43	91.5	747	8	ADG57511	Adg57511	Novel	hum	908	42	89.4	93	3	AAI60134	AAI60134	Zea may
836	43	91.5	747	8	ADG56959	Adg56959	Novel	hum	909	42	89.4	94	4	ADG27717	ADG27717	Human nov
837	43	91.5	747	8	ADG55855	Adg55855	Novel	hum	910	42	89.4	103	3	AAI60133	AAI60133	Zea may
838	43	91.5	747	8	ADG58615	Adg58615	Novel	hum	911	42	89.4	108	5	ABP60752	ABP60752	Chlorobiu
839	43	91.5	747	8	ADG70981	Adg70981	Novel	hum	912	42	89.4	110	6	AAU56505	AAU56505	Propionib
840	43	91.5	747	8	ADG58063	Adg58063	Novel	hum	913	42	89.4	110	6	AAU56505	AAU56505	Propionib
841	43	91.5	747	8	ADG53647	Adg53647	Novel	hum	914	42	89.4	111	3	AAI12494	AAI12494	Zea may
842	43	91.5	747	8	ADG71533	Adg71533	Novel	hum	915	42	89.4	139	4	ABP68209	ABP68209	Drosophil
843	43	91.5	747	8	ADG50632	Adg50632	Novel	hum	916	42	89.4	169	9	ABM91297	ABM91297	M. xanthu
844	43	91.5	747	8	ADG81720	Adg81720	Novel	hum	917	42	89.4	174	7	ADY74512	ADY74512	Mycobacte
845	43	91.5	747	8	ADH30682	Adh30682	Novel	hum	918	42	89.4	183	3	AAI11492	AAI11492	Arabidops
846	43	91.5	747	8	ADH12049	Adh12049	Novel	hum	919	42	89.4	183	5	ABP99365	ABP99365	Arabidops
847	43	91.5	747	8	ADG50008	Adg50008	Novel	hum	920	42	89.4	193	3	AAI11491	AAI11491	Arabidops
848	43	91.5	747	8	ADG51880	Adg51880	Novel	hum	921	42	89.4	201	8	ADY72965	ADY72965	Plant ful
849	43	91.5	747	8	ADG52471	Adg52471	Novel	hum	922	42	89.4	217	8	ADY07461	ADY07461	Plant ful
850	43	91.5	747	8	ADG54139	Adg54139	Novel	hum	923	42	89.4	372	8	ADY72752	ADY72752	Plant ful
851	43	91.5	747	8	ADG49384	Adg49384	Novel	hum	924	42	89.4	382	1	ADY10333	ADY10333	Plant ful
852	43	91.5	747	8	ADG81168	Adg81168	Novel	hum	925	42	89.4	432	1	AAI92149	AAI92149	Large env
853	43	91.5	747	8	ADG56407	Adg56407	Novel	hum	926	42	89.4	432	1	AAI92148	AAI92148	Large env
854	43	91.5	747	8	ADH12673	Adh12673	Novel	hum	927	42	89.4	459	2	AAI28890	AAI28890	Mouse Tcf
855	43	91.5	747	8	ADG48760	Adg48760	Novel	hum	928	42	89.4	459	5	AAI99985	AAI99985	Murine T-
856	43	91.5	747	8	ADG61519	Adg61519	Novel	hum	929	42	89.4	525	3	AAI25294	AAI25294	Bucalypcu
857	43	91.5	747	8	ADH28606	Adh28606	Novel	hum	930	42	89.4	553	3	AAI97403	AAI97403	Human apo
858	43	91.5	747	8	ADG54751	Adg54751	Novel	hum	931	42	89.4	606	4	AAI69121	AAI69121	Arabidops
859	43	91.5	747	8	ADG59791	Adg59791	Novel	hum	932	42	89.4	662	2	AAI68401	AAI68401	FelV-B en
860	43	91.5	747	8	ADG51256	Adg51256	Novel	hum	933	41	87.2	45	4	ABP66271	ABP66271	Drosophil
861	43	91.5	747	8	ADH43547	Adh43547	Novel	hum	934	41	87.2	65	5	ABP60608	ABP60608	Human ORF
862	43	91.5	747	8	ADG59200	Adg59200	Novel	hum	935	41	87.2	107	5	ABP60758	ABP60758	Corynebac
863	43	91.5	747	8	ADG62656	Adg62656	Novel	hum	936	41	87.2	108	5	ABP60751	ABP60751	Buchnera
864	43	91.5	747	8	ADH181215	Adh181215	Novel	hum	937	41	87.2	108	5	ABP60750	ABP60750	Buchnera
865	43	91.5	747	8	ADH25681	Adh25681	Novel	neu	938	41	87.2	120	9	ABP40665	ABP40665	L. pneumo
866	43	91.5	747	8	ADG09958	Adg09958	Novel	hum	939	41	87.2	120	9	ABP37345	ABP37345	L. pneumo
867	43	91.5	747	8	ADH15429	Adh15429	Novel	hum	940	41	87.2	126	6	ADP36599	ADP36599	Actinecto
868	43	91.5	747	8	ADG09306	Adg09306	Novel	hum	941	41	87.2	142	4	ABP64146	ABP64146	Actinecto
869	43	91.5	747	8	ADH114761	Adh114761	Novel	hum	942	41	87.2	188	4	AAU39188	AAU39188	Propionib
870	43	91.5	747	8	ADH18336	Adh18336	Novel	hum	943	41	87.2	188	6	ABM35707	ABM35707	Propionib
871	43	91.5	747	8	ADJ63637	Adj63637	Novel	hum	944	41	87.2	353	7	ABO77648	ABO77648	Pseudomon
872	43	91.5	747	8	ADJ77532	Adj77532	Novel	hum	945	40	85.1	160	4	ABP60122	ABP60122	Drosophil
873	43	91.5	747	8	ADK82892	Adk82892	Novel	hum	946	39	83.0	103	5	ABP48767	ABP48767	Listeria
874	43	91.5	747	8	ADJ65654	Adj65654	Novel	hum	947	39	83.0	105	5	ABP60796	ABP60796	Treponema
875	43	91.5	747	8	ADM27790	Adm27790	Novel	hum	948	39	83.0	112	5	AAU83688	AAU83688	Human PRO
876	43	91.5	747	8	ADM17458	Adm17458	Novel	hum	949	39	83.0	161	9	ABM92721	ABM92721	M. xanthu
877	43	91.5	747	8	ADL07292	Adl07292	Novel	hum	950	39	83.0	165	7	ADG36909	ADG36909	B. subtil
878	43	91.5	747	8	ADM42514	Adm42514	Novel	hum	951	39	83.0	172	2	AAI80812	AAI80812	Amino aci
879	43	91.5	747	8	ADM28376	Adm28376	Novel	hum	952	39	83.0	172	2	AAI37845	AAI37845	Human XAG
880	43	91.5	747	8	ADJ195858	Adj195858	Novel	hum	953	39	83.0	172	2	AAI03237	AAI03237	Human XAG
881	43	91.5	747	8	ADJ196410	Adj196410	Novel	hum	954	39	83.0	172	2	AAI03236	AAI03236	Human XAG
882	43	91.5	747	8	ADG32362	Adg32362	Novel	hum	955	39	83.0	172	2	AAI03236	AAI03236	Human XAG
883	43	91.5	747	8	ADG32362	Adg32362	Novel	hum	956	39	83.0	172	2	AAI03236	AAI03236	Human XAG
884	43	91.5	747	8	ADU50414	Adu50414	Novel	hum	957	39	83.0	172	3	AAI24432	AAI24432	Human PRO
885	43	91.5	747	8	ADU50414	Adu50414	Novel	hum	958	39	83.0	172	3	AAI24432	AAI24432	Human PRO
886	43	91.5	747	8	ADM49663	Adm49663	Novel	hum	959	39	83.0	172	4	AAI24432	AAI24432	Human PRO
887	43	91.5	747	8	ADZ03337	Adz03337	Novel	hum	960	39	83.0	172	4	AAI24432	AAI24432	Human PRO
888	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	961	39	83.0	172	5	ABP84930	ABP84930	Human PRO
889	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	962	39	83.0	172	5	ABP84930	ABP84930	Human PRO
890	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	963	39	83.0	172	5	ABP84930	ABP84930	Human PRO
891	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	964	39	83.0	172	5	ABP84930	ABP84930	Human PRO
892	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	965	39	83.0	172	6	ABP84930	ABP84930	Human PRO
893	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	966	39	83.0	172	6	ABP84930	ABP84930	Human PRO
894	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	967	39	83.0	172	6	ABP84930	ABP84930	Human PRO
895	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	968	39	83.0	172	6	ABP84930	ABP84930	Human PRO
896	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	969	39	83.0	172	6	ABP84930	ABP84930	Human PRO
897	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	970	39	83.0	172	6	ABP84930	ABP84930	Human PRO
898	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	971	39	83.0	172	7	ABP84930	ABP84930	Human PRO
899	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	972	39	83.0	172	7	ABP84930	ABP84930	Human PRO
900	43	91.5	747	8	ADZ52354	Adz52354	Novel	hum	973	39	83.0	172	7	ABP84930	ABP84930	Human PRO

974	39	83.0	172	7	ADB73331	Adb73331	Novel	hum
975	39	83.0	172	7	ADB78413	Adb78413	Novel	hum
976	39	83.0	172	7	ADB85061	Adb85061	Human	PRO
977	39	83.0	172	7	ADB78167	Adb78167	Novel	hum
978	39	83.0	172	7	ADB87233	Adb87233	Human	PRO
979	39	83.0	172	7	ADB84815	Adb84815	Human	PRO
980	39	83.0	172	7	ADB83930	Adb83930	Novel	hum
981	39	83.0	172	7	ADB73085	Adb73085	Novel	hum
982	39	83.0	172	7	ADC36923	Adc36923	Human	PRO
983	39	83.0	172	7	ADC21913	Adc21913	Human	PRO
984	39	83.0	172	7	ADC49944	Adc49944	Novel	hum
985	39	83.0	172	7	ADC49143	Adc49143	Novel	hum
986	39	83.0	172	7	ADC49660	Adc49660	Novel	hum
987	39	83.0	172	7	ADC47521	Adc47521	Novel	hum
988	39	83.0	172	7	ADC47266	Adc47266	Novel	hum
989	39	83.0	172	7	ADC78141	Adc78141	Novel	hum
990	39	83.0	172	7	ADD06376	Add06376	Novel	hum
991	39	83.0	172	7	ADD10517	Add10517	Human	sec
992	39	83.0	172	7	ADC7895	Adc7895	Novel	hum
993	39	83.0	172	7	ADD11477	Add11477	Novel	hum
994	39	83.0	172	7	ADD50858	Add50858	Novel	hum
995	39	83.0	172	7	ADD51104	Add51104	Novel	hum
996	39	83.0	172	7	ADD37270	Add37270	Human	sec
997	39	83.0	172	7	ADD50585	Add50585	Human	PRO
998	39	83.0	172	7	ADD50339	Add50339	Human	PRO
999	39	83.0	172	7	ADD51350	Add51350	Novel	hum
1000	39	83.0	172	8	ADC48897	Adc48897	Novel	hum

ALIGNMENTS

RESULT 1
ID AAP71087 standard; peptide; 6 AA.

XX	XX	AAP71087;
XX	XX	25-MAR-2003 (revised)
DT	DT	31-OCT-2002 (revised)
DT	DT	06-JUN-1991 (first entry)
XX	XX	Sequence of thioredoxin analogue.
XX	XX	Redox active peptide; antioxidant; stress; ischaemia; lipid peroxidation;
KM	KM	food industry; cosmetics; antibiotic.
XX	XX	Unidentified.
XX	XX	OS
XX	XX	Key
FT	FT	Misc-difference 1 Location/Qualifiers
FT	FT	/note="optional, and may optionally be joined to a
FT	FT	terminal blocking sp."
FT	FT	Misc-difference 6 /note="see above"
XX	XX	EP237189-A.
PN	PN	16-SEP-1987.
XX	XX	10-FEB-1987; 87EP-00301150.
XX	XX	10-FEB-1986; 86US-00828112.
PR	PR	14-MAR-1986; 86US-00839857.
PR	PR	20-OCT-1986; 86US-00921287.
XX	XX	(REPK) REPLIGEN CORP.
PA	PA	Piglet VP, Willis CD;
PI	PI	WPI; 1987-258442/37.
DR	DR	New and known thioredoxin derivs. and analogues - useful for preventing
PT	PT	

PT metal catalysed oxidative damage in biological reactions and disease states.
XX
XX Claim 7; Page 7; 7pp; English.
PS
XX It is a redox active peptide which can be used in cpds. to treat stress and ischaemia, for inhibiting lipid peroxidn. due to drugs or toxic effects, as anti-inflammatory agents, to prevent DNA damage, and to maintain the biological activity of antibiotics or proteins. Thioredoxin can be used as a general antioxidant in the food and cosmetic industry. It may be used in prodn. processes for antibiotics, proteins or polypeptides. Therapeutic dose is 1 microgram/kg - 10mg/kg. (Updated on 31-Oct-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
CC
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WCGPCK 6
Db 1 WCGPCK 6
RESULT 2
ID ABP54936 standard; peptide; 6 AA.
XX
XX ABP54936;
XX
XX 08-JAN-2003 (first entry)
DT
XX
DE Active site peptide of thioredoxin.
XX
XX Thioredoxin; organoarsenical; arsenoxide; antiarthritic; antiout;
KM osteopathic; antirheumatic; arthritis; therapy.
XX
XX Homo sapiens.
OS
XX WO200274305-A1.
PN
XX
XX 26-SEP-2002.
PD
XX
XX 19-MAR-2002; 2002WO-AU000310.
PF
XX
XX 19-MAR-2001; 2001AU-00003798.
PR
XX
XX (UNIX) UNISEARCH LTD.
PA
XX
PI Hogg PJ, Donoghue N;
XX
XX WPI; 2002-750519/81.
DR
XX
XX Use of an impermeable cell membrane compound for the treatment of arthritis in vertebrates.
PT
XX
XX Example 2 (b); Page 42; 91pp; English.
PS
XX
XX The present sequence is that of a hexapeptide comprising the active site sequence of thioredoxin. The hexapeptide was used in an example from the invention that examined the binding of 4-(N-(S-glutathionylacetyl)amino)phenylarsenoxide (GSAO) to peptide and protein dithiols. The results indicated that GSAO selectively binds proteins containing closely spaced thiols. The invention provides a method for the treatment and/or prophylaxis of arthritis using a compound of formula A-(L-Y)P, where A is a cell-membrane impermeable pendant group, L is a linker and/or spacer, Y is an arsenoxide or arsenoxide equivalent, and P is an integer from 1 to 10. The compound, e.g. GSAO, is useful for the treatment of arthritic conditions such as calcific periarthritis, entropathic, chronic, thumb, hip, peripheral, psoriatic, rheumatoid, septic or Jaccoud's arthritis, gout, hand or knee osteoarthritis,

CC juvenile osteoarthritis, oligoarthritis, and polyarthritis (all claimed).
 CC The compound blocks angiogenesis in the synovial tissue and leucocyte
 CC ingress that triggers inflammation, with no signs or symptoms of toxicity
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 3
 ADA08451
 ID ADA08451 standard; peptide; 6 AA.

AC ADA08451;

DT 06-NOV-2003 (first entry)

DE Mammalian peptide found in thioredoxin and protein disulphide isomerase.

XX Anti-angiogenesis; plasmin fragment; plasminogen; plasminogen activator;
 KM plasmin reductase; reduced plasmin protein; anti-angiogenesis activator;
 KM urokinase-type plasminogen activator; A61; annexin II heterotetramer;
 KM annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
 KM protein disulphide isomerase; modulating angiogenesis; mammalian;
 KM cleavage peptide.

XX Mammalia.

OS US2003083234-A1.

PN 01-MAY-2003.

PD 26-NOV-2002; 2002US-00304287.

PR 28-NOV-2001; 2001US-0333866P.

XX (WALS/) WALSMAN D.

PA (KMOM/) KMOM M.

PI Waisman D, Kwon M,

DR WPI; 2003-596985/56.

XX Producing an anti-angiogenesis plasmin fragment, useful for modulating,
 PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
 PT plasminogen polypeptide with a plasminogen activator and a plasmin
 PT reductase.

PS Example 2; Page 6; 29pp; English.

XX The present invention relates to a method for producing an anti-
 CC angiogenesis plasmin fragment. The method comprises contacting a
 CC plasminogen polypeptide with a plasminogen activator and a plasmin
 CC reductase, where a reduced plasmin protein is produced and the anti-
 CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
 CC released from the reduced plasmin protein. The plasminogen activator is
 CC preferably a urokinase-type plasminogen activator. The angiogenesis
 CC plasmin fragment is A61. The plasmin reductase is selected from annexin
 CC II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
 CC disulphide isomerase. The annexin II heterotetramer is associated with a
 CC cell membrane. The method of the invention is useful for modulating (e.g.
 CC promoting or inhibiting) angiogenesis. The present sequence represents a
 CC mammalian cleavage peptide found in thioredoxin and protein disulphide
 CC isomerase.

XX Sequence 6 AA;

Query Match 100.0%; Score 47; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 4
 ADM32929
 ID ADM32929 standard; peptide; 6 AA.

AC ADM32929;

DT 17-JUN-2004 (first entry)

DE Amino acid sequence of the thioredoxin active site.

XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KM lung disease; cystic fibrosis.

XX Synthetic.

OS Key Location/Qualifiers

FT Active-site 1..6 /note= "active site of thioredoxin"

FT Modified-site 2 /note= "this residue is in a reduced state"

FT Modified-site 5 /note= "this residue is in a reduced state"

XX WO2004024868-A2.

XX 25-MAR-2004.

PD 10-SEP-2003; 2003WO-US028526.

PR 10-SEP-2002; 2002US-0409960P.

PR 11-APR-2003; 2003US-0462082P.

XX (NATJ-) NAT JEWISH MEDICAL & RES CENT.

PI White CW;

DR WPI; 2004-270016/25.

XX Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.

PS Claim 13; Page 51; 69pp; English.

XX The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive
 CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for

Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|
|
|
|
|
DB 1 WCGPCK 6

RESULT 7

ID ADQ97008 standard; peptide, 6 AA.

AC ADQ97008;

DT 07-OCT-2004 (first entry)

DE Thiorodoxin and protein disulphide isomerase common sequence.

KW p11 protein; plasminogen activation; tumour growth; metastasis; treating.

OS Synthetic.

PN US2004142897-A1.

PD 22-JUL-2004.

PF 12-DEC-2003; 2003US-00735577.

PR 28-NOV-2001; 2001US-0333866P.

PR 26-NOV-2002; 2002US-00304287.

PR 13-DEC-2002; 2002US-0433140P.

PA (WAIS/) WAISMAN D M.

PI Waisman DM;

DR WPI; 2004-579971/56.

PT New composition which modulates the activity of a p11 protein and effects a change in the level of plasminogen activation by a cell useful for treating cancer or reducing p11 protein activity in cancer cells.

PS Example 2; SEQ ID NO 4; 66p; English.

CC The invention relates to a composition which modulates the activity of a p11 protein and effects a change in the level of plasminogen activation by a cell. The composition is useful for reducing p11 protein activity in cancer cells. They are also useful for inhibiting tumour growth or metastasis or treating cancer. The present sequence represents the amino acid sequence of the thiorodoxin and protein disulphide isomerase common sequence involved with cleavage, formation and reshuffling of disulphide bonds.

SQ Sequence 6 AA;

Query Match 100.0%; Score 47; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|
|
|
|
|
DB 1 WCGPCK 6

RESULT 8

ID AAW45003 standard; peptide, 12 AA.

AC AAW45003;

DT 27-APR-1998 (first entry)

DE Immunomodulatory peptide D7233.

XX Immunomodulator; immunosuppressant; immunostimulator; treatment;
KW transplant rejection; autoimmune disease; cancer; infection.

OS Synthetic.

PN WO9739023-A1.

PD 23-OCT-1997.

PF 04-APR-1997; 97WO-SE000574.

PR 12-APR-1996; 96SE-00001422.

PR 23-SEP-1996; 96SE-00003469.

PA (ASTR) ASTRA AB.

PI Bergstrand H, Eriksson T, Lindvall M, Saerstrand B;

DR WPI; 1997-526397/48.

PT Nucleic acids encoding cysteine- or methionine-containing peptide(s) which have immunostimulatory or immunosuppressive activity - can be used to treat, e.g. cancers, infection, autoimmune disease or transplant rejection.

PS Claim 12; Page 155; 183pp; English.

CC The present peptide is an immunosuppressant or immunostimulator. An immunosuppressant can be used to treat transplant rejection or autoimmune disease, e.g. rheumatoid arthritis, systemic lupus erythematosus, Sjogren's syndrome, scleroderma, mixed connective tissue disease, dermatomyositis, polymyositis, Reiter's syndrome, Behcet's disease, type 1 diabetes, Hashimoto's thyroiditis, Graves' disease, multiple sclerosis, myasthenia gravis, encephalomyelitis, pemphigus vulgaris, vegetans or foliaceus, Senear-Usher syndrome or Brazilian pemphigus. An immunostimulator can be used to treat conditions such as cancer or infection.

SQ Sequence 12 AA;

Query Match 100.0%; Score 47; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.3; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|
|
|
|
|
DB 1 WCGPCK 6

RESULT 9

ID AAY09429 standard; peptide, 12 AA.

AC AAY09429;

DT 14-JUL-1999 (first entry)

DE Immunoreactive peptide SEQ ID NO:54.

KW Immunoreactive; immunomodulation; immunosuppression; immunostimulation; immune response; immunoreactive; autoimmune disease.

OS Synthetic.

PN WO9919347-A1.

PD 22-APR-1999.

PF 06-OCT-1998; 98WO-SE001801.

PR 10-OCT-1997; 97US-00949024.

PA (ASTR) ASTRA AB.
 XX
 PI Bergstrand H, Eriksson T, Lindvall M, Saernstrand B;
 XX
 DR WPI; 1999-287953/24.
 XX
 PT Synthetic genes encoding immunoreactive peptides containing cysteine or
 XX methionine.
 PS Claim 32; Page 52; 104pp; English.
 CC
 CC The present invention describes nucleic acid molecules comprising a
 CC coding sequence encoding an immunoreactive peptide and further encoding a
 CC protein targeting sequence. The nucleic acid is administered to a patient
 CC so that its expression product, an immunoreactive peptide, modulates an
 CC immune response in a patient. The nucleic acid can also be used to treat
 CC cancer, either after surgery to remove a portion of the cancer or after
 CC ionizing radiation. A cytokine is also administered in conjunction with
 CC the nucleic acid. Cells containing the nucleic acid molecule can also be
 CC used for treatment. The immunoreactive peptide is immunosuppressive and can
 CC be used in patients with autoimmune disease. The present sequence
 CC represents a specifically claimed immunoreactive peptide from the present
 CC invention
 CC
 SQ Sequence 12 AA;
 XX

Query Match 100.0%; Score 47; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 1 WCGPCK 6

RESULT 10
 AAU08670
 ID AAU08670 standard; protein; 52 AA.
 XX
 AC AAU08670;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Thioresoxin domain markov model sequence #1.
 XX
 KM Thioresoxin; 22105; cytosratic; cardiant; haemostatic;
 KM cellular proliferative disorder; differentiative disorder; cancer;
 KM carcinoma; sarcoma; tumour; haemopoetic neoplastic disorder; leukemia;
 KM chronic myelogenous leukemia; cardiovascular disorder; atherosclerosis;
 KM ischaemia; thrombosis; hypertension.
 XX
 OS Synthetic.
 XX
 PN WO200166756-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US007139.
 XX
 PR 07-MAR-2000; 2000US-0187447P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Curtis RAJ;
 XX
 DR WPI; 2001-589945/66.
 XX
 PT Novel thioresoxin polypeptides and polynucleotides for treating a
 PT disorder associated with aberrant cellular proliferation or
 PT differentiation, e.g., cancer and to identify modulators for therapeutic
 PT use.
 XX
 PS Disclosure; Fig 3A; 126pp; English.

XX The invention relates to a novel human thioresoxin polypeptide, 22105,
 CC fragments of it and allelic variants. 22105 is useful for identifying a
 CC compound which modulates the activity or expression of the polypeptide
 CC and nucleic acid, where the binds to the polypeptide, and the binding is
 CC detected by direct detection of a test compound/polypeptide binding, by
 CC using a competition binding assay or an assay for 22105-mediated signal
 CC transduction, and the activity of the polypeptide is a redox activity or
 CC the ability to modulate protein processing, protein folding and protein
 CC secretion. Anti-22105 antibody is useful for detecting the presence of
 CC 22105 in a sample. A modulator of 22105 is useful for treating or
 CC preventing a disorder such as cellular proliferative or differentiative
 CC disorder (e.g. cancers, carcinomas, sarcomas and tumours), haemopoetic
 CC neoplastic disorder (e.g. leukemia and chronic myelogenous leukemia) or
 CC cardiovascular disorder (e.g. atherosclerosis, ischaemia, thrombosis,
 CC hypertension), characterised by aberrant activity or expression of a
 CC 22105 nucleic acid or polypeptide in a subject, where the agent is
 CC preferably a peptide, a phosphopeptide, a small molecule, an antibody or
 CC their combination, or an antisense, a ribozyme, a triple helix molecule,
 CC a 22105 nucleic acid or their combination (many examples of each disorder
 CC are given in the specification). The present sequence represents a
 CC thioresoxin domain sequence derived from a hidden markov model
 CC
 SQ Sequence 52 AA;
 XX

Query Match 100.0%; Score 47; DB 4; Length 52;
 Best Local Similarity 100.0%; Pred. No. 7.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 20 WCGPCK 25

RESULT 11
 AAR42822
 ID AAR42822 standard; protein; 80 AA.
 XX
 AC AAR42822;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAY-1994 (first entry)
 XX
 DE rECEP 84.
 XX
 KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KM therapy; thioresoxin.
 XX
 OS Homo sapiens.
 XX
 PN WO9320107-A1.
 XX
 PD 14-OCT-1993.
 XX
 PF 06-APR-1993; 93WO-US003310.
 XX
 PR 06-APR-1992; 92US-00862832.
 PR 06-JUL-1992; 92US-00906842.
 XX
 PA (BIGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Silberstein DS, Balcewicz-Sablinska MK;
 XX
 DR WPI; 1993-336837/42.
 DR N-PSDB; AAQ49405.
 XX
 XX Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.
 XX
 PS Example 3; Page 67; 96pp; English.
 XX
 CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
 CC Enhancing Factor (ECEF); Thioresoxin and ADF) and encoding a polypeptide

CC of 104 amino acids has been found to support the growth of an EBV
 CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
 CC expression of IL-2 receptors in a large granular lymphocyte cell line
 CC from an ATL patient in the manner of IL-1 and to mediate the growth
 CC inhibitory properties of interferon gamma. Recombinant ECEF (ECEP) 80 is
 CC a truncated version of the 104 amino acid polypeptide comprising the
 CC first 80 amino acids of the molecule. Some shortened ECEP's are useful
 CC because they retain eosinophil stimulating activity but lack
 CC proinflammatory dihalol reductase activity. In particular they can be
 CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
 CC field.)

CC Sequence 80 AA;

QY Query Match 100.0%; Score 47; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 30 WCGPCK 35

RESULT 12

AA42821
 ID AA42821 standard; protein; 84 AA.

AC AA42821;

DT 25-MAR-2003 (revised)

DT 04-MAY-1994 (first entry)

XX

DE RECF 84.

KW Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KW therapy; thioedoxin.

XX Homo sapiens.

XX WO320107-A1.

PD 14-OCT-1993.

PF 06-APR-1993; 93WO-US003310.

PR 06-APR-1992; 92US-00862832.

PR 06-JUL-1992; 92US-00906842.

PA (BGM) BRIGHAM & WOMENS HOSPITAL.

PI Silberstein DS, Balcewicz-Sablinska MK;

DR WPI; 1993-336837/42.

DR N-PSDB; AAQ49404.

PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.

PS Example 3; Page 66; 96pp; English.

CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
 CC Enhancing Factor (ECF); thioedoxin and ADP) and encoding a polypeptide
 CC of 104 amino acids has been found to support the growth of an EBV
 CC transformed B lymphocyte cell line in the manner of IL-1; to induce the
 CC expression of IL-2 receptors in a large granular lymphocyte cell line
 CC from an ATL patient in the manner of IL-1 and to mediate the growth
 CC inhibitory properties of interferon gamma. Recombinant ECEF (ECEP) 84 is
 CC a truncated version of the 104 amino acid polypeptide comprising the
 CC first 84 amino acids of the molecule. Some shortened ECEP's are useful
 CC because they retain eosinophil stimulating activity but lack
 CC proinflammatory dihalol reductase activity. In particular they can be
 CC used for killing tumour cells. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX SQ Sequence 84 AA;

QY Query Match 100.0%; Score 47; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 30 WCGPCK 35

RESULT 13

ADJ68506
 ID ADJ68506 standard; protein; 84 AA.

AC ADJ68506;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SegID312.

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; anticholinergic;

KW osteopathic; ophthalmological; cyostatic.

XX Homo sapiens.

XX WO2003087768-A2.

PD 23-OCT-2003.

PF 04-APR-2003; 2003WO-US010870.

PR 12-APR-2002; 2002US-0372843P.

PR 17-JUN-2002; 2002US-0389987B.

PR 20-SEP-2002; 2002US-0412418P.

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.

PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SM, Glenn GM;

PI Warnock DE;

DR WPI; 2003-845369/78.

PT Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function.
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.

PS Claim 1; SEQ ID NO 312; 180pp; English.

CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, anticholinergic, osteopathic, ophthalmological and
 CC cyostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.

SQ Sequence 84 AA;
 Query Match 100.0%; Score 47; DB 7; Length 84;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 30 WCGPCK 35
 Db
 RESULT 14
 ABP60794
 ID ABP60794 standard; protein; 91 AA.
 XX
 AC ABP60794;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Thiocapsa roseopersicina thioredoxin SEQ ID NO:143.
 XX
 KM Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KM vasotropic; vulnerary; antibacterial; immunosuppressive; antilicer;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Thiocapsa roseopersicina.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742900.
 XX
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN-) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M;
 DR WPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PT
 PS Claim 81; Page 243; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP6077 to

CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 CC
 SQ Sequence 91 AA;
 Query Match 100.0%; Score 47; DB 5; Length 91;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 32 WCGPCK 37
 Db
 RESULT 15
 AAB49948
 ID AAB49948 standard; protein; 95 AA.
 XX
 AC AAB49948;
 XX
 DT 07-MAR-2001 (first entry)
 XX
 DE A. oryzae protein disulfide isomerase #3.
 XX
 KM Disulphide bond; allergy; protein disulfide isomerase variant; detergent;
 KM food additive; cosmetic.
 XX
 OS Aspergillus oryzae.
 XX
 PN WO200070064-A1.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-DK000265.
 XX
 PR 17-MAY-1999; 99DK-00000683.
 XX
 PR 18-MAY-1999; 99DK-00000689.
 PR 02-JUN-1999; 99US-0137068P.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Hjort CM;
 PI
 DR WPI; 2001-070776/08.
 DR N-PSDB; AAC89030.
 XX
 PT Protein disulfide isomerase variant having increased reducing properties
 PT and decreased redox potential than native proteins, used to reduce
 PT allergenicity of allergic proteins in feed, food or cosmetic products.
 PT
 PS Claim 2; Page 76-77; 82pp; English.
 XX
 CC The present invention provides variants of the Aspergillus oryzae protein
 CC disulfide isomerase enzyme. These are capable of reducing disulphide
 CC bonds in proteins, which may be the cause of allergies in humans. The
 CC proteins can be used to reduce the allergenicity of foods, to treat
 CC scleroderms, in detergents, in food additives and in cosmetics
 CC
 SQ Sequence 95 AA;
 Query Match 100.0%; Score 47; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 37 WCGPCK 42
 Db
 RESULT 16
 ABP60779
 ID ABP60779 standard; protein; 102 AA.
 XX


```

AC ABP60779;
XX
DT 06-SEP-2002 (first entry)
XX
DE Mycoplasma pneumoniae thioresoxin SEQ ID NO:128.
XX
KW Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
KW vasotropic; vulnery; antibacterial; immunosuppressive; anticulcer;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease.
XX
OS Mycoplasma pneumoniae.
XX
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742900.
XX
PR 05-JUL-2001; 2001US-0302885P.
XX
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
XX WPI; 2002-508806/54.
XX
PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
PS Claim 81; Page 238; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 102 AA;
XX
Query Match 100.0%; Score 47; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

ABP60755
XX
ID ABP60755 standard; protein; 102 AA.
XX
AC ABP60755;
XX
DT 07-AUG-2003 (revised)
XX
DT 06-SEP-2002 (first entry)
XX
DE Peitact sp thioresoxin SEQ ID NO:104.
XX
KW Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
KW oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
KW vasotropic; vulnery; antibacterial; immunosuppressive; anticulcer;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease.
XX
OS Unidentified.
XX
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742900.
XX
PR 05-JUL-2001; 2001US-0302885P.
XX
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
XX WPI; 2002-508806/54.
XX
PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
PS Claim 81; Page 230; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchopulmonary disease, psoriasis,
CC malignancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention. (Updated on 07-AUG-2003 to correct OS field.)
XX
SQ Sequence 102 AA;
XX
Query Match 100.0%; Score 47; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Db 27 WCGPCK 32

RESULT 18
ABP60756
ID ABP60756 standard; protein; 102 AA.
XX
AC ABP60756;
XX
DT 06-SEP-2002 (first entry)
XX
DE Chlamydia trachomatis thio redoxin SEQ ID NO:105.
XX
KW Multimeric protein; redox protein; thio redoxin; thio redoxin reductase;
KW oil body; ophthalmological; antidiabetic; cyostatic; antipsoriatic;
KW vasotrophic; vulnery; antibacterial; immunosuppressive; antileuc;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease.
XX
OS Chlamydia trachomatis.
XX
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742900.
PR 05-JUL-2001; 2001US-0302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
DR MPI; 2002-508806/54.
XX
PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
PS Claim 81; Page 230; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malinancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
|||||
Db 27 WCGPCK 32

RESULT 19
ABP60753
ID ABP60753 standard; protein; 102 AA.
XX
AC ABP60753;
XX
DT 06-SEP-2002 (first entry)
XX
DE Chlamydia muridarum thio redoxin SEQ ID NO:102.
XX
KW Multimeric protein; redox protein; thio redoxin; thio redoxin reductase;
KW oil body; ophthalmological; antidiabetic; cyostatic; antipsoriatic;
KW vasotrophic; vulnery; antibacterial; immunosuppressive; antileuc;
KW food product; milk; wheat; oxidative stress; cataract; diabetes;
KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
KW gastro oesophageal reflux disease.
XX
OS Chlamydia muridarum.
XX
PN WO200250289-A1.
XX
PD 27-JUN-2002.
XX
PF 19-DEC-2001; 2001WO-US050240.
XX
PR 19-DEC-2000; 2000US-00742900.
PR 05-JUL-2001; 2001US-0302885P.
PR 04-DEC-2001; 2001US-0006038.
XX
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
PI Del Val G, Zaplachinski S, Moloney M;
XX
DR MPI; 2002-508806/54.
XX
PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.
XX
PS Claim 81; Page 229; 362pp; English.
XX
CC The present invention describes a method (M1) for producing an oil body
CC associated with a recombinant multimeric protein complex (MPC). M1
CC comprises producing in a cell comprising oil bodies a first and second
CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
CC P2 to form the MPC and associating the complex with an occlusion body
CC (OB) through an OB-targeting-protein capable of associating with OB and
CC P1. M1 is useful for producing an oil body associated with a recombinant
CC MPC. The oil bodies are further formulated for use in the preparation of
CC a food product such as milk or wheat based food product, personal care
CC product which reduces the oxidative stress on the surface area of the
CC human body or used to lighten the skin, or a pharmaceutical composition
CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
CC malinancies, reperfusion injury, wound healing, sepsis, gastro
CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
CC ABP60964 represent sequence given in the exemplification of the present
CC invention
XX
SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 27 WCGPCK 32

RESULT 20

ABP60777
 ID ABP60777 standard; protein; 102 AA.

AC ABP60777;
 XX

DT 06-SEP-2002 (first entry)

DE Mycoplasma genitalium thioedoxin SEQ ID NO:126.

XX Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytoprotic; antiproliferative;
 KW vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro oesophageal reflux disease; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Mycoplasma genitalium.

OS Mycoplasma genitalium.

PN WO200250289-A1.

XX 27-JUN-2002.

XX 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 05-JUL-2001; 2001US-0302885P.

PR 04-DEC-2001; 2001US-0006038.

PA (SEMB-) SEMBIOSYS GENETICS INC.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;

PI Del Val G, Zaplachinski S, Moloney M;

XX WPI; 2002-508806/54.

XX Producing oil body associated with recombinant multimeric protein complex

XX e.g. redox proteins and immunoglobulins comprises producing recombinant

XX polypeptides capable of forming the complex in cells comprising oil

XX bodies.

XX Claim 81; Page 237; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 and ABP60677 to
 CC ABP60694 represent sequence given in the exemplification of the present
 CC invention

XX SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 5; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 29 WCGPCK 34

RESULT 21

ADB09186
 ID ADB09186 standard; protein; 102 AA.

AC ADB09186;
 XX

DT 20-NOV-2003 (first entry)

DE Allotococcus oclis antigenic protein SEQ ID NO:3126.

XX Allotococcus oclis; antigenic protein; immunogenic; immunisation;

KW gene therapy; Gram-positive bacterium; infection.

XX Allotococcus oclis.

OS Allotococcus oclis.

PN WO2003048304-A2.

XX 12-JUN-2003.

XX 25-NOV-2002; 2002WO-US036123.

PR 29-NOV-2001; 2001US-0333777P.

PR 18-NOV-2002; 2002US-0426742P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Fletcher LD, McMichael JC, Russell DP, Zagursky RJ;

PI WPI; 2003-505284/47.

XX N-PSDB; ADB09185.

XX New Allotococcus oclis polynucleotides and polypeptides, useful for

XX treating and diagnosing diseases, drug screening assays and monitoring of

XX effects during drug clinical trials.

XX Claim 33; SEQ ID NO 3126; 1019pp; English.

XX The present invention describes an isolated polynucleotide (1) of
 CC Allotococcus oclis genomic DNA, which encodes an antigenic protein.
 CC Allotococcus oclis is a Gram-positive bacterium. Also described: (1)
 CC an isolated polypeptide that is encoded by the polynucleotide (1); (2) an
 CC expression vector comprising the novel isolated polynucleotide (1), its
 CC complement, degenerate variant or fragment; (3) a genetically engineered
 CC host cell, transfected, transformed or infected with the vector of (2);
 CC (4) an antibody specific for the polypeptide of (1); (5) an immunogenic
 CC composition comprising the polypeptide, its complement, biological
 CC equivalent or fragment, or the polynucleotide that is comprised in the
 CC expression vector; (6) a pharmaceutical composition comprising the
 CC polypeptide of (1) and a carrier; (7) a protein chip comprising an array
 CC of the polypeptides of (1), their biological equivalent or fragment; (8)
 CC immunising against Allotococcus oclis by administering to a host the
 CC immunogenic composition; (9) detecting and/or identifying Allotococcus
 CC oclis in the biological sample; (10) a kit comprising a container
 CC containing the novel polynucleotide, its degenerate variant or fragment,
 CC or the antibody of (4); and (11) producing a polypeptide by culturing the
 CC genetically engineered host cell under conditions suitable to produce the
 CC polypeptide from the culture. (I) can be used in gene therapy. The
 CC polynucleotides, polypeptides, antibodies and compositions of the present
 CC invention can be used for treating and diagnosing diseases, drug
 CC screening assays and monitoring of effects during drug clinical trials.
 CC The polynucleotides are useful for expressing and detecting Allotococcus

CC otitidis. The present sequence represents an *Alloicoccus otitidis*
 CC antigen protein from the present invention.
 XX
 CC
 SQ Sequence 102 AA;

Query Match 100.0%; Score 47; DB 6; Length 102;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 27 WCGPCK 32

RESULT 22
 ABP60747
 ID ABP60747 standard; protein; 103 AA.
 XX
 AC ABP60747;
 XX

DT 06-SEP-2002 (first entry)

DE *Bacillus subtilis* thioredoxin SEQ ID NO:96.

XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoptic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antilcer;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.

XX *Bacillus subtilis*.

XX WO200250289-A1.

PD 27-JUN-2002.

XX 19-DEC-2001; 2001WO-US050240.

XX 19-DEC-2000; 2000US-00742900.

PR 05-JUL-2001; 2001US-0302885P.

PR 04-DEC-2001; 2001US-0006038.

XX (SEMB-) SEMBIOSYS GENETICS INC.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Van Rooyen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;

PI Del Val G, Zaplachinski S, Moloney M;

XX WPI; 2002-50886/54.

DR WPI; 2002-50886/54.

XX Claim 81; Page 227; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,

CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89559 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 CC

SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 27 WCGPCK 32

RESULT 23
 ABG93246
 ID ABG93246 standard; protein; 103 AA.
 XX
 AC ABG93246;
 XX

DT 21-NOV-2002 (first entry)

DE *C. albicans* BAX-associated protein fragment SEQ ID 450.

XX Bax; Bax-resistance; cytosolic; fungicide; immunosuppressive; virucide;
 KM vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
 KM apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
 KM neurodegeneration; cell death.

XX *Candida albicans*.

XX WO200264766-A2.

PD 22-AUG-2002.

XX 21-DEC-2001; 2001WO-EP015398.

XX 22-DEC-2000; 2000EP-00870318.

PR 04-JAN-2001; 2001EP-00870002.

PR 09-JAN-2001; 2001EP-00870003.

XX (JANC) JANSSEN PHARM NV.

PA Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

PI WPI; 2002-667002/71.

DR N-PADB; ABQ76512.

XX New isolated nucleic acid representing a synthetic BAX-gene, useful as

PT medicament for treating, preventing and/or alleviating yeast or fungal

PT infections or proliferative disorders, or for preventing apoptosis in

PT certain diseases.

XX Claim 36; Fig 2; 344pp; English.

XX This invention describes a novel nucleic acid representing a synthetic
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
 CC resistant yeast or fungi, identifying, or obtaining and identifying
 CC Candida spp. sequences that are differentially expressed in a pathway
 CC eventually leading to programmed cell death or identifying inhibitors or
 CC inhibitor sequences of Bax-induced cell death. The products of the
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and
 CC vasotropic activity and can be used in vaccines or for gene therapy. The
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
 CC antibodies and antibodies are useful as medicaments or in
 CC preparing a medicament for treating, preventing and/or alleviating
 CC diseases associated with yeast or fungi or proliferative disorders,
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds
 CC or polypeptides, or the genetically modified organism are useful for
 CC preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 24

ABG93156
ID ABG93156 standard; protein; 103 AA.

XX
AC ABG93156;

XX
DT 21-NOV-2002 (first entry)

XX
DE S. cerevisiae BAX-associated protein fragment SEQ ID 270.

XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
XX vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
XX apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX neurodegeneration; cell death.

XX
OS Saccharomyces cerevisiae.

XX
PN WO200264766-A2.

XX
PD 22-AUG-2002.

XX
PF 21-DEC-2001; 2001WO-EP015398.

XX
PR 22-DEC-2000; 2000EP-00870318.

XX
PR 04-JAN-2001; 2001EP-00870002.

XX
PR 09-JAN-2001; 2001EP-00870003.

XX
PA (JANC) JANSSEN PHARM NV.

XX
PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX
DR WPI; 2002-667002/71.

XX
DR N-PSDB; ABQ76422.

XX
PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
XX medicament for treating, preventing and/or alleviating yeast or fungal
XX infections or proliferative disorders, or for preventing apoptosis in
XX certain diseases.

XX
PS Claim 36; Fig 1; 34pp; English.

XX
CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX
SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 25

ABG93328
ID ABG93328 standard; protein; 103 AA.

XX
AC ABG93328;

XX
DT 21-NOV-2002 (first entry)

XX
DE C. albicans BAX-associated protein fragment SEQ ID 614.

XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
XX vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
XX apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
XX neurodegeneration; cell death.

XX
OS Candida albicans.

XX
PN WO200264766-A2.

XX
PD 22-AUG-2002.

XX
PF 21-DEC-2001; 2001WO-EP015398.

XX
PR 22-DEC-2000; 2000EP-00870318.

XX
PR 04-JAN-2001; 2001EP-00870002.

XX
PR 09-JAN-2001; 2001EP-00870003.

XX
PA (JANC) JANSSEN PHARM NV.

XX
PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;

XX
DR WPI; 2002-667002/71.

XX
DR N-PSDB; ABQ76594.

XX
PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
XX medicament for treating, preventing and/or alleviating yeast or fungal
XX infections or proliferative disorders, or for preventing apoptosis in
XX certain diseases.

XX
PS Claim 36; Fig 2; 34pp; English.

XX
CC This invention describes a novel nucleic acid representing a synthetic
CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
CC resistant yeast or fungi, identifying, or obtaining and identifying
CC Candida spp. sequences that are differentially expressed in a pathway
CC eventually leading to programmed cell death or identifying inhibitors or
CC inhibitor sequences of Bax-induced cell death. The products of the
CC invention have cytostatic, fungicide, immunosuppressive, virucide and
CC vasotropic activity and can be used in vaccines or for gene therapy. The
CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
CC antisense molecules and antibodies are useful as medicaments or in
CC preparing a medicament for treating, preventing and/or alleviating
CC diseases associated with yeast or fungi or proliferative disorders, such
CC as cancer, or for preventing apoptosis in certain diseases. The compounds
CC or polypeptides, or the genetically modified organism are useful for
CC preparing a medicament for modifying the endogenic flora of humans and

CC other mammals. The vaccine is useful for immunising against yeast or
CC fungal infections. Apoptosis-related diseases include autoimmune disease,
CC ischaemia, diseases related with viral infections or neurodegenerations.
CC This sequence represents a polypeptide associated with the Bax gene
CC described in the disclosure of the invention

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
29 WCGPCK 34

Db

RESULT 26

ABP73948
ID ABP73948 standard; protein; 103 AA.

XX AC ABP73948;

XX DT 30-JAN-2003 (first entry)

XX DE Candida albicans essential protein SEQ ID NO 7785.

XX KM Fungus; yeast; tetracyclin; promoter; GRACE strain; biosynthesis;

XX KW signal transduction; DNA replication; cell division; growth;

XX KM proliferation; Candida albicans; fungicide; antifungal.

XX OS Candida albicans.

XX PN WO200253728-A2.

XX PD 11-JUL-2002.

XX PF 26-DEC-2001; 2001WO-US049486.

XX PR 29-DEC-2000; 2000US-0259128P.

XX PR 20-FEB-2001; 2001US-00792024.

XX PR 22-AUG-2001; 2001US-0314050P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;

XX DR WPI; 2002-566694/60.

XX DR N-PSDB; AB232498.

XX PT Constructing strains for identifying gene products as effective targets
XX PT for therapeutic intervention, by inactivating in the strain one allele of
XX PT a gene and placing other allele of the gene under conditional expression.

XX PS Claim 44; SEQ ID NO 7785; 167bp + Sequence Listing; English.

XX CC The invention relates to constructing (M1) a strain of diploid fungal
XX CC cells in which both alleles of a gene are modified, comprising modifying

XX CC one allele by insertion or replacement by a cassette having an
XX CC expressible selectable marker and modifying other allele by

XX CC recombination, of a promoter replacement fragment with a heterologous
XX CC promoter, so that expression of the second allele is regulated by the

XX CC promoter. (M1) is useful for constructing a strain of diploid fungal
XX CC cells in which both alleles of a gene are modified. The diploid fungal

XX CC cells having both alleles modified are useful for identifying a gene that
XX CC is essential to the survival or growth of a fungus, a gene that

XX CC contributes to the virulence and/or pathogenicity of a fungus, a gene
XX CC that contributes to the resistance and/or pathogenicity of a fungus, a gene

XX CC agent, an antifungal agent that inhibits the growth of a diploid fungus
XX CC and for identifying a therapeutic agent for treatment of a mammalian

XX CC disease. (M1) is useful for identifying a compound which modulates the
XX CC activity of a gene product, preferably enzymatic activity, carbon

XX CC compound catabolism, biosynthetic, transporter, transcriptional,

CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office

XX SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 5; Length 103;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
29 WCGPCK 34

Db

RESULT 27

ABR41607
ID ABR41607 standard; protein; 103 AA.

XX AC ABR41607;

XX DT 02-JUN-2003 (first entry)

XX DE Human DITHP electron transfer-associated protein.

XX KM Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;

XX KM cancer; cell proliferative disorder; autoimmune disorder;

XX KM inflammatory disorder; infection; hormonal disorder; metabolic disorder;

XX KM neurological disorder; gastrointestinal disorder; transport disorder;

XX KM connective tissue disorder; drug screening; proteome analysis;

XX KM gene therapy; antisense therapy; genotyping; transgenic animal; knock in;

XX KM disease model; toxicological testing; transcript imaging;

XX KM electron transfer-associated protein.

XX OS Homo sapiens.

XX PN WO200297031-A2.

XX PD 05-DEC-2002.

XX PF 27-MAR-2002; 2002WO-US010056.

XX PR 28-MAR-2001; 2001US-0279619P.

XX PR 29-MAR-2001; 2001US-0280067P.

XX PR 29-MAR-2001; 2001US-0280068P.

XX PR 16-MAY-2001; 2001US-0291280P.

XX PR 17-MAY-2001; 2001US-0291829P.

XX PR 17-MAY-2001; 2001US-0291849P.

XX PR 19-JUN-2001; 2001US-0299428P.

XX PR 20-JUN-2001; 2001US-0299776P.

XX PR 20-JUN-2001; 2001US-0300001P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

XX PI Duffour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;

XX PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstlin EH;

XX PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;

XX PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX DR WPI; 2003-129518/12.

XX DR N-PSDB; ACC46545.

XX PT Novel human diagnostic and therapeutic polypeptide useful for identifying
XX PT test compound which specifically binds to a polypeptide encoded by human
XX PT diagnostic and therapeutic polynucleotide, and to induce antibodies.

XX PS Claim 27; SEQ ID NO 1142; 591bp; English.

XX The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC6080-ACC6749) and to their encoded
 CC proteins (DITHP, ABR41135-ABR41812). The invention also relates to
 CC polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
 CC detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is associated with
 CC electron transfer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at http://wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 6; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 26 WCGPCK 31

RESULT 28
 ADK90669
 ID ADK90669 standard; protein; 103 AA.
 AC ADK90669;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Baker's yeast thioredoxin 2 (THX2) protein SeqID 14.
 XX
 KW baker's yeast; THX2; transgenic; abiotic stress response; crop plant;
 KW oxidoreductase stress-related protein; ORSRP; environmental stress;
 KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;
 KW thioredoxin; THX; Quantitative Trait Locus; QTL.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO2004018687-A2.
 XX
 PD 04-MAR-2004.
 XX
 PF 01-JUL-2003; 2003WO-EP006994.
 XX
 PR 07-AUG-2002; 2002EP-00017671.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Chardonnais A, Puzio P;
 XX
 DR WPI; 2004-226856/21.
 DR N-PSDB; ADK90668.

XX New transgenic plant cell transformed by oxidoreductase stress-related
 PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
 PT plant with increased environmental stress tolerance.
 XX

PS Example 2; SEQ ID NO 14; 140pp; English.

XX This invention relates to novel transgenic plant cells transformed by
 CC genes encoding proteins associated with the abiotic stress response.
 CC Specifically, it refers to transgenic crop plants expressing the
 CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
 CC increased tolerance and/or resistance to environmental stresses such as
 CC salinity, drought, temperature, chemicals or pathogens. The present
 CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
 CC thioredoxin (THX) proteins, where expression is under the control of an
 CC inducible tissue-specific or developmentally-specific promoter and
 CC furthermore it provides antisense oligos and RNA interference molecules
 CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
 CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
 CC associated with environmental stress tolerance. This polypeptide sequence
 CC is a baker's yeast THX protein of the invention.

SQ Sequence 103 AA;

Query Match 100.0%; Score 47; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 29
 ADM32933
 ID ADM32933 standard; protein; 103 AA.
 XX
 AC ADM32933;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Amino acid sequence of a thioredoxin polypeptide.
 XX
 KW mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
 KW lung disease; cystic fibrosis; enzyme.
 XX
 OS Saccharomyces cerevisiae.
 OS Synthetic.
 XX
 PN WO2004024868-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 10-SEP-2003; 2003WO-US028526.
 XX
 PR 10-SEP-2002; 2002US-0409960P.
 XX
 PR 11-APR-2003; 2003US-0462082P.
 XX
 PA (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 XX
 PI White CW;
 XX
 DR WPI; 2004-270016/25.
 XX
 PF Increasing the liquefaction of excessively viscous or cohesive mucus or
 PT sputum comprises contacting the mucus or sputum with a composition
 PT comprising a protein or peptide containing a thioredoxin active-site in
 PT reduced state.
 XX
 PS Disclosure; Page 64; 69pp; English.
 XX
 CC The specification describes a method for increasing the liquefaction of
 CC mucus or sputum in a patient that has excessively viscous or cohesive

CC mucus or sputum. The method comprises contacting the mucus or sputum of
 CC the patient with a composition comprising a protein or peptide containing
 CC a thioredoxin active site in reduced state. The mucus or sputum to be
 CC contacted is located in the respiratory tract, gastrointestinal tract or
 CC reproductive tract of the patient. The composition is administered to the
 CC patient in a pharmaceutical carrier. The protein has a half-life in the
 CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
 CC volume of a sample of mucus or sputum from the patient shows a
 CC statistically significant increase after administration of the
 CC composition. The protein comprises thioredoxin selected from prokaryotic
 CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
 CC thioredoxin. The composition further comprises nicotinamide-adenine
 CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
 CC thioredoxin active site of the protein, and thioredoxin reductase. The
 CC method and composition are useful for decreasing the viscosity and
 CC cohesiveness of, and increasing the liquefaction of, excessively or
 CC abnormally viscous or cohesive mucus or sputum. These may be used for
 CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
 CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
 CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
 CC which may be used in the method of the invention.

CC Sequence 103 AA;

Query Match 100.0%; Score 47; DB 8; Length 103;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 29 WCGPCK 34

RESULT 30

ID AAR42820 standard; protein; 104 AA.

XX AAR42820;

XX 25-MAR-2003 (revised)

DT 04-MAY-1994 (first entry)

XX RECEF 104.

KM Eosinophil cytotoxicity enhancing factor; ECEF; stimulation; diagnosis;
 KW therapy; thioredoxin.

XX Homo sapiens.

XX WO9320107-A1.

XX 14-OCT-1993.

XX 06-APR-1993; 93WO-US003310.

XX 06-APR-1992; 92US-00862832.

XX 06-JUL-1992; 92US-00906842.

XX (BGM) BRIGHAM & WOMENS HOSPITAL.

XX Silberstein DS, Balcewicz-Sablinska MK;

XX WPI; 1993-336837/42.

XX N-PSDB; AAQ49403.

XX Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having

PT Eosinophil-stimulating activity, for use in diagnosis and therapy.

XX Example 3; Page 65; 96pp; English.

CC A 14 kDa molecule designated various names (Eosinophil Cytotoxicity-
 CC Enhancing Factor (ECEF); thioredoxin and ADF) has been found to support
 CC the growth of an BBV transformed B lymphocyte cell line in the manner of

CC IL-1; to induce the expression of IL-2 receptors in a large granular
 CC lymphocyte cell line from an ATL patient in the manner of IL-1 and to
 CC modulate the growth inhibitory properties of interferon gamma. Recombinant
 CC ECEF (RECEF) 104 is the full length 104 amino acid polypeptide encoded by
 CC this molecule and was produced for comparison studies against shortened
 CC versions of the polypeptide. Some shortened ECEF's are useful because
 CC they retain eosinophil stimulating activity but lack proinflammatory
 CC dihol reductase activity. In particular they can be used for killing
 CC tumour cells. (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 104 AA;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 DB 30 WCGPCK 35

RESULT 31

ID AAR47855 standard; protein; 104 AA.

XX AAR47855;

XX 25-MAR-2003 (revised)

DT 18-JUL-1994 (first entry)

XX Human ADF-polypeptide.

KM ADF; thioredoxin; pancreatitis; amylase; lipase; free radicals;

KW protein folding; denaturing; renaturing.

XX Homo sapiens.

XX EP579958-A1.

XX 26-JAN-1994.

XX 18-JUN-1993; 93EP-00109794.

XX 19-JUN-1992; 92JP-00161454.

XX (AJIN) AJINOMOTO KK.

XX Asano T, Kennochi T, Isono K, Hirakawa T, Hamuro J;

XX WPI; 1994-027626/04.

XX N-PSDB; AAQ55111.

XX Use of a polypeptide having human ADF (thioredoxin) activity - for the

PT prophylaxis or therapeutic treatment of pancreatitis or diseases which

XX accompany pancreatic disorders.

XX Claim 2; Page 9; 15pp; English.

CC The ADF polypeptide suppresses the release of the pancreatic enzymes
 CC amylase and lipase into the blood thereby suppressing pancreatitis. The
 CC ADF is also capable of eliminating free radicals which can cause organ
 CC damage, as well as refolding denatured proteins which have been denatured
 CC by free radicals. The ADF may be isolated from cultured human derived
 CC cells and prepared by chemical synthesis or recombinant techniques
 CC (Updated on 25-MAR-2003 to correct PN field.)

CC Sequence 104 AA;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 30 WCGSPCK 35

RESULT 32

AAR72389

ID AAR72389 standard; protein; 104 AA.

AC AAR72389;

DT 10-NOV-1995 (first entry)

DE Recombinant human ADF.

KW ADF; inflammation; radiation sickness; fermentation; recombinant.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Active-site 31..34

PN JP07079780-A.

PD 28-MAR-1995.

PF 20-SEP-1993; 93JP-00233361.

PR 20-SEP-1993; 93JP-00233361.

PA (AJIN) AJINOMOTO KK.

DR WPI; 1995-157850/21.

DR N-PSDB; AAO87817.

PT Prepn. of recombinant human ADF by direct expression in E. coli - for
 PT treating inflammation and radiation sickness caused by commercially
 PT produced free radical(s).

PS Claim 2; Page 7-8; 11pp; Japanese.

CC The DNA sequence encoding human ADF was inserted into a plasmid which was
 CC then used to transform E.coli. The E.coli was then cultured and the
 CC recombinantly produced ADF harvested. Human ADF can be used as a treating
 CC agent for inflammation and radiation sickness

SQ Sequence 104 AA;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6

Db 30 WCGSPCK 35

RESULT 33

AAG80708

ID AAG80708 standard; protein; 104 AA.

AC AAG80708;

DT 18-MAR-2002 (first entry)

DE S. cerevisiae TRX2 protein.

KW TRX2; yeast; thioredoxin; lesion; intracellular redox.

OS Saccharomyces cerevisiae.

PN JP2001288103-A.

PD 16-OCT-2001.

XX 02-MAR-2000; 2000JP-00057204.
 PF 02-FEB-2000; 2000JP-00025258.

XX (ORIY) ORIENTAL YEAST CO LTD.
 XX

XX WPI; 2002-117628/16.
 DR N-PSDB; ABA97065.

PT A thioredoxin composition stable in solution used for treating and/or
 PT preventing lesions and diseases related to intracellular redox condition.

PS Claim 4; Page 14-15; 19pp; Japanese.

CC This invention describes a novel thioredoxin (TRX) composition, stable in
 CC solution which contains a yeast TRX derived from Saccharomyces cerevisiae
 CC X2180-1A. The TRX composition of the invention can be used for treating
 CC and/or preventing lesions and diseases related to intracellular redox
 CC conditions. This sequence represents the S. cerevisiae TRX2 protein
 CC described in the method of the invention

SQ Sequence 104 AA;

Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6

Db 30 WCGSPCK 35

RESULT 34

ABP60927

ID ABP60927 standard; protein; 104 AA.

AC ABP60927;

DT 06-SEP-2002 (first entry)

DE Staphylococcus aureus thioredoxin reductase SEQ ID NO:276.

KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KW vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro oesophageal reflux disease.

KW Staphylococcus aureus.

PN WO200250289-A1.

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 05-JUL-2001; 2001US-0302885P.

PR 04-DEC-2001; 2001US-00060038.

PA (SEMB-) SEMBIOSYS GENETICS INC.

PI (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK;
 XX Del Val G, Zaplachinski S, Moloney M;
 DR WPI; 2002-508806/54.

PT Producing oil body associated with recombinant multimeric protein complex

PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 82; Page 323; 362pp; English.

The present invention describes a method (M1) for producing an oil body associated with a recombinant multi-metric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition used to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, emphysema, bronchiolopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN85953 to ABN86067 to ABP00964 represent sequence given in the exemplification of the present invention

SQ Sequence 104 AA;

```

Query Match Similarity      100.0%; Score 47; DB 5; Length 104;
Beet Local Similarity      100.0%; Pred. No. 14;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 WCGPCK 6
        |||||
Db      28 WCGPCK 33

```

RESULT 35
ABP60803
ID ABP60803 standard; protein; 104 AA

DT 06-SEP-2002 (first entry)

DE Homo sapiens thioredoxin SEQ ID NO:152.

KM Multimeric propeptide; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antiparasitic;
 KM vasotropic; vulniferous; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; catenact; diathee;
 KM chronic obstructive pulmonary disease; emphysema; emphysema; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.

OS Homo sapiens.

PN WO200250289-A1.

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS IN

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Van Rooijen G, Deckers H, Heifetz PB,

PI Del Val G, Zaplachinski S, Moloney M;

XX

DR WPI; 2002-508806/54.

PT Producing oil body associated with recombinant multimeric protein complex
PT e.g. redox proteins and immunoglobulins comprises producing recombinant
PT polypeptides capable of forming the complex in cells comprising oil
PT bodies.

PS Claim 81; Page 246; 362pp; English.

The present invention describes a method (M1) for producing an oil body associated with a recombinant multimeric protein complex (MPC). M1 comprises producing in a cell comprising oil bodies a first and second recombinant polypeptide (P1, P2), where P1 is capable of associating with P2 to form the MPC and associating the complex with an occlusion body (OB) through an OB-targeting-protein capable of associating with OB and P1. M1 is useful for producing an oil body associated with a recombinant MPC. The oil bodies are further formulated for use in the preparation of a food product such as milk or wheat based food product, personal care product which reduces the oxidative stress on the surface area of the human body or used to lighten the skin, or a pharmaceutical composition to treat chronic obstructive pulmonary disease (COPD), cataracts, diabetes, emphysema, bronchiolopulmonary disease, psoriasis, malignancies, reperfusion injury, wound healing, sepsis, gastro intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD (gastro oesophageal reflux disease). ABN959563 to ABN89593 and ABF60677 to ABP00964 represent sequence given in the exemplification of the present invention.

SQ Sequence 104 AA;

Query Match	100.0%;	Score 47;	DB 5;	Length 104;
Best Local Similarity	100.0%;	Pred. No. 14;		
Matches 6; Conservative	0;	Mismatches	0;	Gaps 0

RESULT 36
ABP60797
ID ABP60797 standard; protein; 104 AA

DT 06-SEP-2002 (first entry)

DE Bos taurus thioredoxin SEQ ID NO:146.

KM Multimeric protein; redox protein; thiorodoxin; chlorodioxin reductase;
KM oil body; ophthalmological; antidiabetic; cytosolic; antiperoxidic;
KM vasotropic; vulnary; antibacterial; immunosuppressive; antilicer;
KM Food product; milk; wheat; oxidative stress; cataract; diabetes;
KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
KM gastro oesophageal reflux disease

OS Bos taurus.

PN WO200250289-A1

PD 27-JUN-2002.

PF 19-DEC-2001; 2001WO-US050240.

PR 19-DEC-2000; 2000US-00742900.

PR 04-DEC-2001; 2001US-00006038.

PA (SEMB-) SEMBIOSYS GENETICS IN

PA (SYGN) SYNGENTA PARTICIPATIONS AG

XX

PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M,
 XX
 DR MPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 244; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 Db 30 WCGSPCK 35
 RESULT 37
 ABP60812
 ID ABP60812 standard; protein; 104 AA.
 AC ABP60812;
 XX
 DT 06-SRP-2002 (first entry)
 XX
 DE Ovis aries thiredoxin SEQ ID NO:161.
 XX
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytoskeletal; antipsoriatic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Ovis aries.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00060638.
 XX

PA (SEMR-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M,
 XX
 DR MPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 249; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 Db 30 WCGSPCK 35
 RESULT 38
 ABP60805
 ID ABP60805 standard; protein; 104 AA.
 AC ABP60805;
 XX
 DT 06-SRP-2002 (first entry)
 XX
 DE Macaca mulatta thiredoxin SEQ ID NO:154.
 XX
 XX Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytoskeletal; antipsoriatic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 OS Macaca mulatta.
 XX
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2000; 2000US-00742900.
 PR

PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M;
 XX MPI; 2002-508806/54.
 DR
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 247; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
 CC malinancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 XX
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 30 WCGPCK 35
 XX
 RESULT 39
 ID ABP60806
 XX ABP60806 standard; protein; 104 AA.
 AC
 XX ABP60806;
 DT 06-SEP-2002 (first entry)
 XX
 DE Mus musculus thioedoxin SEQ ID NO:155.
 XX
 DE
 KM Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 XX Mus musculus.
 OS
 PN WO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX

PF 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2000; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M;
 XX MPI; 2002-508806/54.
 DR
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81; Page 247; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiolopulmonary disease, psoriasis,
 CC malinancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 XX
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 30 WCGPCK 35
 XX
 RESULT 40
 ID ABP60809
 XX ABP60809 standard; protein; 104 AA.
 AC
 XX ABP60809;
 DT 06-SEP-2002 (first entry)
 XX
 DE Oryctolagus cuniculus thioedoxin SEQ ID NO:158.
 XX
 DE
 KM Multimeric protein; redox protein; thioedoxin; thioedoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytostatic; antipsoriatic;
 KM vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KM bronchiolopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX
 XX Oryctolagus cuniculus.
 OS
 PN WO200250289-A1.
 XX

XX 27-JUN-2002.
 PD 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2001; 2001WO-US050240.
 PR 19-DEC-2000; 2000US-00742900.
 XX 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 DR
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PS Claim 81; Page 248; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 30 WCGSPCK 35
 RESULT 41
 ABP60810
 ID ABP60810 standard; protein; 104 AA.
 AC ABP60810;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Rattus norvegicus thioresoxin SEQ ID NO:159.
 XX
 XX Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
 KM vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KM gastro oesophageal reflux disease.
 XX

OS Rattus norvegicus.
 XX
 PN WO200250289-A1.
 XX
 XX 27-JUN-2002.
 PD 19-DEC-2001; 2001WO-US050240.
 XX
 XX 19-DEC-2001; 2001WO-US050240.
 PR 19-DEC-2000; 2000US-00742900.
 XX 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 PI Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 DR
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 PS Claim 81; Page 248-249; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 104 AA;
 Query Match 100.0%; Score 47; DB 5; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 30 WCGSPCK 35
 RESULT 42
 ABP60801
 ID ABP60801 standard; protein; 104 AA.
 AC ABP60801;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Gallus gallus thioresoxin SEQ ID NO:150.
 XX
 XX Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
 KM oil body; ophthalmological; antidiabetic; cytosolic; antipsoriatic;
 KM vasotropic; vulnary; antibacterial; immunosuppressive; antitumor;
 KM food product; milk; wheat; oxidative stress; cataract; diabetes;
 KM chronic obstructive pulmonary disease; emphysema; psoriasis; sepsis;
 KM bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KM

KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 XX gastro oesophageal reflux disease.
 OS Gallus gallus.
 XX WO200250289-A1.
 PN WO200250289-A1.
 XX 27-JUN-2002.
 PD 27-JUN-2002.
 XX 19-DEC-2001; 2001WO-US050240.
 PF 19-DEC-2001; 2001WO-US050240.
 XX 19-DEC-2001; 2000US-00742900.
 PR 05-JUL-2001; 2001US-0302885P.
 PR 04-DEC-2001; 2001US-0006038.
 XX (SEMB-) SEMBIOSYS GENETICS INC.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;
 XX WPI; 2002-508806/54.
 DR WPI; 2002-508806/54.
 XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX Claim 81; Page 245-246; 362pp; English.
 PS The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, emphysema, bronchiopulmonary disease, psoriasis,
 CC malnutrition, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease), ABN89569 to ABN89593 and ABP60677 to
 CC ABP6964 represent sequence given in the exemplification of the present
 CC invention
 XX SQ Sequence 104 AA;
 XX
 XX Query Match 100.0%; Score 47; DB 5; Length 104;
 XX Best Local Similarity 100.0%; Pred. No. 14;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 XX |||||
 DB 30 WCGPCK 35
 XX
 XX RESULT 43
 XX ABG93115
 ID ABG93115 standard; protein; 104 AA.
 XX
 XX ABG93115;
 AC
 XX 21-NOV-2002 (first entry)
 DT 21-NOV-2002 (first entry)
 XX
 XX S. cerevisiae BAX-associated protein fragment SEQ ID 188.
 DE
 XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
 KM vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
 KW apoptosis; fungal; yeast; infection; autoimmune disease; leukaemia;

KW neurodegeneration; cell death.
 XX Saccharomyces cerevisiae.
 OS
 XX WO200264766-A2.
 PN WO200264766-A2.
 XX 22-AUG-2002.
 PD 22-AUG-2002.
 XX 21-DEC-2001; 2001WO-EP015398.
 PF 21-DEC-2001; 2001WO-EP015398.
 XX 22-DEC-2000; 2000EP-008700318.
 PR 04-JAN-2001; 2001EP-00870002.
 PR 09-JAN-2001; 2001EP-00870003.
 XX (JANC) JANSSEN PHARM NV.
 PA
 XX Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
 PI WPI; 2002-667002/71.
 DR N-PSDB; ABQ76381.
 XX
 XX New isolated nucleic acid representing a synthetic BAX-gene, useful as
 PT medicament for treating, preventing and/or alleviating yeast or fungal
 PT infections or proliferative disorders, or for preventing apoptosis in
 PT certain diseases.
 XX Claim 36; Fig 1; 34pp; English.
 PS This invention describes a novel nucleic acid representing a synthetic
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
 CC resistant yeast or fungi, identifying, or obtaining and identifying
 CC Candida spp. sequences that are differentially expressed in a pathway
 CC eventually leading to programmed cell death or identifying inhibitors or
 CC inhibitor sequences of Bax-induced cell death. The products of the
 CC invention have cytostatic, fungicide; immunosuppressive, virucide and
 CC vasotropic activity and can be used in vaccines or for gene therapy. The
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
 CC antisense molecules and antibodies are useful as medicaments or in
 CC preparing a medicament for treating, preventing and/or alleviating
 CC diseases associated with yeast or fungi or proliferative disorders, such
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds
 CC or polypeptides, or the genetically modified organism are useful for
 CC preparing a medicament for modifying the endogenic flora of humans and
 CC other mammals. The vaccine is useful for immunising against yeast or
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,
 CC leukaemia, diseases related with viral infections or neurodegenerations.
 CC This sequence represents a polypeptide associated with the Bax gene
 CC described in the disclosure of the invention
 XX SQ Sequence 104 AA;
 XX
 XX Query Match 100.0%; Score 47; DB 5; Length 104;
 XX Best Local Similarity 100.0%; Pred. No. 14;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 XX |||||
 DB 30 WCGPCK 35
 XX
 XX RESULT 44
 XX ADK90667
 ID ADK90667 standard; protein; 104 AA.
 XX
 XX ADK90667;
 AC
 XX 20-MAY-2004 (first entry)
 DT 20-MAY-2004 (first entry)
 XX
 XX Baker's yeast thioredoxin 1 (THX1) protein SeqID 12.
 DE
 XX Baker's yeast; THX1; transgenic; abiotic stress response; crop plant;
 KM oxidoreductase stress-related protein; ONSRP; environmental stress;
 KW salinity; drought; temperature; chemical; pathogen; glutaredoxin; GRX;

```

KW chioredoxin; THX; Quantitative Trait Locus; QTL.
XX
OS Saccharomyces cerevisiae.
XX
PN WO2004018687-A2.
XX
PD 04-MAR-2004.
XX
PF 01-JUL-2003; 2003WO-EP006994.
XX
PR 07-AUG-2002; 2002EP-00017671.
XX
PA (BADI ) BASF PLANT SCI GMBH.
XX
PI Chardonnais A, Puzio P;
XX
DR WPI; 2004-226856/21.
XX
DR N-PSDB; ADR90666.
XX
PT New transgenic plant cell transformed by oxidoreductase stress-related
PT protein (ORSRP) coding nucleic acid, useful for producing a transgenic
XX plant with increased environmental stress tolerance.
XX
PS Example 2; SEQ ID NO 12; 140bp; English.
XX
CC The invention relates to novel transgenic plant cells transformed by
CC genes encoding proteins associated with the abiotic stress response.
CC Specifically, it refers to transgenic crop plants expressing the
CC heterologous oxidoreductase stress-related protein (ORSRP) that confers
CC increased tolerance and/or resistance to environmental stresses such as
CC salinity, drought, temperature, chemicals or pathogens. The present
CC invention describes the ORSRPs as heat-stable glutaredoxin (GRX) and/or
CC thioredoxin (THX) proteins, where expression is under the control of an
CC inducible tissue-specific or developmentally-specific promoter and
CC furthermore it provides antisense oligos and RNA interference molecules
CC to inhibit ORSRP expression. In addition, these nucleic acids are useful
CC as Quantitative Trait Locus (QTL) markers that can map genetic loci
CC associated with environmental stress tolerance. This polypeptide sequence
CC is a baker's yeast THX protein of the invention.
XX
SQ Sequence 104 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
DB 30 WCGPCK 35
XX
RESULT 45
AD059801
ID AD059801 standard; protein; 104 AA.
XX
AC AD059801;
XX
DT 15-JUL-2004 (first entry)
XX
DE B. subtilis metabolic pathway gene, trxA, protein.
XX
KW chip; metabolic pathway; acoA; ahpc; ahpf; citB; clpC; clpP; codY; csps;
KW csps; des; dnaK; eno; glrA; groEL; groL; ibpA; ibpF; katA; katB; lcpP;
KW lch; opuAB; phoA; phoD; pscs; purC; purN; pyrB; pyrF; sigB; trxA; trxA;
KW ydJf; fermentation monitoring; process control; increased efficiency.
XX
OS Bacillus subtilis.
XX
PN DE10242433-A1.
XX
PD 25-MAR-2004.
XX
PF 11-SEP-2002; 2002DE-01042433.

```

```

XX
PR 11-SEP-2002; 2002DE-01042433.
XX
PA (HENK ) HENKEL KGAA.
XX
PA (UYGR ) UNIV GREIFSWALD.
XX
PI Feesche J, Maurer K, Breves R, Schweder T, Hecker M, Juegen B,
XX Voigt B;
XX
DR WPI; 2004-271050/26.
XX
DR N-PSDB; AD059800.
XX
PT Chip carrying probes for specific genes, useful for rapid monitoring of
XX organism status, particularly during fermentation.
XX
PS Disclosure; SEQ ID NO 78; 138bp; German.
XX
CC The invention relates to a chip that carries probes for at least one
CC regulated genes involved in the corresponding metabolic pathways in other
CC organisms. The specified genes are acoA, ahpc, citB, clpC, clpP,
CC codY, csps, des, dnaK, eno, glrA, groEL, groL, ibpA, ibpF, katA,
CC katB, lcpP, lch, opuAB, phoA, phoD, pscs, purC, purN, pyrB, pyrF, sigB,
CC trxA, trxA and ydJf. The specification includes a table identifying the
CC products of these genes. The chips are used to determine the
CC physiological condition of organisms being used in a biological process,
CC especially for monitoring fermentations for production of a protein or
CC low molecular weight compound, but also for laboratory-scale cloning and
CC expression analysis. The method is quicker than gel electrophoretic
CC methods currently used, so allows a more rapid intervention for process
CC control and thus increased efficiency. The present sequence represents
XX the amino acid sequence of a B. subtilis metabolic pathway gene protein.
XX
SQ Sequence 104 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 104;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
DB 28 WCGPCK 33
XX
RESULT 46
AD588157
ID AD588157 standard; protein; 104 AA.
XX
AC AD588157;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human protein of a TNF-alpha signalling pathway protein complex Seqid 12.
XX
KW protein complex; tumour necrosis factor-alpha signalling pathway;
KW TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
KW inflammatory bowel disease; infectious disease; septic shock;
KW bacterial infection; neurological disease; stroke-induced inflammation;
KW neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
KW antirheumatic; cytoskeletal; antibacterial; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004035783-A2.
XX
PD 29-APR-2004.
XX
PF 24-SEP-2003; 2003WO-EP050655.
XX
PR 26-SEP-2002; 2002EP-00021809.
XX
PR 10-FEB-2003; 2003EP-00100274.
XX
PA (CELL-) CELLZOME AG.
XX

```

PI Bouwmeester T, Huhse B, Bauch A, Ruffner H, Bauer A, Kuester B;
 XX Supert3-Furga G, Kruse U;
 XX WPI; 2004-348460/32.
 DR
 XX
 PT New protein complex comprising at least one first and second protein of
 PT the Tumor Necrosis Factor-alpha (TNF-alpha)-signaling pathway, useful for
 PT diagnosing or treating inflammation, neurological diseases, infectious
 PT diseases or cancer.
 XX
 PS Example; SEQ ID NO 12, 1980pp; English.
 XX
 CC This invention relates to novel protein complexes of the tumour necrosis
 CC factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to
 CC methods for preparing these complexes comprising at least two component
 CC proteins, as well as screening methods to identify modulators of the
 CC pathway, which include antibodies, agonists and antagonists thereof. The
 CC present invention describes a protein complex and kit that are useful for
 CC diagnosing, prognosing or treating chronic inflammatory diseases such as
 CC rheumatoid arthritis and inflammatory bowel disease; infectious diseases
 CC such as septic shock and bacterial infections; neurological diseases such
 CC as stroke-induced inflammation in neurons; neurodegenerative diseases and
 CC cancer. Accordingly, these complexes can be used for the development of
 CC pharmaceutical compositions that exhibit anti-inflammatory, antiarthritic,
 CC antineumatic, cytostatic and antibacterial activities and can be used
 CC for gene therapy purposes. In particular, the invention further provides
 CC siRNA-oligonucleotides useful for inhibiting protein expression for in
 CC vitro or cell culture assays. This polypeptide is a human protein that
 CC can be used in combination with other proteins provided in the
 CC specification to form novel complexes of the TNF-alpha signalling pathway
 CC of the invention.
 CC
 SQ Sequence 104 AA;
 XX
 XX
 Query Match 100.0%; Score 47; DB 8; Length 104;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 30 WCGSPCK 35
 XX
 RESULT 47
 AAP92141
 ID AAP92141 standard; protein; 105 AA.
 XX
 AC AAP92141;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-JUN-1990 (first entry)
 XX
 DE Recombinant human adult T cell leukaemia derived factor.
 XX
 KM Human adult T cell leukaemia derived factor; hADF; cancer;
 KM immunodeficiency disease.
 XX
 OS Homo sapiens.
 XX
 PI Key Location/Qualifiers
 FH Region 2..105
 FT /note= "Claim 1"
 XX
 PN EP299206-A.
 XX
 PD 18-JAN-1989.
 XX
 PF 10-JUN-1988; 88BP-00109311.
 XX
 PR 12-JUN-1987; 87JP-00146348.
 PR 31-MAY-1988; 88DP-00134218.
 XX
 PA (AJIN) AJINOMOTO KK.

XX
 PI Yodoi J, Tagaya Y, Maeda M, Matsui H, Kondo N, Hamuro J;
 XX
 DR WPI; 1989-016762/03.
 DR N-PSDB; AAN93083.
 XX
 PT Recombinant human adult T cell leukaemia derived factor polypeptide -
 PT used for treating cancer, immuno-deficiency disease etc.
 XX
 PS Disclosure; Page; 24pp; English.
 XX
 CC DNA encoding the polypeptide was sequenced from a gene bank prep. from
 CC mRNA isolated from ATL-2 cells from patient with adult T leukaemia virus.
 CC Vectors contg. the DNA can be used to transform host cells for prodn. of
 CC hADF polypeptide. The polypeptide causes differentiation and induces
 CC growth of lymphocytes and fibroblasts. The N-terminal Met is optional.
 CC Similar peptides with deletions, sustrs. and allelic derivs. may also be
 CC used. See also AAP94809. (Updated on 25-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 105 AA;
 XX
 XX
 Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGSPCK 6
 DB 31 WCGSPCK 36
 XX
 RESULT 48
 AAR42819
 ID AAR42819 standard; protein; 105 AA.
 XX
 AC AAR42819;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAY-1994 (first entry)
 XX
 DE ECFE/thioredoxin/ADF.
 XX
 KM Eosinophil cytotoxicity enhancing factor; ECFE; stimulation; diagnosis;
 KM therapy; thioredoxin.
 XX
 OS Homo sapiens.
 XX
 PN WO9320107-A1.
 XX
 PD 14-OCT-1993.
 XX
 PF 06-APR-1993; 93WO-US003310.
 XX
 PR 06-APR-1992; 92US-00862832.
 PR 06-JUL-1992; 92US-00906842.
 XX
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 PI Silberstein DS, Balcewicz-Sablinska MK;
 XX
 DR WPI; 1993-336837/42.
 DR N-PSDB; AAQ49402.
 XX
 PT Shortened Eosinophil Cytotoxicity-Enhancing Factor proteins - having
 PT Eosinophil-stimulating activity, for use in diagnosis and therapy.
 XX
 PS Disclosure; Fig 6; 96pp; English.
 XX
 CC A 14 kDa molecule was isolated by three separate groups and found to
 CC support the growth of an EBV transformed B lymphocyte cell line in the
 CC manner of IL-1. It was also found to induce the expression of IL-2
 CC receptors in a large granular lymphocyte cell line from an ATL patient in
 CC the manner of IL-1. The molecule has been designated various names, these
 CC being Eosinophil Cytotoxicity-Enhancing Factor; (ECFE) thioredoxin and

CC ADF. The molecule has also been found to mediate the growth inhibitory
 CC properties of interferon gamma. Some shortened ECF's are useful because
 CC they retain eosinophil stimulating activity but lack proinflammatory
 CC dihalol reductase activity. In particular they can be used for killing
 CC tumour cells. (Updated on 25-Mar-2003 to correct PN field.)

SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 49
 AAR37700
 ID AAR37700 standard; protein; 105 AA.

XX AAR37700;

DT 09-NOV-1993 (first entry)

DE ADF.

KM Human; ADF; transgenic; mouse; beta-actin; promoter; terminator;
 KW resistant; stress; anti-inflammatory drugs.

OS Homo sapiens.

PN JP05130819-A.

PD 28-MAY-1993.

PF 12-NOV-1991; 91JP-00295618.

PR 12-NOV-1991; 91JP-00295618.

PA (AJIN) AJINOMOTO KK.

DR WPI; 1993-208254/26.

DR N-PSDB; AAQ43433.

PT New human ADF transgenic mouse - is resistant to stress and is useful for
 PT prepn. of antiinflammatory drugs.

PS Claim 3; Page 5; 10pp; Japanese.

CC This sequence represents human ADF. The DNA encoding this sequence may be
 CC used in the production of a transgenic mouse. The transgenic mouse
 CC contains, in the 5' to 3' direction, a human beta-actin promoter, the
 CC human ADF coding gene, a termination codon, a human beta-actin poly(A)
 CC signal and a human beta-actin terminator. The transgenic mouse is
 CC resistant to stress. It is useful in the research of the mechanism of
 CC stress and for the development of anti-inflammatory drugs

SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 50
 AAR47856
 ID AAR47856 standard; protein; 105 AA.

AC AAR47856;

XX 25-MAR-2003 (revised)

DT 18-JUL-1994 (first entry)

DE Human ADF-polypeptide.

KM ADF; thioredoxin; pancreatitis; amylase; lipase; free radicals;
 KW protein folding; denaturing; renaturing.

OS Homo sapiens.

PN EP579958-A1.

PD 26-JAN-1994.

PF 18-JUN-1993; 93BP-00109794.

PR 19-JUN-1992; 92JP-00161454.

PA (AJIN) AJINOMOTO KK.

PI Asano T, Kermochi T, Isono K, Hirakawa T, Hamuro J;

DR WPI; 1994-027626/04.

DR N-PSDB; AAQ55112.

PT Use of a polypeptide having human ADF (thioredoxin) activity - for the
 PT prophylaxis or therapeutic treatment of pancreatitis or diseases which
 PT accompany pancreatic disorders.

PS Claim 2; Page 12; 15pp; English.

CC The ADF polypeptide suppresses the release of the pancreatic enzymes
 CC amylase and lipase into the blood thereby suppressing pancreatitis. The
 CC ADF is also capable of eliminating free radicals which can cause organ
 CC damage, as well as refolding denatured proteins which have been denatured
 CC by free radicals. The ADF may be isolated from cultured human derived
 CC cells and prepared by chemical synthesis or recombinant techniques
 CC (Updated on 25-Mar-2003 to correct PN field.)

SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 31 WCGPCK 36

RESULT 51

AAR72390
 ID AAR72390 standard; protein; 105 AA.

XX AAR72390;

DT 10-NOV-1995 (first entry)

DE Recombinant human ADF.

KM ADF; inflammation; radiation sickness; fermentation; recombinant.

OS Homo sapiens.

FT Key Location/Qualifiers
 FT Active-site 32..35

PN JP07079780-A.

PD 28-MAR-1995.

```

PF 20-SEP-1993; 93JP-00233361.
XX
PR 20-SEP-1993; 93JP-00233361.
XX
PA (AJIN ) AJINOMOTO KK.
XX
DR WPI; 1995-157850/21.
XX
DR N-PSDB; AA087818.
XX
PT Prepn. of recombinant human ADF by direct expression in E. coli - for
PT treating inflammation and radiation sickness caused by commercially
PT produced free radical(s).
XX
PS Claim 3; Page 8; 11pp; Japanese.
XX
CC The DNA sequence encoding human ADF was inserted into a plasmid which was
CC then used to transform E.coli. The E.coli was then cultured and the
CC recombinantly produced ADF harvested. Human ADF can be used as a treating
CC agent for inflammation and radiation sickness
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGPCK 6
DB 31 MCGPCK 36

RESULT 52
AAW69567
ID AAW69567 standard; protein; 105 AA.
XX
AC AAW69567;
XX
DT 15-OCT-1998 (first entry)
XX
DB Human thioredoxin mutant C62S/C69S/C73S.
XX
KW Human; thioredoxin; mutant; variant; TRX; AP-1; transcriptional activity;
KW Ref-1.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 62 /note= "Cys in wild type"
FT Misc-difference 69 /note= "Cys in wild type"
FT Misc-difference 73 /note= "Cys in wild type"
XX
EP853088-A2.
XX
PD 15-JUL-1998.
XX
PE 14-JAN-1998; 98EP-00100535.
XX
PR 14-JAN-1997; 97JP-00004489.
XX
PA (ORIV ) ORIENTAL YEAST CO LTD.
PA (YODO/) YODOI J.
XX
PI Yodoi J;
XX
DR WPI; 1998-364621/32.
XX
PT New thioredoxin variants with amino acid substitutions for cysteine
PT except at active centre for increasing stability in non-reducing
PT conditions - used with Ref-1 to enhance AP-1 transcriptional activity.

```

```

XX
PS Example 3; Page; 14pp; English.
XX
CC The present sequence represents a human thioredoxin (TRX) variant derived
CC from the wild-type sequence (obtained from Genbank), as stated in the
CC specification. TRX variants can be made stable under non-reducing
CC conditions by substituting at least one or all Cys residues by other
CC amino acid residues, except that Cys residues in the active centre of TRX
CC remain unmodified. Also described in the present invention is a factor
CC for enhancing the transcriptional activity of AP-1 which comprises the
CC TRX variant and Ref-1 associated with each other via an S-S bond. TRX
CC variants can be used with Ref-1 to enhance AP-1 transcriptional activity.
CC TRX variants do not form multimers and are stable under non-reducing
CC conditions
XX
SQ Sequence 105 AA;

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGPCK 6
DB 31 MCGPCK 36

RESULT 53
AAV25908
ID AAV25908 standard; protein; 105 AA.
XX
AC AAV25908;
XX
DT 06-OCT-1999 (first entry)
XX
DE Human thioredoxin protein.
XX
KW Thioredoxin; thioredoxin reductase; human; antisense; primer; metastasis;
KW cytosolic; tumour growth inhibitor; detection; nuclease resistant;
KW phosphorothioate linkage.
XX
OS Homo sapiens.
XX
PN WO938963-A1.
XX
PD 05-AUG-1999.
XX
PE 29-JAN-1999; 99WO-CA000077.
XX
PR 30-JAN-1998; 98US-0073196P.
XX
PA (GENE-) GENESENSE TECHNOLOGIES INC.
XX
PI Wright JA, Young AH, Lee YS;
XX
DR WPI; 1999-469328/39.
XX
DR N-PSDB; AA200544.
XX
PT Antisense oligonucleotides against thioredoxin and thioredoxin reductase
PT genes, useful for inhibiting tumor growth and metastasis.
XX
PS Disclosure; Fig 2; 88pp; English.
XX
CC This invention describes novel antisense oligonucleotides against
CC thioredoxin and thioredoxin reductase gene which have cytostatic activity
CC and are useful for inhibiting tumour growth and metastasis in mammals.
CC They may also be used as hybridization probes to detect the presence of
CC the thioredoxin and thioredoxin reductase mRNAs in mammalian cells. They
CC may also be used as molecular weight markers. The antisense
CC oligonucleotides are nuclease resistant due to the presence of
CC phosphorothioate internucleotide linkages. This sequence represents the
CC human thioredoxin protein
XX
SQ Sequence 105 AA;

```

Query Match 100.0%; Score 47; DB 2; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 54
 AAG03956
 ID AAG03956 standard; protein; 105 AA.

AC AAG03956;
 XX 06-OCT-2000 (first entry)
 DT Human secreted protein, SEQ ID NO: 8037.
 XX
 DE Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GBST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 XX
 DR N-PSDB; AAC03962.

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 8037; 71bp + Sequence listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

XX Sequence 105 AA;

Qy Query Match 100.0%; Score 47; DB 3; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 55
 ABP60700

ID ABP60700 standard; protein; 105 AA.

XX ABP60700;

AC 06-SEP-2002 (first entry)

DT Human thioredoxin protein SEQ ID NO:47.

XX
 DE Human thioredoxin protein SEQ ID NO:47.
 XX
 KW Multimeric protein; redox protein; thioredoxin; thioredoxin reductase;
 KW oil body; ophthalmological; antidiabetic; cyostatic; antiposrotic;
 KW vasotropic; vulnary; antibacterial; immunosuppressive; antilester;
 KW food product; milk; wheat; oxidative stress; cataract; diabetes;
 KW chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 KW bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 KW gastro intestinal bleeding; intestinal bowel disease; ulcer;
 KW gastro oesophageal reflux disease.

XX Homo sapiens.

XX WO200250289-A1.

XX 27-JUN-2002.

XX 19-DEC-2001; 2001WO-US050240.

XX 19-DEC-2000; 2000US-00742900.

XX 05-JUL-2001; 2001US-0302885P.

XX 04-DEC-2001; 2001US-00006038.

XX (SEMB-) SEMBIOSYS GENETICS INC.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Van Rooijen G, Deckers H, Helfetz PB, Briggs SP, Dalmia BK;
 PI Del Val G, Zaplachinski S, Moloney M;

XX WPI; 2002-508806/54.

XX N-PSDB; ABR89591.

XX Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.

XX Disclosure; Page 203; 362pp; English.

XX The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malignancies, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease). ABR89569 to ABR89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention

XX Sequence 105 AA;

Qy Query Match 100.0%; Score 47; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 56
 ID ABP60757 standard; protein; 105 AA.
 XX
 AC ABP60757;
 XX
 DT 06-SEP-2002 (first entry)
 XX
 DE Corynebacterium nephridii thioresoxin SEQ ID NO:106.
 XX
 XX Multimeric protein; redox protein; thioresoxin; thioresoxin reductase;
 XX oil body; ophthalmological; antidiabetic; cytostatic; antiproliferative;
 XX vasotropic; vulnery; antibacterial; immunosuppressive; antitumor;
 XX food product; milk; wheat; oxidative stress; cataract; diabetes;
 XX chronic obstructive pulmonary disease; envenomation; psoriasis; sepsis;
 XX bronchiopulmonary disease; malignancy; reperfusion injury; wound healing;
 XX gastro intestinal bleeding; intestinal bowel disease; ulcer;
 XX gastro oesophageal reflux disease.
 XX
 OS Corynebacterium nephridii.
 XX
 PN MO200250289-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050240.
 XX
 PR 19-DEC-2000; 2000US-00742800.
 XX
 PR 05-JUL-2001; 2001US-0302885P.
 XX
 PR 04-DEC-2001; 2001US-00006038.
 XX
 PA (SEMB-) SEMBIOSYS GENETICS INC.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Van Rooijen G, Deckers H, Heifetz PB, Briggs SP, Dalmia BK,
 PI Del Val G, Zaplachinski S, Moloney M;
 XX
 DR MPI; 2002-508806/54.
 XX
 PT Producing oil body associated with recombinant multimeric protein complex
 PT e.g. redox proteins and immunoglobulins comprises producing recombinant
 PT polypeptides capable of forming the complex in cells comprising oil
 PT bodies.
 XX
 PS Claim 81, Page 230; 362pp; English.
 XX
 CC The present invention describes a method (M1) for producing an oil body
 CC associated with a recombinant multimeric protein complex (MPC). M1
 CC comprises producing in a cell comprising oil bodies a first and second
 CC recombinant polypeptide (P1, P2), where P1 is capable of associating with
 CC P2 to form the MPC and associating the complex with an occlusion body
 CC (OB) through an OB-targeting-protein capable of associating with OB and
 CC P1. M1 is useful for producing an oil body associated with a recombinant
 CC MPC. The oil bodies are further formulated for use in the preparation of
 CC a food product such as milk or wheat based food product, personal care
 CC product which reduces the oxidative stress on the surface area of the
 CC human body or used to lighten the skin, or a pharmaceutical composition
 CC used to treat chronic obstructive pulmonary disease (COPD), cataracts,
 CC diabetes, envenomation, bronchiopulmonary disease, psoriasis,
 CC malnutrition, reperfusion injury, wound healing, sepsis, gastro
 CC intestinal (GI) bleeding, intestinal bowel disease (IBD), ulcers, GERD
 CC (gastro oesophageal reflux disease), ABN89569 to ABN89593 and ABP60677 to
 CC ABP60964 represent sequence given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 105 AA;
 XX

Query Match 100.0%; Score 47; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 57
 ID ABG93363 standard; protein; 105 AA.
 XX
 AC ABG93363;
 XX
 DT 21-NOV-2002 (first entry)
 XX
 DE Human BAX-associated protein fragment SEQ ID 684.
 XX
 XX Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide;
 XX vasotropic; vaccine; gene therapy; proliferative disorder; cancer;
 XX apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia;
 XX neurodegeneration; cell death.
 XX
 OS Homo sapiens.
 XX
 PN MO200264766-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 21-DEC-2001; 2001WO-EP015398.
 XX
 PR 22-DEC-2000; 2000EP-00870318.
 XX
 PR 04-JAN-2001; 2001EP-00870002.
 XX
 PR 09-JAN-2001; 2001EP-00870003.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Contreras RH, Eberhardt I, Luyten WHML, Reekmans RJ;
 XX
 DR MPI; 2002-667002/71.
 XX
 DR N-PSDB; ABQ76629.
 XX
 PT New isolated nucleic acid representing a synthetic BAX-gene, useful as
 PT medicament for treating, preventing and/or alleviating yeast or fungal
 PT infections or proliferative disorders, or for preventing apoptosis in
 PT certain diseases.
 XX
 PS Claim 36; Fig 2; 344pp; English.
 XX
 CC This invention describes a novel nucleic acid representing a synthetic
 CC Bax gene. The Bax gene of the invention is useful for identifying Bax-
 CC resistant yeast or fungi, identifying, or obtaining and identifying
 CC Candida spp. sequences that are differentially expressed in a pathway
 CC eventually leading to programmed cell death or identifying inhibitors or
 CC inhibitor sequences of Bax-induced cell death. The products of the
 CC invention have cytostatic, fungicide, immunosuppressive, virucide and
 CC vasotropic activity and can be used in vaccines or for gene therapy. The
 CC isolated nucleic acids, polypeptides, pharmaceutical compositions,
 CC antisense molecules and antibodies are useful as medicaments or in
 CC preparing a medicament for treating, preventing and/or alleviating
 CC diseases associated with yeast or fungi or proliferative disorders, such
 CC as cancer, or for preventing apoptosis in certain diseases. The compounds
 CC or polypeptides, or the genetically modified organism are useful for
 CC preparing a medicament for modifying the endogenous flora of humans and
 CC other mammals. The vaccine is useful for immunising against yeast or
 CC fungal infections. Apoptosis-related diseases include autoimmune disease,
 CC ischaemia, diseases related with viral infections or neurodegenerations.
 CC This sequence represents a polypeptide associated with the Bax gene
 CC described in the disclosure of the invention
 XX
 SQ Sequence 105 AA;
 XX

Query Match 100.0%; Score 47; DB 5; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 58

ABO07225
 ID ABO07225 standard; protein; 105 AA.

AC ABO07225;

DT 13-AUG-2003 (first entry)

DE Human p53 modifying protein, SEQ ID 185.

KW Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
 KW antipapillary; p53 pathway; breast cancer; colon cancer; kidney cancer;
 KW lung cancer; ovarian cancer; angiogenesis; cell cycle;
 KW apoptotic disorder; cell proliferation disorder.

OS Homo sapiens.

PN WO200299122-A1.

PD 12-DEC-2002.

PF 03-JUN-2002; 2002WO-US017382.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

PA (EXEL-) EXELIXIS INC.

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP,

DR WPI; 2003-156859/15.

DR N-PSDB; ACD13398.

PT Identifying modulators of the p53 pathway for use in treating apoptotic

PT or cell proliferation disorders, comprises screening for agents that

PT modulate activity of a human ortholog of genes that modify the p53

PT pathway in Drosophila.

PS Example 2; Page 536; 678pp; English.

CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to a HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a control; and (d) determining
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood of disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer.
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,

CC apoptotic or cell proliferation disorders. The present sequence
 CC represents a human p53 pathway modifying protein

CC Sequence 105 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 6; Length 105;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 59

ABR92158
 ID ABR92158 standard; protein; 105 AA.

AC ABR92158;

DT 10-SEP-2003 (first entry)

DE Human cervical cancer cell marker protein SEQ ID NO:226.

KW Human; cervical cancer; cervical cancer marker; cancer therapy;
 KW detection; gene therapy; vaccine.

OS Homo sapiens.

PN WO2002101075-A2.

PD 19-DEC-2002.

PF 12-JUN-2002; 2002WO-US018638.

PR 13-JUN-2001; 2001US-0298155P.

PR 13-JUN-2001; 2001US-0298159P.

PR 14-NOV-2001; 2001US-0335936P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;

PI Gannavarapu M, Glatt K, Hoersch S;

DR WPI; 2003-156867/15.

DR N-PSDB; ACF12941.

PS Claim 4; Page 377-378; 386pp; English.

CC ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
 CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
 CC normal indicates the presence of cervical cancer. Also described: (1) a
 CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
 CC assessing (M1) whether a patient is afflicted with cervical cancer,
 CC comprising comparing the level of expression of a marker in a patient's
 CC sample, and the normal level of expression of the marker in a control non
 CC -cervical cancer sample, where a significant increase in the level of
 CC expression of the marker in the patient's sample relative to that in the
 CC control sample is an indication that the patient is afflicted with
 CC cervical cancer. (I) has cytostatic activity, and can be used in gene
 CC therapy and in vaccines. (I) is useful in detecting, characterizing,
 CC preventing and treating human cervical cancers. (I) may also be used in
 CC various prognostic and diagnostic assays, pharmacogenomics and in
 CC monitoring clinical trials

SO Sequence 105 AA;

Query Match 100.0%; Score 47; DB 6; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 31 WCGPCK 36

RESULT 60
ADD67269
ID ADD67269 standard; protein; 105 AA.

AC ADD67269;

DT 15-JAN-2004 (first entry)

DE Thioedoxin protein SEQ ID NO:127.

KW apparatus combination; binding site collection; pattern recognition;
KM profiling; screening.

XX Mus musculus.

PN WO2003062402-A2.

PD 31-JUL-2003.

PF 24-JAN-2003; 2003WO-US002397.

PR 24-JAN-2002; 2002US-0352011P.

PA (POIN-) POINTILLISTE INC.

PI Ault-Riche D, Kasaner PD;

DR WPI; 2003-636736/60.

PT New combination comprising an addressable collection of binding sites,
PT software comprising instructions for pattern recognition and an imager
PT for detecting patterns, useful for profiling a sample.

PS Example 7; SEQ ID NO 127; 309pp; English.

XX The present invention describes a combination of apparatus (I)
CC comprising: (a) an addressable collection of binding sites; and (b)
CC software comprising instructions for pattern recognition and/or an imager
CC for detecting patterns. The addressable collection of binding sites
CC comprises: (a) capture agents, where each capture agent is preselected to
CC specifically bind to a pre-selected tag; and (b) tagged reagents, each
CC comprising one of the pre-selected tags, where each locus in the
CC collection comprises the same capture agent, where the tagged reagent
CC comprises a molecule and a tag, each tag is pre-selected to specifically
CC bind to a capture agent, where each tag is bound to a capture agent,
CC forming a complex of the tagged reagent with the capture agent, where
CC each locus comprises tagged reagents and where each of the different
CC molecules at each locus comprises the same pre-selected tag. Also
CC described: (1) a system for profiling samples; (2) a method for profiling
CC a sample; (3) a computer system or computer readable medium comprising
CC the database produced by the method of profiling a sample; (4) a method
CC for preparing a capture system that displays a collection of binding
CC sites; (5) a positionally addressable collection of binding sites
CC comprising capture agents bound to a solid support and tagged reagents;
CC and (6) a method for screening samples. The combination (I) is useful for
CC profiling a sample. The present sequence is used in the exemplification
CC of the present invention.

XX Sequence 105 AA;

Query Match 100.0%; Score 47; DB 7; Length 105;

Best Local Similarity 100.0%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |

Db 31 WCGPCK 36

RESULT 61
ADP30728
ID ADP30728 standard; protein; 105 AA.

AC ADP30728;

DT 12-FEB-2004 (first entry)

DE Rat angiogenesis modulating protein #146.

XX rat; angiogenesis; angiogenesis modulating protein;

KW retinal neovascularization or diseases associated with chronic inflammation;

KM chronic inflammation; myocardial ischemia; stroke;

XX coronary artery disease; peripheral vascular disease.

OS Rattus norvegicus.

PN US2003162706-A1.

PD 28-AUG-2003.

PF 10-DEC-2002; 2002US-00316253.

PR 08-FEB-2002; 2002US-0355295P.

PR 26-JUN-2002; 2002US-0391758P.

PA (PROC) PROCTER & GAMBLE CO.

PI Peters KG, Thompson LJ, Wang F, Greis KD;

DR WPI; 2003-711557/67.

DR N-PADB; ADP30727.

PT Treating angiogenesis-mediated disorder, e.g., retinal or choroidal

PT neovascularization or diseases associated with chronic inflammation,

PT myocardial ischemia, stroke, coronary artery disease or peripheral

PT vascular disease.

PS Claim 2; SEQ ID NO 291; 26pp; English.

XX The invention relates to a method of treating an angiogenesis-mediated
CC disorder in a subject. The method is useful for treating angiogenesis-
CC mediated disorder, e.g., retinal or choroidal neovascularization or
CC diseases associated with chronic inflammation, myocardial ischemia,
CC stroke, coronary artery disease or peripheral vascular disease. The
CC present sequence is used in the exemplification of the invention.

XX Sequence 105 AA;

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 31 WCGPCK 36

RESULT 62
ADJ70213
ID ADJ70213 standard; protein; 105 AA.

AC ADJ70213;

DT 06-MAY-2004 (first entry)

DE Human heat mitochondrial protein as a therapeutic target SeqID2019.

XX mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 OS Homo sapiens.
 XX
 XX MO2003087768-A2.
 PN
 XX 23-OCT-2003.
 PD
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 XX 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 XX (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghost SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 DR WPI; 2003-845369/78.
 XX
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 PS
 XX Claim 1; SEQ ID NO 2019; 180bp; English.
 CC This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, neurotropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytoskeletal activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 47; DB 7; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 31 WCGPCK 36
 RESULT 63
 ADL47593
 ID ADL47593 standard; protein; 105 AA.
 XX
 AC ADL47593;
 XX
 XX 06-MAY-2004 (first entry)
 DT
 XX
 DE Wild-type Trx coding sequence, SEQ ID 1.
 XX Antidiabetic; Antiarteriosclerotic; Neuroprotective; Neurotropic;
 KW Antiparinsonian; Anticonvulsant; Cardiant; Cardiovascular;
 KW Antirheumatic; Antiarthritic; Cytostatic; Antiporiatic; Gene Therapy;
 XX

KW thiorodoxin; Trx; atherosclerosis; diabetes; apoptotic disease;
 KW mitochondrial disease; cardiac dysfunction;
 KW angiogenesis dependent disease; neurodegenerative disease;
 KW rheumatoid arthritis; cancer; psoriasis.
 OS Unidentified.
 XX
 XX MO2004013283-A2.
 PN
 XX 12-FEB-2004.
 PD
 XX
 XX 22-JUL-2003; 2003WO-US022847.
 XX
 XX 02-AUG-2002; 2002US-0401073P.
 PR
 XX (UYRP) UNIV ROCHESTER.
 PA
 XX Min W, Yingmei L;
 PI
 XX
 XX WPI; 2004-157111/15.
 DR N-PSDB; ADL47596.
 XX
 XX New mutant thiorodoxin molecule which is resistant to oxidizing effects
 PT of cytokines or reactive oxygen species, useful for treating or
 PT diagnosing atherosclerosis, diabetes, Alzheimer's disease, myocardial
 PT infarction or cancer.
 PS
 XX Disclosure; SEQ ID NO 1; 145bp; English.
 CC The present invention relates to mutant thiorodoxin (Trx) proteins and
 CC their coding sequences, where the thiorodoxin molecule is resistant to
 CC the oxidizing effects of cytokines or reactive oxygen species or
 CC resistant to S-nitrosylation of a SH-group by nitrous oxide. The mutant
 CC Trx proteins are useful for treating or diagnosing atherosclerosis,
 CC diabetes, apoptotic disease, mitochondrial dysfunction disease or cardiac
 CC dysfunction. Mitochondrial dysfunction diseases include Kearns-Sayre
 CC syndrome or encephalomyopathy lactic acidosis and stroke-like episodes.
 CC Apoptotic diseases include neurodegenerative diseases, e.g. Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, amyotrophic lateral
 CC sclerosis, multiple sclerosis or peripheral neuropathy. Cardiac
 CC dysfunction includes myocardial infarction, cardiomyopathy, arterial
 CC hypertension or heart failure. The mutant Trx proteins are also useful
 CC for treating or diagnosing angiogenesis dependent diseases, e.g.
 CC rheumatoid arthritis, cancer or psoriasis. The present sequence is the
 CC wild-type Trx protein, from which the mutants of the invention were
 CC generated.
 XX
 SQ Sequence 105 AA;
 Query Match 100.0%; Score 47; DB 8; Length 105;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 31 WCGPCK 36
 RESULT 64
 ADL82895
 ID ADL82895 standard; protein; 105 AA.
 XX
 AC ADL82895;
 XX
 XX 17-JUN-2004 (first entry)
 DT
 XX
 DE Human PRO38337, SEQ ID 97.
 XX
 XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; Pro; B cell related disorder; cancer;
 KW Immune-mediated inflammatory disease; human.
 XX

OS Homo sapiens.
XX
XX WO2004024097-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 15-SEP-2003; 2003WO-US029097.
XX
XX PR 16-SEP-2002; 2002US-0411392P.
XX
XX PA (GENTH) GENENTECH INC.
XX
XX PI Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
XX Wu TD;
XX
XX DR MPI: 2004-329389/30.
XX N-PSDB; ADL82894.
XX
XX PT New PRO polypeptide, useful for diagnosing and treating a B cell related
XX disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
XX mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
XX
XX PS Claim 10; Fig 97; 695pp; English.
XX
XX CC The present invention relates to PRO proteins and their coding sequences.
XX CC The PRO proteins are useful for diagnosing and treating a B cell related
XX disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
XX antigen unresponsiveness, selective IgA deficiency, selective IgM
XX deficiency, selective deficiency of IgG subclasses, immunodeficiency with
XX hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's
XX lymphoma, intermediate lymphoma, follicular lymphoma, type II
XX hypersensitivity, rheumatoid arthritis, autoimmune mediated hemolytic
XX anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
XX ankylosing spondylitis. The PRO proteins are also useful for preparing a
XX medicament for treating a condition that is responsive to the PRO
XX protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
XX coding sequences are useful as hybridization probes in chromosome and
XX gene mapping, in preparing PRO proteins, or in generating transgenic
XX animals or knockout animals, which in turn are useful in the development
XX and screening of therapeutically useful reagents.
XX
XX SQ Sequence 105 AA;
XX
XX
XX Query Match 100.0%; Score 47; DB 8; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WCGPCK 6
XX |||||
XX Db 31 WCGPCK 36
XX
XX
XX RESULT 65
XX ADM32938
XX ID ADM32938 standard; protein; 105 AA.
XX
XX AC ADM32938;
XX
XX DT 17-UTN-2004 (first entry)
XX
XX DE Amino acid sequence of a thioredoxin polypeptide.
XX
XX KM mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
XX lung disease; cystic fibrosis; enzyme.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN WO2004024868-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 10-SEP-2003; 2003WO-US028526.
XX

XX
XX PR 10-SEP-2002; 2002US-0409960P.
XX PR 11-APR-2003; 2003US-0462082P.
XX
XX PA (MAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX PI White CW;
XX
XX DR MPI: 2004-270016/25.
XX
XX PT Increasing the liquefaction of excessively viscous or cohesive mucus or
XX sputum comprises contacting the mucus or sputum with a composition
XX comprising a protein or peptide containing a thioredoxin active-site in
XX reduced state.
XX
XX PS Disclosure; Page 66-67; 69pp; English.
XX
XX CC The specification describes a method for increasing the liquefaction of
XX mucus or sputum in a patient that has excessively viscous or cohesive
XX mucus or sputum. The method comprises contacting the mucus or sputum of
XX the patient with a composition comprising a protein or peptide containing
XX a thioredoxin active site in reduced state. The mucus or sputum to be
XX contacted is located in the respiratory tract, gastrointestinal tract or
XX reproductive tract of the patient. The composition is administered to the
XX patient in a pharmaceutical carrier. The protein has a half-life in the
XX volume of about 5 minutes to about 24 hours. The liquid phase of a total
XX volume of a sample of mucus or sputum from the patient shows a
XX statistically significant increase after administration of the
XX composition. The protein comprises thioredoxin selected from prokaryotic
XX thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
XX thioredoxin. The composition further comprises nicotinamide-adenine
XX dinucleotide phosphate (reduced form) (NADPH) for reducing the
XX thioredoxin active site of the protein, and thioredoxin reductase. The
XX method and composition are useful for decreasing the viscosity and
XX cohesiveness of, and increasing the liquefaction of excessively or
XX abnormally viscous or cohesive mucus or sputum. These may be used for
XX treating lung diseases (i.e. cystic fibrosis) in which abnormal or
XX excessive viscosity or cohesiveness of mucus or sputum is a symptom or
XX cause of the disease. ADM32938ADM32941 represent thioredoxin polypeptides
XX which may be used in the method of the invention.
XX
XX SQ Sequence 105 AA;
XX
XX
XX Query Match 100.0%; Score 47; DB 8; Length 105;
XX Best Local Similarity 100.0%; Pred. No. 14;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 WCGPCK 6
XX |||||
XX Db 31 WCGPCK 36
XX
XX
XX RESULT 66
XX ADM32935
XX ID ADM32935 standard; protein; 105 AA.
XX
XX AC ADM32935;
XX
XX DT 17-UTN-2004 (first entry)
XX
XX DE Amino acid sequence of a thioredoxin polypeptide.
XX
XX KM mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
XX lung disease; cystic fibrosis; enzyme.
XX
XX OS Mus musculus.
XX OS Synthetic.
XX
XX PN WO2004024868-A2.
XX
XX PD 25-MAR-2004.
XX
XX PF 10-SEP-2003; 2003WO-US028526.
XX

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
XX
XX White CW;
XX
XX WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
PS Disclosure; Page 65; 69pp; English.
XX
XX The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
RESULT 67
ADM32936
ID ADM32936 standard; protein; 105 AA.
XX
AC ADM32936;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KW lung disease; cystic fibrosis; enzyme.
XX
XX Rattus norvegicus.
OS Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
XX
XX White CW;
XX
XX WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
PS Disclosure; Page 65-66; 69pp; English.
XX
XX The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
RESULT 68
ADM32937
ID ADM32937 standard; protein; 105 AA.
XX
AC ADM32937;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
XX mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KW lung disease; cystic fibrosis; enzyme.
XX
XX Bos taurus.
OS Synthetic.
XX
PN WO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
XX
XX White CW;
XX
XX WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
XX
PS Disclosure; Page 66; 69pp; English.
XX
CC The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may be used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
XX
RESULT 69
ADM32934
ID ADM32934 standard; protein; 105 AA.
XX
AC ADM32934;
XX
DT 17-JUN-2004 (first entry)
XX
DE Amino acid sequence of a thioredoxin polypeptide.
XX
KM mucus; sputum; thioredoxin; active site; cohesive mucus; cohesive sputum;
KM lung disease; cystic fibrosis; enzyme.
XX
OS Gallus gallus.
OS Synthetic.
XX
PN MO2004024868-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028526.

XX 10-SEP-2002; 2002US-0409960P.
PR 11-APR-2003; 2003US-0462082P.
XX
XX (NAME-) NAT JEWISH MEDICAL & RES CENT.
XX
XX White CW;
XX
XX WPI; 2004-270016/25.
XX
PT Increasing the liquefaction of excessively viscous or cohesive mucus or
PT sputum comprises contacting the mucus or sputum with a composition
PT comprising a protein or peptide containing a thioredoxin active-site in
PT reduced state.
XX
XX
PS Disclosure; Page 64-65; 69pp; English.
XX
CC The specification describes a method for increasing the liquefaction of
CC mucus or sputum in a patient that has excessively viscous or cohesive
CC mucus or sputum. The method comprises contacting the mucus or sputum of
CC the patient with a composition comprising a protein or peptide containing
CC a thioredoxin active site in reduced state. The mucus or sputum to be
CC contacted is located in the respiratory tract, gastrointestinal tract or
CC reproductive tract of the patient. The composition is administered to the
CC patient in a pharmaceutical carrier. The protein has a half-life in the
CC patient of about 5 minutes to about 24 hours. The liquid phase of a total
CC volume of a sample of mucus or sputum from the patient shows a
CC statistically significant increase after administration of the
CC composition. The protein comprises thioredoxin selected from prokaryotic
CC thioredoxin, yeast thioredoxin, plant thioredoxin and mammalian
CC thioredoxin. The composition further comprises nicotinamide-adenine
CC dinucleotide phosphate (reduced form) (NADPH) for reducing the
CC thioredoxin active site of the protein, and thioredoxin reductase. The
CC method and composition are useful for decreasing the viscosity and
CC cohesiveness of, and increasing the liquefaction of excessively or
CC abnormally viscous or cohesive mucus or sputum. These may be used for
CC treating lung diseases (i.e. cystic fibrosis) in which abnormal or
CC excessive viscosity or cohesiveness of mucus or sputum is a symptom or
CC cause of the disease. ADM32930ADM32941 represent thioredoxin polypeptides
CC which may be used in the method of the invention.
XX
SQ Sequence 105 AA;
XX
Query Match 100.0%; Score 47; DB 8; Length 105;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 31 WCGPCK 36
XX
RESULT 70
AD019655
ID AD019655 standard; protein; 105 AA.
XX
AC AD019655;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO polypeptide #292.
XX
KM Human; PRO; immune related disorder; systemic lupus erythematosus;
KM rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KM systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KM autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KM diabetes mellitus; renal disease; demyelinating disease;
KM central nervous system; peripheral nervous system;
KM demyelinating polyneuropathy; Guillain-Barre syndrome;
KM chronic inflammatory demyelinating polyneuropathy.
XX
XX Homo sapiens.
XX

PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM,
 PI Wood WI, Wu TD;
 XX
 DR WPI: 2004-420067/39.
 DR N-PSDB; ADO19654.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7, SEQ ID NO 584; 1731BP; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating polynuropathy,
 CC central or peripheral nervous system, demyelinating polynuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polynuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 CC
 SQ Sequence 105 AA;
 QY 1 WCGPCK 6
 Db 31 WCGPCK 36

Search completed: February 23, 2006, 00:37:12
 Job time : 163 secs

This Page Blank (uspro)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:38:49 / Search time 23.5 Seconds
(without alignments)
24.566 Million cell updates/sec

Title: US-10-660-118a-3
Perfect score: 47
Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	89	E84409	thioredoxin [impor
2	47	100.0	102	G64213	thioredoxin - Myco
3	47	100.0	102	S73896	thioredoxin - Myco
4	47	100.0	102	B71503	probable thioredox
5	47	100.0	102	C81600	thioredoxin TC0826
6	47	100.0	103	TXBY2	thioredoxin II - Y
7	47	100.0	103	T39085	thioredoxin II - f
8	47	100.0	104	A28086	thioredoxin - rabp
9	47	100.0	104	B37192	thioredoxin - Bac1
10	47	100.0	104	TXBY1	thioredoxin I - ye
11	47	100.0	104	S77780	thioredoxin - Myco
12	47	100.0	104	A59394	thioredoxin - Clos
13	47	100.0	104	B84037	thioredoxin trxa l
14	47	100.0	104	E89885	thioredoxin [impor
15	47	100.0	105	A30006	thioredoxin - chic
16	47	100.0	105	JH0568	thioredoxin [valid
17	47	100.0	105	JSD067	thioredoxin - rhes
18	47	100.0	105	S04107	thioredoxin - mous
19	47	100.0	105	S04352	thioredoxin - rat
20	47	100.0	105	TXRX	thioredoxin - cory
21	47	100.0	105	B97700	thioredoxin [impor
22	47	100.0	105	D97279	thioredoxin [impor
23	47	100.0	106	S33357	thioredoxin - Stre
24	47	100.0	106	H64622	thioredoxin - He11
25	47	100.0	106	A49888	thioredoxin - Pen1
26	47	100.0	106	AG2579	thioredoxin C-1 tr
27	47	100.0	107	A26622	thioredoxin - Chro
28	47	100.0	107	S47867	thioredoxin-like p
29	47	100.0	107	T02814	thioredoxin TRXRp1
30	47	100.0	107	AH3504	thioredoxin C-1 (l
31	47	100.0	107	E64047	thioredoxin - Haem
32	47	100.0	108	G82991	thioredoxin PA5240
33	47	100.0	108	AD0471	thioredoxin 1 [imp
34	47	100.0	108	D82338	thioredoxin VC0306
35	47	100.0	109	S35497	thioredoxin - Salm
36	47	100.0	109	TXEC	thioredoxin [valid
37	47	100.0	109	S27053	thioredoxin - Emer
38	47	100.0	109	AF0922	thioredoxin [impor
39	47	100.0	110	A87688	thioredoxin [impor
40	47	100.0	110	C81090	thioredoxin NMB136
41	47	100.0	110	B81850	thioredoxin 1 NMA1
42	47	100.0	113	S57175	thioredoxin h, cyt
43	47	100.0	115	T29044	hypothetical prote
44	47	100.0	116	B70851	probable trxc prot
45	47	100.0	117	E70107	thioredoxin (trxa)
46	47	100.0	118	S34812	thioredoxin h2 - c
47	47	100.0	121	T39387	thioredoxin h1 - f
48	47	100.0	127	S19498	thioredoxin homolo
49	47	100.0	127	B91218	thioredoxin 1 [imp
50	47	100.0	127	C86064	thioredoxin 1 [imp
51	47	100.0	129	B96621	probable thioredox
52	47	100.0	129	T08084	dynein light chain
53	47	100.0	130	D71707	thioredoxin (trxa)
54	47	100.0	133	F97361	thioredoxin C-1 (l
55	47	100.0	145	S70356	thioredoxin C3 - c
56	47	100.0	148	B96721	probable thioredox
57	47	100.0	156	T08086	dynein light chain
58	47	100.0	177	T09495	thioredoxin m - ra
59	47	100.0	179	T00893	thioredoxin m - ra
60	47	100.0	181	TXSPM	thioredoxin m prec
61	47	100.0	182	T07837	thioredoxin f prec
62	47	100.0	182	S20929	thioredoxin f prec
63	47	100.0	182	E96539	hypothetical prote
64	47	100.0	185	D95115	thioredoxin family
65	47	100.0	186	S85044	probable M-type th
66	47	100.0	190	F04661	thioredoxin f prec
67	47	100.0	191	T12261	thioredoxin f prec
68	47	100.0	191	H97984	conserved hypotet
69	47	100.0	290	T40552	thioredoxin-like p
70	47	100.0	322	AH3011	thioredoxin trxa l
71	47	100.0	329	AH3559	thioredoxin [impor
72	47	100.0	331	G98272	probable thioredox
73	47	100.0	458	S77662	thioredoxin-disulf
74	47	100.0	88	B46264	thioredoxin 2 - al
75	47	93.6	102	H66572	thioredoxin [impor
76	47	93.6	102	D72052	thioredoxin CP0088
77	47	93.6	103	AC1582	thioredoxin [impor
78	47	93.6	103	AC1582	thioredoxin [impor
79	47	93.6	104	A28215	thioredoxin - Rhod
80	47	93.6	104	H95206	thioredoxin [impor
81	47	93.6	104	H98071	thioredoxin-disulf
82	47	93.6	104	C46264	thioredoxin 3 - al
83	47	93.6	104	D86830	thioredoxin [impor
84	47	93.6	104	C81432	thioredoxin Cj0147
85	47	93.6	105	A46264	thioredoxin 1 - al
86	47	93.6	106	A35135	thioredoxin - Rhod
87	47	93.6	107	A32956	thioredoxin m - Sy
88	47	93.6	107	TXAI	thioredoxin 1 - An
89	47	93.6	107	S31915	thioredoxin - red
90	47	93.6	107	S73146	thioredoxin A - re
91	47	93.6	107	S46521	thioredoxin - Porp
92	47	93.6	107	S46958	thioredoxin A - Sy
93	47	93.6	107	B53307	thioredoxin - Stre
94	47	93.6	107	AD1813	thioredoxin [impor
95	47	93.6	108	AH2101	thioredoxin [impor
96	47	93.6	109	A55124	hypothetical prote
97	47	93.6	109	S77444	thioredoxin A - Gr
98	47	93.6	110	S46522	thioredoxin - Stre
99	47	93.6	110	T35576	thioredoxin - Stre
100	47	93.6	110	T42061	thioredoxin [impor
101	47	93.6	110	AD2039	thioredoxin h - Ar
102	47	93.6	114	JQ2242	thioredoxin

103	44	93.6	116	2	T10739	176	39	83.0	181	2	S45556	thioredoxin relate
104	44	93.6	119	2	T10170	177	39	83.0	197	2	T29930	hypothetical prote
105	44	93.6	118	2	T50867	178	39	83.0	351	2	T18066	hypothetical prote
106	44	93.6	122	2	T04090	179	39	83.0	358	2	T17619	hypothetical prote
107	44	93.6	123	2	B70873	180	39	83.0	2567	2	A49551	filamin, Muller ce
108	44	93.6	125	2	T50866	181	39	83.0	5825	2	T11217	polyprotein - lava
109	44	93.6	126	1	S16590	182	38	80.9	40	2	B41440	protein disulfide-
110	44	93.6	131	2	T50862	183	38	80.9	63	2	PK0084	thioredoxin h2 - s
111	44	93.6	131	2	T50863	184	38	80.9	72	2	S15137	thioredoxin h2 - s
112	44	93.6	131	2	T50864	185	38	80.9	100	2	T49043	hypothetical prote
113	44	93.6	131	2	T50865	186	38	80.9	106	2	AE1428	thioredoxin homolo
114	44	93.6	133	2	S58123	187	38	80.9	106	2	AD1802	thioredoxin homolo
115	44	93.6	139	2	G70464	188	38	80.9	134	2	C69410	thioredoxin (trx-3
116	44	93.6	139	2	H91059	189	38	80.9	151	2	AB3263	thiol:disulfide in
117	44	93.6	139	2	G85059	190	38	80.9	154	2	H83526	probable thioredox
118	44	93.6	139	2	AB0831	191	38	80.9	176	1	A47384	cytochrome c bioge
119	44	93.6	139	2	B65036	192	38	80.9	318	2	S67190	disulfide isomeras
120	44	93.6	140	1	S57774	193	38	80.9	338	2	C82590	thioredoxin Xr2174
121	44	93.6	141	2	G75455	194	38	80.9	359	2	T03644	probable protein d
122	44	93.6	142	2	G75612	195	38	80.9	359	2	T37880	probable protein d
123	44	93.6	145	2	AD0397	196	38	80.9	361	2	T00437	probable protein d
124	44	93.6	150	2	D81247	197	38	80.9	364	2	T09614	probable protein d
125	44	93.6	167	2	T03957	198	38	80.9	369	2	T47259	probable protein d
126	44	93.6	172	1	S38909	199	38	80.9	378	2	A47300	cell adhesion prot
127	44	93.6	173	2	F84530	200	38	80.9	431	2	S45038	protein disulfide-
128	44	93.6	174	2	T29491	201	38	80.9	439	2	S19656	protein disulfide-
129	44	93.6	185	2	F75549	202	38	80.9	440	2	JC4369	p5 protein precurs
130	44	93.6	194	2	T00482	203	38	80.9	440	2	T15352	hypothetical prote
131	44	93.6	216	2	S72901	204	38	80.9	440	2	T01115	probable protein d
132	44	93.6	216	2	A70545	205	38	80.9	443	2	D86183	hypothetical prote
133	44	93.6	222	2	H87210	206	38	80.9	481	2	JC5378	protein disulfide-
134	44	93.6	250	2	B87921	207	38	80.9	482	2	S34275	protein disulfide-
135	44	93.6	268	2	C38095	208	38	80.9	485	2	S71863	protein disulfide-
136	44	93.6	281	2	S49353	209	38	80.9	488	1	JC2385	protein disulfide-
137	44	93.6	282	2	S49352	210	38	80.9	488	2	T23055	hypothetical prote
138	44	93.6	299	2	B87262	211	38	80.9	489	2	S68280	protein disulfide-
139	44	93.6	340	2	T33313	212	38	80.9	491	2	S71862	protein disulfide-
140	44	93.6	366	2	S61796	213	38	80.9	492	2	T38093	probable protein d
141	44	93.6	606	2	T31557	214	38	80.9	493	2	T34092	hypothetical prote
142	43	91.5	105	2	S76386	215	38	80.9	496	2	A54757	protein disulfide-
143	43	91.5	105	2	AG2042	216	38	80.9	497	1	A32820	protein disulfide-
144	43	91.5	107	2	T33843	217	38	80.9	498	2	S62626	protein disulfide-
145	43	91.5	111	1	A32233	218	38	80.9	501	2	B86351	protein disulfide-
146	43	91.5	115	2	AF2098	219	38	80.9	504	1	A28807	protein disulfide-
147	43	91.5	119	2	T18644	220	38	80.9	504	2	S41661	protein disulfide-
148	43	91.5	119	2	T088271	221	38	80.9	505	1	S55507	protein disulfide-
149	43	91.5	151	2	B96796	222	38	80.9	505	2	S63994	protein disulfide-
150	43	91.5	160	2	A86200	223	38	80.9	505	2	S68363	protein disulfide-
151	43	91.5	242	2	A96499	224	38	80.9	505	2	JC5704	protein disulfide-
152	43	91.5	464	2	T46333	225	38	80.9	505	2	JC2291	protein disulfide-
153	43	91.5	578	2	T02292	226	38	80.9	508	1	A30007	dolichyl-diphospho
154	43	91.5	788	2	T26967	227	38	80.9	508	1	ISHUSS	protein disulfide-
155	42	89.4	108	2	B55124	228	38	80.9	508	1	ISHUSS	protein disulfide-
156	42	89.4	140	2	G87183	229	38	80.9	509	1	A38362	protein disulfide-
157	42	89.4	273	1	B31479	230	38	80.9	509	1	ISHUSS	protein disulfide-
158	42	89.4	534	1	VCWVSF	231	38	80.9	510	1	ISBOSS	protein disulfide-
159	42	89.4	662	1	VCWVLB	232	38	80.9	512	1	ISAASS	protein disulfide-
160	42	89.4	662	1	VCWVGF	233	38	80.9	512	2	A41440	protein disulfide-
161	42	89.4	662	2	A25982	234	38	80.9	513	2	T05974	protein disulfide-
162	42	89.4	668	1	VCWVFP	235	38	80.9	513	2	S69181	protein disulfide-
163	42	89.4	837	1	T02761	236	38	80.9	515	1	ISCHSS	protein disulfide-
164	41	87.2	108	1	S02802	237	38	80.9	515	2	T06262	probable protein d
165	41	87.2	108	2	B84999	238	38	80.9	515	2	S57942	protein disulfide-
166	41	87.2	113	2	F82526	239	38	80.9	517	2	JC7623	protein disulfide-
167	41	87.2	210	2	A87523	240	38	80.9	519	2	S66673	disulfide isomeras
168	41	87.2	289	2	E83138	241	38	80.9	522	1	ISBYS8	protein disulfide-
169	39	83.0	103	2	A11275	242	38	80.9	532	2	T07927	protein disulfide-
170	39	83.0	103	2	A11638	243	38	80.9	584	2	S06318	endoplasmic reticu
171	39	83.0	105	2	G97090	244	38	80.9	638	1	ISMGER	protein disulfide-
172	39	83.0	105	2	D71265	245	38	80.9	643	1	S12476	protein disulfide-
173	39	83.0	146	2	C70314	246	38	80.9	645	1	A23723	protein disulfide-
174	39	83.0	165	2	E69869	247	38	80.9	664	2	S44756	probable protein d
175	39	83.0	178	2	T19587	248	38	80.9	1152	2	F86363	hypothetical prote

249	37	78.7	170	2	H87704	thiol-disulfide in
250	37	78.7	176	1	I64161	cytochrome c bioge
251	37	78.7	363	2	T37630	protein disulfide
252	36	76.6	105	2	E98087	conserved hypotnet
253	36	76.6	106	2	A82870	thioredoxin U0589
254	36	76.6	116	2	D84285	hypothetical prote
255	36	76.6	118	2	S58118	thioredoxin (clone
256	36	76.6	118	2	S58120	thioredoxin (clone
257	36	76.6	119	2	T08142	thioredoxin h homo
258	36	76.6	119	2	D86330	F6p9.21 protein -
259	36	76.6	123	2	T08141	thioredoxin h homo
260	36	76.6	123	2	T14379	thioredoxin PBC-2
261	36	76.6	125	2	S58119	thioredoxin (clone
262	36	76.6	133	2	C90180	thioredoxin (trxA-
263	36	76.6	135	2	C90393	hypothetical prote
264	36	76.6	140	2	T15738	thioredoxin 2 VCA0
265	36	76.6	149	2	B82423	hypothetical prote
266	36	76.6	151	2	T23939	hypothetical prote
267	36	76.6	151	2	T32957	hypothetical prote
268	36	76.6	155	2	T29947	hypothetical prote
269	36	76.6	170	2	E63891	cytochrome c bioge
270	36	76.6	177	2	B83840	thioredoxin (thiol
271	36	76.6	200	2	H71366	probable thioredox
272	36	76.6	221	2	T04271	probable thioredox
273	36	76.6	227	2	B70790	hypothetical prote
274	36	76.6	229	1	D43685	nonstructural prot
275	36	76.6	229	1	D43685	nonstructural prot
276	36	76.6	278	2	E83336	cytochrome c bioge
277	36	76.6	357	2	S23526	cinnamyl-alcohol d
278	36	76.6	357	2	S23525	cinnamyl-alcohol d
279	36	76.6	380	2	G01639	transmembrane prot
280	36	76.6	445	1	B65000	NAHD2 dehydrogenas
281	36	76.6	445	1	AB0797	NAHD2 dehydrogenas
282	36	76.6	445	2	AB5869	NAHD dehydrogenase
283	36	76.6	445	2	H91024	NAHD dehydrogenase
284	36	76.6	448	2	F83316	NAHD dehydrogenase
285	36	76.6	461	2	AE0311	NAHD2 dehydrogenas
286	36	76.6	562	2	A55588	mannosyl-glycoprot
287	36	76.6	603	2	UC7900	beta-N-acetylgluco
288	36	76.6	654	2	B56011	transcription fact
289	36	76.6	961	1	TSHUP4	chromospondin 4 p
290	36	76.6	1021	2	I39207	leukocyte surface
291	36	76.6	1023	2	G96509	pro-pol-dutrase po
292	36	76.6	1182	2	T29097	transcription fact
293	36	76.6	2109	2	I38414	transcription fact
294	36	76.6	2148	2	A56011	thioredoxin (trx-4
295	35	74.5	105	2	H69517	secreted protein,
296	35	74.5	168	2	AF0632	secreted periplasm
297	35	74.5	169	2	H81980	probable periplasm
298	35	74.5	169	2	B81036	thioredoxin NMB184
299	35	74.5	188	2	A75532	cytochrome c bioge
300	35	74.5	203	2	AC3483	thiol:disulfide in
301	35	74.5	221	2	S40401	thioredoxin-1like p
302	35	74.5	222	2	AD2999	thiol:disulfide in
303	35	74.5	222	2	E98284	thiol:disulfide in
304	35	74.5	395	2	B72381	alcohol dehydrogen
305	35	74.5	401	2	A13312	ATP synthase beta
306	35	74.5	552	2	F75311	ABC transporter, A
307	35	74.5	566	2	T06724	protein disulfide-
308	35	74.5	574	2	T25887	hypothetical prote
309	35	74.5	601	2	T21814	hypothetical prote
310	34	72.3	105	2	E86673	thioredoxin H-type
311	34	72.3	108	2	F83309	probable thioredox
312	34	72.3	122	2	T28977	hypothetical prote
313	34	72.3	128	2	AD3300	thioredoxin (impor
314	34	72.3	158	2	S62213	calcium channel be
315	34	72.3	167	2	G64183	hypothetical prote
316	34	72.3	185	2	A81327	probable lipoprote
317	34	72.3	199	2	A97682	thiol disulfide in
318	34	72.3	199	2	A12906	thiol:disulfide in
319	34	72.3	211	2	A82614	thioredoxin XP1990
320	34	72.3	251	2	S23821	hypothetical prote
321	34	72.3	251	2	C45557	regulatory protein
322	32	72.3	263	1	ASLJFP	vif protein - fe1i
323	34	72.3	271	2	G82838	formamidyrimidin
324	34	72.3	292	2	H84285	succinate dehydrog
325	34	72.3	337	2	B95288	probable zinc-bind
326	34	72.3	367	1	A46355	site-specific DNA-
327	34	72.3	367	1	T18185	probable site-spec
328	34	72.3	407	2	T24951	hypothetical prote
329	34	72.3	436	2	T27039	hypothetical prote
330	34	72.3	483	2	B82722	hypothetical prote
331	34	72.3	485	2	I39557	ribulose-bisphosph
332	34	72.3	486	2	I39559	ribulose-bisphosph
333	34	72.3	508	1	SYNHT	histidine-tRNA lig
334	34	72.3	508	2	E96804	probable thioredox
335	34	72.3	623	2	T16384	hypothetical prote
336	34	72.3	625	2	T10661	serine/threonine-s
337	34	72.3	687	2	T39838	hypothetical prote
338	34	72.3	961	2	H86181	hypothetical prote
339	34	72.3	1007	2	T01437	hypothetical prote
340	34	72.3	1041	2	T29010	hypothetical prote
341	34	72.3	1041	2	T08839	polypeptide - marm
342	34	72.3	2970	2	S42768	ary protein - Eura
343	33	70.2	62	2	S15676	chorionic gonadotr
344	33	70.2	67	2	A55210	hem 5'-region hyp
345	33	70.2	74	2	S25773	testis-specific pr
346	33	70.2	80	2	I65235	testicular luteini
347	33	70.2	118	2	PN0141	lutropin beta chai
348	33	70.2	118	2	PN0139	lutropin beta chai
349	33	70.2	119	2	AC1465	lutropin beta chai
350	33	70.2	123	2	D75363	hypothetical prote
351	33	70.2	130	2	C87136	thioredoxin (impor
352	33	70.2	132	2	D39741	cytochrome c bioge
353	33	70.2	138	2	S00512	lutropin beta chai
354	33	70.2	139	2	I52320	testicular luteini
355	33	70.2	141	1	UTR0B	lutropin beta chai
356	33	70.2	141	1	UTR0B	lutropin beta chai
357	33	70.2	141	1	UTR0B	lutropin beta chai
358	33	70.2	141	1	UTR0B	lutropin beta chai
359	33	70.2	141	1	UTR0B	lutropin beta chai
360	33	70.2	141	1	UTR0B	lutropin beta chai
361	33	70.2	141	1	UTR0B	lutropin beta chai
362	33	70.2	157	2	S16728	polyferredoxin 2x2
363	33	70.2	163	2	E72473	probable thioredox
364	33	70.2	170	2	S01449	hypothetical prote
365	33	70.2	195	2	S24228	BHV-1 protein homo
366	33	70.2	216	2	PR0375	natural killer cel
367	33	70.2	277	2	AE2947	hypothetical prote
368	33	70.2	277	2	D98335	ABC transporter, A
369	33	70.2	283	2	C86535	hypothetical prote
370	33	70.2	283	2	H72087	hypothetical prote
371	33	70.2	291	2	S77611	killer toxin KPI p
372	33	70.2	293	2	JN0651	rRNA methyltransfe
373	33	70.2	299	2	G96902	transcription regu
374	33	70.2	302	1	WZBE9	gene y protein - h
375	33	70.2	309	2	AB0838	virulence protein
376	33	70.2	310	2	D63386	unknown protein [i
377	33	70.2	332	1	WGSMMH	hydroxymycin B phosp
378	33	70.2	345	2	S72708	biotin synthase (i
379	33	70.2	345	2	S72708	biotin synthase (E
380	33	70.2	347	2	T17645	hypothetical prote
381	33	70.2	349	2	G70542	biotin synthase (E
382	33	70.2	359	1	JT0391	site-specific DNA
383	33	70.2	359	2	A27159	potassium channel
384	33	70.2	363	2	B97199	uncharacterized co
385	33	70.2	367	2	H96764	protein RING zinc
386	33	70.2	398	1	S24802	polyferredoxin 6x2
387	33	70.2	415	2	S51977	FUN9 protein - yea
388	33	70.2	416	2	S51961	FUN50 protein - yea
389	33	70.2	426	2	B36467	hypothetical prote
390	33	70.2	433	2	B84566	hypothetical prote
391	33	70.2	442	2	AD2475	hypothetical prote
392	33	70.2	458	2	D70325	hypothetical prote
393	33	70.2	483	2	H87492	Yif family protei
394	33	70.2	489	2	JC4324	Yifnositilbene alph

395	33	70.2	527	2	T37055	probable oxidoredu
396	33	70.2	535	2	S58324	oestrogen receptor
397	33	70.2	535	2	T00824	probable thiodox
398	33	70.2	537	2	T48599	hypothetical prote
399	33	70.2	539	2	H97279	phosphoenolpyruvat
400	33	70.2	551	2	S77442	cytochrome-c oxida
401	33	70.2	563	2	AD2011	hypothetical prote
402	33	70.2	572	2	S14200	GRESAG protein - T
403	33	70.2	582	2	S10099	transcription fact
404	33	70.2	608	2	E84750	hypothetical prote
405	33	70.2	608	2	T03278	gene ERTIN protein
406	33	70.2	613	2	UC7762	SOX-3 protein - gu
407	33	70.2	678	1	I77530	proprotein convert
408	33	70.2	692	2	A97013	hypothetical prote
409	33	70.2	695	2	E70923	hypothetical prote
410	33	70.2	773	2	J02187	P87 protein - Card
411	33	70.2	956	1	A46016	thrombospondin 3 -
412	33	70.2	956	1	A57121	jagged protein pre
413	33	70.2	1257	2	A56136	hypothetical prote
414	33	70.2	1257	2	T01020	variant-specific s
415	33	70.2	2228	2	T14029	polyprotein - dour
416	33	70.2	3005	2	T08841	hypothetical prote
417	32	68.1	75	2	T21519	thiodoxin M-2 -
418	32	68.1	126	2	S74493	chotriogonadotropin
419	32	68.1	169	1	KTH08	hypothetical prote
420	32	68.1	171	2	AC2081	hypothetical prote
421	32	68.1	174	2	AD2081	hypothetical prote
422	32	68.1	187	2	T36816	hypothetical prote
423	32	68.1	202	2	T50635	hypothetical prote
424	32	68.1	220	2	T30688	hypothetical prote
425	32	68.1	244	2	T40018	glutaredoxin-like
426	32	68.1	277	2	I52825	gene MAC25 protein
427	32	68.1	280	2	F96608	probable chitinase
428	32	68.1	282	2	S50031	protaacyclin-stimu
429	32	68.1	309	2	I41075	site-specific DNA-
430	32	68.1	312	2	E85073	hypothetical prote
431	32	68.1	314	1	T50537	succinate dehydrog
432	32	68.1	316	1	G90406	succinate dehydrog
433	32	68.1	317	1	T45163	succinate dehydrog
434	32	68.1	317	2	D90446	alcohol dehydrogen
435	32	68.1	325	2	B70000	cytochrome-c oxida
436	32	68.1	344	2	UC7920	35k hemin binding
437	32	68.1	346	1	H69789	probable alcohol d
438	32	68.1	348	2	E84143	L-1-tiltol 2-dehydro
439	32	68.1	354	2	E81178	probable alcohol d
440	32	68.1	354	2	H81925	probable alcohol d
441	32	68.1	363	2	C83128	2,3-butanediol deh
442	32	68.1	370	2	A86737	(R,R)-butanediol d
443	32	68.1	382	2	S51962	FUN49 protein - ye
444	32	68.1	411	2	A55610	corticotriolin-rele
445	32	68.1	430	2	A56726	corticoliberin rec
446	32	68.1	459	2	JC6520	CRF receptor - mou
447	32	68.1	431	2	I49149	saunagine/corticoc
448	32	68.1	448	2	T48866	hypothetical prote
449	32	68.1	453	2	T15374	hypothetical prote
450	32	68.1	454	2	T21358	hypothetical prote
451	32	68.1	459	2	JC6520	interferon regulat
452	32	68.1	486	2	TJ39456	zinc finger protei
453	32	68.1	488	1	I39769	aldenhyde dehydrog
454	32	68.1	504	2	G02474	interferon regulat
455	32	68.1	525	2	T21357	hypothetical prote
456	32	68.1	669	2	T08827	hypothetical prote
457	32	68.1	744	2	A45622	surface antigen gp
458	32	68.1	755	2	A44315	cartilage oligomer
459	32	68.1	761	2	C64813	ybbu protein - Bac
460	32	68.1	761	2	G90728	probable enzyme [l
461	32	68.1	761	2	H85579	RNA-directed RNA p
462	32	68.1	774	1	P31V50	basic polymerase 2
463	32	68.1	774	2	S13670	receptor-protein t
464	32	68.1	975	2	I48974	protein-tyrosine k
465	32	68.1	976	2	A36355	tyrosine kinase Mp
466	32	68.1	977	2	S49004	hypothetical prote
467	32	68.1	1073	2	T01955	
468	32	68.1	1103	2	T13590	distal tail fiber
469	32	68.1	1321	2	T29308	hypothetical prote
470	32	68.1	1372	2	T29309	hypothetical prote
471	32	68.1	2703	1	A24420	noctch protein - fr
472	32	68.1	4302	1	A38971	polycystic kidney
473	32	68.1	4302	2	A39804	thrombospondin pre
474	31.5	67.0	1178	2	A39804	neurotoxin p2 - sc
475	31	66.0	35	1	NTSRPM	neurotoxin p2 - sc
476	31	66.0	35	2	A59356	testis-specific pr
477	31	66.0	55	1	S25774	testis-specific pr
478	31	66.0	56	1	WTFP	testis-specific pr
479	31	66.0	56	2	H81133	rubredoxin NMB093
480	31	66.0	63	2	S25772	testis-specific pr
481	31	66.0	65	2	A72324	terredoxin - Therm
482	31	66.0	68	2	S25775	testis-specific pr
483	31	66.0	73	2	A60136	keratin, scale (cl
484	31	66.0	98	1	KRGLBS	keratin, feather -
485	31	66.0	114	1	E64423	yein protein homol
486	31	66.0	114	2	D75422	hypothetical prote
487	31	66.0	116	2	S09845	hypothetical prote
488	31	66.0	124	2	T13559	hypothetical prote
489	31	66.0	124	2	A83707	hypothetical prote
490	31	66.0	128	2	J01002	keratin, claw - ch
491	31	66.0	131	2	A87461	hypothetical prote
492	31	66.0	141	2	D82843	DNA polymerase III
493	31	66.0	150	2	H86488	protein T32E20.29
494	31	66.0	155	1	KRCHS	keratin, scale - c
495	31	66.0	158	1	ZBBE11	17k zinc-binding p
496	31	66.0	161	2	T48767	hypothetical prote
497	31	66.0	162	2	T49420	hypothetical prote
498	31	66.0	179	2	A87654	hypothetical prote
499	31	66.0	186	2	T31643	hypothetical prote
500	31	66.0	186	2	T03808	alanine-tRNA ligas
501	31	66.0	190	2	S52130	vascular endotheli
502	31	66.0	190	2	B40080	vascular endotheli
503	31	66.0	192	2	A72645	hypothetical prote
504	31	66.0	195	2	S3967	hypothetical prote
505	31	66.0	201	2	S16897	alanine-tRNA ligas
506	31	66.0	205	2	S16899	alanine-tRNA ligas
507	31	66.0	205	2	F71491	probable UDP-gluc
508	31	66.0	218	2	F81650	UDP-N-acetylglucos
509	31	66.0	220	2	G86164	protein F15K9.8 [i
510	31	66.0	222	2	A59263	tetraogan TSPAN-2
511	31	66.0	232	2	A41551	vascular endotheli
512	31	66.0	232	2	D96663	unknown protein, 5
513	31	66.0	233	2	D84797	hypothetical prote
514	31	66.0	241	2	C82852	competence protein
515	31	66.0	243	2	C75608	hypothetical prote
516	31	66.0	245	2	S30860	hypothetical prote
517	31	66.0	246	2	A43905	sperm outer dense
518	31	66.0	247	2	T33965	hypothetical prote
519	31	66.0	247	2	I48699	outer dense fiber
520	31	66.0	265	2	B48151	sperm tail protein
521	31	66.0	269	2	JC5938	thioredoxin-like p
522	31	66.0	296	2	T07367	protein T33E18.2 [
523	31	66.0	302	2	A96789	hypothetical prote
524	31	66.0	303	2	T47356	lipidic acid synthe
525	31	66.0	321	2	AD0580	MHA3 (keratin acid
526	31	66.0	323	2	I48667	regulatory protein
527	31	66.0	332	2	I48691	sperm tail protein
528	31	66.0	338	2	E82432	hypothetical prote
529	31	66.0	340	1	C70538	probable 6-phospho
530	31	66.0	345	2	T25561	hypothetical prote
531	31	66.0	356	1	A35253	2-dehydro-3-deoxy-
532	31	66.0	356	1	ADRCYH	2-dehydro-3-deoxy-
533	31	66.0	356	2	AB0833	2-dehydro-3-deoxy-
534	31	66.0	356	2	H91061	hypothetical prote
535	31	66.0	356	2	D85906	hypothetical prote
536	31	66.0	356	2	AC0399	2-dehydro-3-deoxy-
537	31	66.0	357	2	D83292	phospho-2-dehydro-
538	31	66.0	362	2	T37455	keratin Ha3-II, ty
539	31	66.0	373	2	T33145	hypothetical prote
540	31	66.0	380	2	A71181	probable isomerase

541	31	66.0	380	2	H75159	3-isopropylmalate	614	31	66.0	842	2	C81396	alanine-tRNA ligase
542	31	66.0	381	2	A33477	protein-glutamine	615	31	66.0	847	2	A64675	alanine-tRNA ligase
543	31	66.0	386	2	T51171	homocitrate hydr	616	31	66.0	847	2	P71842	alanine-tRNA ligase
544	31	66.0	392	2	A60777	keratin 2, type I,	617	31	66.0	860	2	G82310	alanyl-tRNA synth
545	31	66.0	395	1	U00396	nodulation protein	618	31	66.0	873	2	H96503	alanyl-tRNA synth
546	31	66.0	396	2	C84797	hypothetical prote	619	31	66.0	874	2	H93533	protein PgC16.17
547	31	66.0	397	2	G97335	butyllisin-like se	620	31	66.0	874	2	P81063	alanyl-tRNA synth
548	31	66.0	399	2	F82657	beta-ketoacyl-[ACP	621	31	66.0	874	2	C81804	alanine-tRNA ligase
549	31	66.0	404	2	J50073	keratin, 47.6k typ	622	31	66.0	874	2	I64095	alanine-tRNA ligase
550	31	66.0	409	2	T47298	probable replicati	623	31	66.0	875	2	A60401	alanine-tRNA ligase
551	31	66.0	412	1	KRSHL1	keratin, 48k type	624	31	66.0	876	1	SYCAT	alanine-tRNA ligase
552	31	66.0	413	1	S34305	nodulation protein	625	31	66.0	876	2	AP0843	alanine-tRNA ligase
553	31	66.0	413	2	T08297	conserved hypochet	626	31	66.0	876	2	B91073	alanyl-tRNA synth
554	31	66.0	416	2	A61404	keratin A, type I	627	31	66.0	877	2	S76394	hypothetical prote
555	31	66.0	416	2	S60034	keratin, type I, n	628	31	66.0	877	2	H71647	alanine-tRNA ligase
556	31	66.0	416	2	A46559	hypothetical prote	629	31	66.0	878	2	C71305	leucine-tRNA ligase
557	31	66.0	416	2	A99419	3-isopropylmalate	630	31	66.0	878	2	B84977	alanine-tRNA ligase
558	31	66.0	416	2	G69524	3-isopropylmalate	631	31	66.0	878	2	B85917	alanyl-tRNA synth
559	31	66.0	417	2	H72362	3-isopropylmalate	632	31	66.0	878	2	G97865	alanine-tRNA ligase
560	31	66.0	418	2	C72394	hypothetical prote	633	31	66.0	880	2	AC2108	alanyl-tRNA synth
561	31	66.0	419	2	D69051	3-isopropylmalate	634	31	66.0	880	2	H87562	alanyl-tRNA synth
562	31	66.0	419	2	B49418	spermatogenesis fa	635	31	66.0	881	2	A97107	alanyl-tRNA synth
563	31	66.0	420	2	B64425	homocitrate hydr	636	31	66.0	885	2	AG3350	alanyl-tRNA synth
564	31	66.0	422	2	C97290	3-isopropylmalate	637	31	66.0	887	2	AG2806	alanyl-tRNA synth
565	31	66.0	423	2	B75045	probable 3-isoprop	638	31	66.0	889	2	AD2215	two-component hydr
566	31	66.0	424	1	S12793	nodulation protein	639	31	66.0	890	2	F75289	alanyl-tRNA synth
567	31	66.0	424	1	ZZZRCL	nodulation protein	640	31	66.0	900	2	F97585	alanyl-tRNA synth
568	31	66.0	426	1	ZZZRCA	nodulation protein	641	31	66.0	900	2	C64232	alanyl-tRNA synth
569	31	66.0	426	2	A95321	NodN-ACETYLGLUCO	642	31	66.0	900	2	S73748	alanyl-tRNA synth
570	31	66.0	428	2	A69085	3-isopropylmalate	643	31	66.0	906	2	D82899	alanyl-tRNA synth
571	31	66.0	432	2	C70381	large subunit of i	644	31	66.0	916	2	C82844	alanyl-tRNA synth
572	31	66.0	433	2	B69495	acetylase (acn) ho	645	31	66.0	955	2	D96538	cytosolic tRNA-Ala
573	31	66.0	434	2	D75373	3-isopropylmalate	646	31	66.0	955	2	A45441	thrombospondin 4 -
574	31	66.0	452	2	T36042	probable plasmid r	647	31	66.0	958	2	S62065	alanine-tRNA ligase
575	31	66.0	455	2	A55050	enigma - human	648	31	66.0	959	2	T38247	probable alanyl-tr
576	31	66.0	463	2	T49460	hypothetical prote	649	31	66.0	965	2	S62935	hypothetical prote
577	31	66.0	464	2	H90140	transcription regu	650	31	66.0	967	1	SYMTAT	alanine-tRNA ligase
578	31	66.0	483	2	AG1898	chloroform reduct	651	31	66.0	968	2	I60107	alanine-tRNA ligase
579	31	66.0	508	1	KRSHL2	keratin type II, m	652	31	66.0	968	2	T29466	hypothetical prote
580	31	66.0	527	2	D84517	probable replicati	653	31	66.0	982	2	T15967	hypothetical prote
581	31	66.0	574	1	HQCLIP	hydrogenase (BC 1,	654	31	66.0	989	2	S32671	alanine-tRNA ligase
582	31	66.0	580	2	S72211	N-acetyl-beta-D-gl	655	31	66.0	1075	2	T00341	hypothetical prote
583	31	66.0	584	1	C8HUA	complement C8 alph	656	31	66.0	1149	2	S67039	DNA-directed RNA p
584	31	66.0	585	2	I46866	complement compone	657	31	66.0	1172	2	P96503	protein PgC16.13
585	31	66.0	597	2	S72468	probable transcrip	658	31	66.0	1196	1	DNBEHR	DNA-binding protei
586	31	66.0	604	2	T36966	hypothetical prote	659	31	66.0	1196	1	DNBEVS	DNA-binding protei
587	31	66.0	616	2	B84500	probable retroelem	660	31	66.0	1196	1	DNBEV1	major DNA-binding
588	31	66.0	633	2	A75069	dipeptide transpor	661	31	66.0	1197	1	A48350	DNA-binding protei
589	31	66.0	642	2	H97019	acetylase A (limpor	662	31	66.0	1364	2	T00250	MEGF2 protein - hu
590	31	66.0	659	2	F70453	acetylase - Aquife	663	31	66.0	1465	2	S31262	TyB protein - years
591	31	66.0	667	1	VCLJGL	env polypeptide pr	664	31	66.0	1467	2	PC1253	TyB protein - years
592	31	66.0	670	2	T33304	hypothetical prote	665	31	66.0	1743	2	T15893	hypothetical prote
593	31	66.0	680	2	UC5133	protein-glutamine	666	31	66.0	1786	1	NMMSB1	laminin beta-1 cha
594	31	66.0	693	1	S61067	homocitrate hydr	667	31	66.0	1802	2	S52611	TyB protein - years
595	31	66.0	695	2	S66662	protein-glutamine	668	31	66.0	1803	2	S56894	TyB protein - years
596	31	66.0	708	2	A53185	G-box-binding fact	669	31	66.0	1983	2	AC1922	two-component hydr
597	31	66.0	712	2	A45638	immunodominant nic	670	31	66.0	2282	2	T42717	DNA-binding protei
598	31	66.0	721	2	T38665	probable homoconi	671	31	66.0	2630	2	T08868	polypeptide PI - A
599	31	66.0	724	2	A48569	antigen Em100 - E1	672	31	66.0	3034	2	T14119	seven-pass transme
600	31	66.0	728	2	S50387	acetylase hydratas	673	31	66.0	4957	2	T03455	ALR protein - huma
601	31	66.0	778	2	T38347	acetylase hydratas	674	31	66.0	5262	2	T03454	ALR protein - huma
602	31	66.0	779	2	S57805	acetylase hydratas	675	31	66.0	5262	2	T03454	thioredoxin - Bac
603	31	66.0	780	2	T52543	acetylase hydratas	676	31	66.0	96	2	A10535	hypothetical prote
604	31	66.0	781	2	A35544	acetylase hydratas	677	31	66.0	105	2	C95223	thioredoxin, proba
605	31	66.0	788	2	S57528	acetylase hydratas	678	31	66.0	119	2	T17930	thioredoxin-like p
606	31	66.0	788	2	S44831	acetylase hydratas	679	31	66.0	130	2	T51879	hypothetical prote
607	31	66.0	789	2	S46631	protein-glutamine	680	31	66.0	133	2	T37311	hypothetical prote
608	31	66.0	817	1	TGHUM1	protein-glutamine	681	31	66.0	150	2	S15914	thioredoxin homolo
609	31	66.0	824	2	B38423	leucine-tRNA ligas	682	31	66.0	236	1	D64740	proline-rich prote
610	31	66.0	824	2	P72408	Na+/H+-exchanging	683	31	66.0	247	2	S31096	protein disulfide
611	31	66.0	832	2	A40205	hypothetical prote	684	31	66.0	255	2	S57381	thioredoxin homolo
612	31	66.0	835	2	T26086	protein-glutamine	685	31	66.0	277	2	S51247	
613	31	66.0	836	2	A54269		686	31	66.0	285	2	S51247	

687	30	63.8	310	2	T17980	hypothetical prote
688	30	63.8	326	1	GOVZML	T2 protein - myxom
689	30	63.8	328	2	D70574	hypothetical prote
690	30	63.8	343	2	T06273	benzothiadiazole-i
691	30	63.8	348	2	C86607	disulfide bond iso
692	30	63.8	348	2	G72016	probable disulfide
693	30	63.8	349	2	E71847	lipopolysaccharide
694	30	63.8	349	2	G64668	lipopolysaccharide
695	30	63.8	357	2	T23460	hypothetical prote
696	30	63.8	367	2	T02767	hypothetical prote
697	30	63.8	367	2	T02990	cinamyl-alcohol d
698	30	63.8	368	2	T38901	probable dimeric d
699	30	63.8	409	2	T03718	suppressor 2 prote
700	30	63.8	432	2	T28931	hypothetical prote
701	30	63.8	437	2	T03161	hypothetical prote
702	30	63.8	470	2	C70672	hypothetical prote
703	30	63.8	483	2	T47974	hypothetical prote
704	30	63.8	496	2	S55665	hypothetical prote
705	30	63.8	510	2	T10494	pectinesterase (EC
706	30	63.8	510	2	T10494	pectinesterase (EC
707	30	63.8	513	2	T34546	hypothetical prote
708	30	63.8	514	2	S48730	Cry j II protein -
709	30	63.8	514	2	JC2498	second major aller
710	30	63.8	514	2	UC7100	polygalacturonase
711	30	63.8	515	2	T03717	GTP-binding protei
712	30	63.8	527	2	P96552	hypothetical prote
713	30	63.8	554	2	T36545	probable spermidin
714	30	63.8	565	2	E91268	thiol disulfide in
715	30	63.8	565	2	C86109	thiol disulfide in
716	30	63.8	565	2	S56364	inner membrane cop
717	30	63.8	567	2	AE1004	thiol,disulfide in
718	30	63.8	567	2	B81408	probable thiol-dis
719	30	63.8	579	2	A64100	inner membrane cop
720	30	63.8	580	2	H86189	hypothetical prote
721	30	63.8	582	2	S69720	hypothetical prote
722	30	63.8	585	2	A10042	thiol,disulfide in
723	30	63.8	600	2	A82043	inner membrane cop
724	30	63.8	751	2	T15403	hypothetical prote
725	30	63.8	758	2	C82784	c-type cytochrome
726	30	63.8	815	2	T15402	hypothetical prote
727	30	63.8	815	2	A48825	Notch homolog Mrc
728	30	63.8	865	2	D72206	valine-tRNA ligase
729	30	63.8	889	2	C72565	probable valyl-tRN
730	30	63.8	1223	2	T10365	helicase - Oxygia
731	30	63.8	1251	2	B86194	hypothetical prote
732	30	63.8	1307	2	S53412	probable membrane
733	30	63.8	1664	2	P84485	probable retroelem
734	30	63.8	2276	2	T00076	hypothetical prote
735	30	63.8	2437	2	S42612	transmembrane prot
736	30	63.8	2524	2	A35844	Xotch protein - Af
737	30	63.8	2531	2	S18188	notch protein homo
738	30	63.8	2531	2	A46019	notch-1 protein -
739	30	63.8	2555	2	A40043	notch protein homo
740	29.5	62.8	570	2	G85046	hypothetical prote
741	29	61.7	113	2	AH2029	hypothetical prote
742	29	61.7	132	1	MFIV2J	matrix protein M2
743	29	61.7	200	2	E81314	probable periplasm
744	29	61.7	227	2	T06634	hypothetical prote
745	29	61.7	230	2	G97215	nifH-related domi
746	29	61.7	250	2	B82821	NADH-ubiquinone ox
747	29	61.7	253	2	D69964	conserved hypochet
748	29	61.7	269	2	E82716	ATP synthase, A ch
749	29	61.7	269	2	S48978	hypothetical prote
750	29	61.7	272	2	B72208	hypothetical prote
751	29	61.7	309	2	I51900	carbonic anhydrase
752	29	61.7	309	2	G70882	probable oxidoredu
753	29	61.7	321	1	F87102	probable phosphos
754	29	61.7	324	1	B70885	probable phosphos
755	29	61.7	354	2	F71721	hypothetical prote
756	29	61.7	374	2	S69627	hypothetical prote
757	29	61.7	385	2	P81341	3-deoxy-manno-occu
758	29	61.7	385	2	T22822	hypothetical prote
759	29	61.7	392	2	A75593	alcohol dehydrogen
760	29	61.7	426	2	F75394	hypothetical prote
761	29	61.7	488	2	T10675	hypothetical prote
762	29	61.7	519	2	I45847	acetylcholine rece
763	29	61.7	591	2	E83039	probable thiol-dis
764	29	61.7	598	2	T45827	pectinesterase-lik
765	29	61.7	600	2	H95379	probable adenine d
766	29	61.7	601	2	F81074	thiol-disulfide in
767	29	61.7	608	2	A53195	afamin precursor
768	29	61.7	613	2	B81868	thiol-disulfide in
769	29	61.7	628	2	AD0632	membrane protein.
770	29	61.7	662	1	A31349	arachidonate 15-1i
771	29	61.7	663	1	A35087	arachidonate 12-1i
772	29	61.7	663	2	S32825	arachidonate 12-1i
773	29	61.7	666	2	T31461	probable magnesium
774	29	61.7	686	2	T15795	hypothetical prote
775	29	61.7	700	2	A33392	protein kinase C (
776	29	61.7	1018	2	S44758	C14B9.6 protein -
777	29	61.7	1165	2	T38867	probable DNA-dirc
778	29	61.7	1422	2	T18404	chromatin remodel
779	29	61.7	1955	1	ACGH	agrin precursor -
780	29	61.7	2052	2	T18290	FYVE finger-contai
781	29	61.7	2137	2	T05244	hypothetical prote
782	29	61.7	2207	2	T24629	glutamate synthase
783	29	61.7	2561	2	T24864	hypothetical prote
784	28.5	60.6	256	2	D97086	formate/nitrite fa
785	28.5	60.6	507	2	S73199	protochlorophyllid
786	28.5	60.6	1171	2	A42916	metabotropic gluta
787	28.5	60.6	1180	2	JC2132	metabotropic gluta
788	28.5	60.6	1212	2	JC2131	metabotropic gluta
789	28	59.6	30	2	S07484	metabotropic gluta
790	28	59.6	39	2	C37264	metabotropic gluta
791	28	59.6	55	1	FEPE	E2 glycoprotein -
792	28	59.6	58	2	S10063	ferredoxin 214Fe-4
793	28	59.6	59	2	S00371	isoprenolign G1 -
794	28	59.6	60	1	TI80R	serum basic protei
795	28	59.6	61	2	S14049	metallothionein pr
796	28	59.6	62	2	T28346	ORF MSV185 hypot
797	28	59.6	65	2	B25103	ferredoxin 214Fe-4
798	28	59.6	66	1	QABPL	restriction inhibi
799	28	59.6	73	2	S30512	restriction inhibi
800	28	59.6	76	2	S10068	cytochrome c-type
801	28	59.6	80	2	T02063	restriction inhibi
802	28	59.6	82	2	T06986	metallothionein-1i
803	28	59.6	88	2	JQ2360	hypothetical prote
804	28	59.6	98	2	D89856	wheat aluminum ind
805	28	59.6	98	2	D89856	hypothetical prote
806	28	59.6	100	1	TI8OSP	basic proteinase i
807	28	59.6	100	1	D89959	spleen basic prote
808	28	59.6	103	2	A86584	hypothetical prote
809	28	59.6	104	2	A71817	CT631 hypothetical
810	28	59.6	104	2	B64702	probable thioredox
811	28	59.6	104	2	S18821	thioredoxin - Heli
812	28	59.6	105	2	D95341	cytochrome c552 pr
813	28	59.6	106	2	H89854	probable CycB2 cyt
814	28	59.6	106	2	E84056	hypothetical prote
815	28	59.6	107	2	G69998	thioredoxin H1 BH3
816	28	59.6	107	2	A60627	thioredoxin H1 hom
817	28	59.6	108	2	A60627	glycoprotein hormo
818	28	59.6	109	2	G65201	hypothetical 11.8
819	28	59.6	112	2	C83864	thioredoxin BH175
820	28	59.6	113	2	T38499	hypothetical prote
821	28	59.6	114	2	E70759	probable fdxa prot
822	28	59.6	116	2	B53701	cryptidin-related p
823	28	59.6	117	2	AC1831	hypothetical prote
824	28	59.6	119	2	I51229	gonadotropin alpha
825	28	59.6	124	2	QQVZEL	F11 protein - vacc
826	28	59.6	130	2	S47637	ribosomal protein
827	28	59.6	130	2	S57137	probable membrane
828	28	59.6	133	2	H42513	J5L 15.2K protein
829	28	59.6	133	2	T28520	hypothetical prote
830	28	59.6	133	2	H72160	hypothetical prote
831	28	59.6	133	2	S33096	M5L protein - vari
832	28	59.6	134	2	T30680	USL protein - vari
	28	59.6	134	2	A54002	hypothetical prote
	28	59.6	134	2	A54002	pollen allergen Lo

833	28	59.6	137	2	A63424	906	28	59.6	290	2	T21185	hypothetical prote
834	28	59.6	138	2	C84491	907	28	59.6	293	2	S63845	transcription elon
835	28	59.6	144	2	G86293	908	28	59.6	294	2	T39774	hypothetical prote
836	28	59.6	144	2	B84728	909	28	59.6	296	2	B71305	hypothetical prote
837	28	59.6	145	2	T34303	910	28	59.6	297	1	S49348	cytochrome-c oxida
838	28	59.6	147	2	AD0421	911	28	59.6	298	2	S39539	osteonectin precu
839	28	59.6	152	2	T04811	912	28	59.6	300	2	S18992	osteonectin precu
840	28	59.6	152	2	S46272	913	28	59.6	301	2	S17361	transcription elon
841	28	59.6	154	2	A96544	914	28	59.6	301	2	S34159	transcription elon
842	28	59.6	154	2	F82633	915	28	59.6	301	2	A29950	transcription elon
843	28	59.6	154	2	A86086	916	28	59.6	301	2	G71206	cryptophan-tRNA Ii
844	28	59.6	162	2	T42001	917	28	59.6	302	1	GEMSN	osteonectin precu
845	28	59.6	163	2	E91238	918	28	59.6	303	1	GEMUN	osteonectin precu
846	28	59.6	166	1	B64019	919	28	59.6	303	2	S72364	transcription elon
847	28	59.6	166	2	T09593	920	28	59.6	303	2	S72365	transcription elon
848	28	59.6	168	2	A31196	921	28	59.6	303	2	T21125	hypothetical prote
849	28	59.6	168	2	D75144	922	28	59.6	304	1	GBRON	osteonectin precu
850	28	59.6	168	2	A71184	923	28	59.6	309	2	A42921	transcription elon
851	28	59.6	170	2	A35944	924	28	59.6	313	2	A87282	MutT/nudix family
852	28	59.6	180	2	B83460	925	28	59.6	314	2	S31868	glucocorticoid rec
853	28	59.6	180	2	S47662	926	28	59.6	316	2	AC0329	conserved hypotet
854	28	59.6	180	2	S47663	927	28	59.6	317	2	B69185	conserved hypotet
855	28	59.6	180	2	T17614	928	28	59.6	318	2	H86342	hypothetical prote
856	28	59.6	185	2	AF0787	929	28	59.6	320	2	T42062	thioredoxin-disulf
857	28	59.6	185	2	A10960	930	28	59.6	321	2	A44230	phthalate dioxygen
858	28	59.6	185	2	A64989	931	28	59.6	322	1	A53307	thioredoxin-disulf
859	28	59.6	185	2	F85858	932	28	59.6	322	2	T36577	thioredoxin reduct
860	28	59.6	185	2	D91014	933	28	59.6	324	2	T42656	hypothetical prote
861	28	59.6	188	2	AD0334	934	28	59.6	326	1	A47016	toluene-4-monooxyg
862	28	59.6	191	2	B84890	935	28	59.6	326	2	A59241	DNA-directed DNA p
863	28	59.6	193	2	AG1279	936	28	59.6	326	2	UC7094	nine-heme cytochro
864	28	59.6	193	2	AG1642	937	28	59.6	328	2	A99416	alcohol dehydrogen
865	28	59.6	195	2	JH0719	938	28	59.6	328	2	DB3275	DNA polymerase III
866	28	59.6	197	2	A82536	939	28	59.6	329	1	A36952	CDP-6'-deoxy-delta
867	28	59.6	198	2	S70515	940	28	59.6	329	2	AE0378	cdp-6'-deoxy-delta-
868	28	59.6	198	2	I52655	941	28	59.6	330	1	GZMSA	Ig gamma-2a chain
869	28	59.6	199	2	H86154	942	28	59.6	332	2	A69224	polyferredoxin 4x2
870	28	59.6	207	2	A69446	943	28	59.6	332	2	T25779	hypothetical prote
871	28	59.6	207	2	T49552	944	28	59.6	332	2	T26145	hypothetical prote
872	28	59.6	213	2	D70592	945	28	59.6	335	2	H87243	hypothetical prote
873	28	59.6	215	2	T01349	946	28	59.6	336	1	C41659	moA/NirX family F
874	28	59.6	215	2	H87196	947	28	59.6	336	2	F81849	benzoate 1,2-dioxy
875	28	59.6	216	2	JX0265	948	28	59.6	336	2	H81091	probable CDP-6-deo
876	28	59.6	218	2	S51381	949	28	59.6	337	2	C83332	probable CDP-6-deo
877	28	59.6	218	2	T45979	950	28	59.6	337	2	A12723	toluate 1,2-dioxyg
878	28	59.6	220	1	A33872	951	28	59.6	337	2	B37505	naphthalene 1,2-di
879	28	59.6	220	1	F72685	952	28	59.6	340	2	T32931	phenol hydroxylase
880	28	59.6	228	2	T01350	953	28	59.6	340	2	C87732	hypothetical prote
881	28	59.6	235	2	JX0167	954	28	59.6	340	2	A10165	protein W03D8.4 Ii
882	28	59.6	236	2	E97101	955	28	59.6	340	2	G96985	probable oxidoredu
883	28	59.6	238	1	A46508	956	28	59.6	341	2	S31571	galactose mutaroca
884	28	59.6	238	1	I38016	957	28	59.6	343	2	T15346	cinamyl-alcohol d
885	28	59.6	238	1	JC2297	958	28	59.6	344	2	I51330	hypothetical prote
886	28	59.6	238	1	S43511	959	28	59.6	346	2	T31263	androgen receptor
887	28	59.6	239	2	F64382	960	28	59.6	348	1	H64657	xylene monooxygena
888	28	59.6	244	2	H84853	961	28	59.6	348	1	S77598	probable cinamyl-
889	28	59.6	245	2	G84853	962	28	59.6	350	2	B37316	cytochrome-c oxida
890	28	59.6	246	2	S38950	963	28	59.6	350	2	S47232	ferredoxin-NAD red
891	28	59.6	247	2	T43136	964	28	59.6	350	2	A71857	phenol 2-monooxyge
892	28	59.6	254	2	B31790	965	28	59.6	352	2	I51282	zinc-dependent alc
893	28	59.6	255	2	T36778	966	28	59.6	353	2	A95312	TRP-1 - axoloti (f
894	28	59.6	257	2	C84890	967	28	59.6	354	2	C95381	probable dioxigena
895	28	59.6	260	2	D64419	968	28	59.6	357	2	T09141	probable oxidoredu
896	28	59.6	263	2	AD0590	969	28	59.6	362	2	S45094	cinamyl-alcohol d
897	28	59.6	270	2	G96914	970	28	59.6	364	2	B69131	cinamyl-alcohol d
898	28	59.6	270	2	T32007	971	28	59.6	366	2	G82970	cryptophan-tRNA Ii
899	28	59.6	273	2	PC4153	972	28	59.6	370	2	B83191	probable ferredoxi
900	28	59.6	274	2	T03797	973	28	59.6	370	2	F64476	alcohol dehydrogen
901	28	59.6	274	2	T39703	974	28	59.6	371	2	D90192	alcohol dehydrogen
902	28	59.6	275	2	G84368	975	28	59.6	373	1	A33419	alcohol dehydrogen
903	28	59.6	280	2	S26831	976	28	59.6	373	1	DERTA	alcohol dehydrogen
904	28	59.6	287	2	T44961	977	28	59.6	373	1	S68061	alcohol dehydrogen
905	28	59.6	288	2	S27842	978	28	59.6	374	1	A56643	alcohol dehydrogen

979 28 59.6 374 1 DEHUC2 alcohol dehydrogen
980 28 59.6 374 2 D72477 probable cryptocop
981 28 59.6 376 1 JC4967 alcohol dehydrogen
982 28 59.6 376 1 S51187 alcohol dehydrogen
983 28 59.6 376 2 JC7759 alcohol dehydrogen
984 28 59.6 377 2 AB0183 alcohol dehydrogen
985 28 59.6 378 2 C85431 hypotheical prote
986 28 59.6 378 2 AF3320 flavohemoprotein
987 28 59.6 379 2 H69512 hypotheical prote
988 28 59.6 381 1 JN0447 alcohol dehydrogen
989 28 59.6 385 2 C75020 tryptophanyl-tRNA
990 28 59.6 386 1 S31140 alcohol dehydrogen
991 28 59.6 387 2 H72299 hypotheical prote
992 28 59.6 393 2 T41211 hypotheical wtf1
993 28 59.6 394 2 A97244 moaA/NtrJ family F
994 28 59.6 399 1 G2MSAM Ig gamma-2a chain
995 28 59.6 399 2 AE3148 glycosyltransferas
996 28 59.6 399 2 F98139 sqdx protein (impo
997 28 59.6 401 2 E88969 protein F15E11.7
998 28 59.6 403 2 JC5269 neuron-specific st
999 28 59.6 404 2 G69332 heterodisulfide re
1000 28 59.6 405 1 G2MSBM Ig gamma-2b chain

ALIGNMENTS

RESULT 1
E84409
Chlorodoxin [imported] - Halobacterium sp. NRC-1
C/Species: Halobacterium sp. NRC-1
C/Date: 02-Feb-2001 #sequence_rev1sion 02-Feb-2001 #text_change 05-Oct-2004
C/Accession: E84409
R/NG: M.V.; Kennedy, S.P.; Mainaiz, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leichauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabluc Jung, K.H.; Alam, M.; Fretlaas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: E84409
A>Status: preliminary
A:Residues: 1-89 <STO>
A:Cross-references: UNIPROT:Q9HMD0; UNIPARC:UPI0000063B9A; GB:AE004437; NID:g10581982; F C:Genetics:
A:Gene: trxA2
C:Superfamily: chlorodoxin
Query Match 100.0%; Score 47; DB 2; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 12 WCGPCK 17
RESULT 2
G64213
Chlorodoxin - Mycoplasma genitalium
C/Species: Mycoplasma genitalium
C/Date: 17-Nov-1995 #sequence_rev1sion 16-Aug-1996 #text_change 05-Oct-2004
C/Accession: G64213
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.; C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: G64213
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-102 <TIGR>
A:Cross-references: UNIPROT:P47370; UNIPARC:UPI0000136E89; GB:U39691; GB:L43967; NID:g10 A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: chlorodoxin; chlorodoxin homology
C:Keywords: redox-active disulfide
F:9-90/Domain: chlorodoxin homology <THR>
F:30-33/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 3
S73896
Chlorodoxin - Mycoplasma pneumoniae (strain ATCC 29342)
N/Alternate names: hypothetical protein A65_off102
C/Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C/Date: 27-Feb-1997 #sequence_rev1sion 25-Apr-1997 #text_change 09-Jul-2004
C/Accession: S73896
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73896
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-102 <HM>
A:Cross-references: UNIPROT:P75512; UNIPARC:UPI0000136E8A; EMBL:AE000056; GB:U00089; NIC A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: chlorodoxin; chlorodoxin homology
F:9-90/Domain: chlorodoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 4
B71503
probable chlorodoxin - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C/Species: Chlamydia trachomatis
C/Date: 13-Sep-1998 #sequence_rev1sion 13-Sep-1998 #text_change 05-Oct-2004
C/Accession: B71503
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: B71503
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-102 <ARN>
A:Cross-references: UNIPROT:O84544; UNIPARC:UPI0000136E75; GB:AE001324; GB:AE001273; NII A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: trxA
C:Superfamily: chlorodoxin; chlorodoxin homology
Query Match 100.0%; Score 47; DB 2; Length 102;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 5

C81660

thioredoxin TC0826 [imported] - Chlamydia muridarum (strain N19g)

C:Species: Chlamydia muridarum, Chlamydia trachomatis MOPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004

C:Accession: C81660

R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of Chlamydia trachomatis MOPn and Chlamydia pneumoniae AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: C81660

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-102 <TET>

A:Cross-references: UNIPROT:Q9PJK3, UNIPARC:UPI0000057A90; GB:AE002349; GB:AE002160; NID

A:Experimental source: strain N19g (MOPn)

C:Genetics:

A:Gene: TC0826

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 102;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 6

TXBY2

thioredoxin II - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein L1933; protein YLR043c

C:Species: Saccharomyces cerevisiae

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 05-Oct-2004

C:Accession: S15048; A39847; S15360; S64870; B38669

R:Gap, Z. R.

J. Biol. Chem. 266, 1692-1696, 1991

A:Title: Yeast thioredoxin genes.

A:Reference number: A38669; MUID:91107668; PMID:1988444

A:Accession: S15048

A:Molecule type: DNA

A:Residues: 1-103 <GAN>

A:Cross-references: UNIPROT:P22217, UNIPARC:UPI000004F943; EMBL:M59169; NID:G173027; PID

R:Miller, E.G.D.

J. Biol. Chem. 266, 9194-9202, 1991

A:Title: Thioredoxin deficiency in yeast prolongs S phase and shortens the G1 interval

A:Reference number: A39847; MUID:91225027; PMID:2026619

A:Accession: A39847

A:Molecule type: DNA

A:Residues: 1-103 <MU>

A:Cross-references: UNIPARC:UPI000004F943; GB:M62647; NID:G173047; PIDN:AAA35177.1; PID:

R:Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.

Eur. J. Biochem. 23, 328-335, 1971

A:Title: Yeast thioredoxin. Amino-acid sequence around the active-center disulfide of th

A:Reference number: S05793; MUID:72100583; PMID:4945270

A:Accession: S15360

A:Molecule type: protein

A:Residues: 26-34 <HAL>

A:Cross-references: UNIPARC:UPI0000171E21

R:Koetter, P.; Rose, M.; Entian, K.D.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64863

A:Accession: S64870

A:Molecule type: DNA

A:Residues: 1-103 <KOE>

A:Cross-references: UNIPARC:UPI000004F943; EMBL:Z73215; NID:G1360372; PIDN:CAA97572.1; I

A:Note: experimental_source strain S288C

C:Genetics:

A:Gene: SGD:TRX1; TR-II; MIPS:YLR043C

A:Cross-references: SGD:S0004033; MIPS:YLR043C

A:Map position: 12R

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F/2-103/Product: thioredoxin II #status predicted <MAT>

F/9-90/Domain: thioredoxin homology <THR>

F/30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 103;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 7

T39085

thioredoxin II - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: thioredoxine 2

C:Species: Schizosaccharomyces pombe

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39085; T46567

R:Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, September 1997

A:Reference number: Z21826

A:Accession: T39085

A:Status: preliminary

A:Molecule type: translated from GB/EMBL/DBJ

A:Residues: 1-103 <GEN>

A:Cross-references: UNIPROT:O14463; UNIPARC:UPI000016205F; EMBL:Z99532; PIDN:CAB16724.1,

A:Experimental source: strain 972h-; cosmid c7d4

R:Lenner, G.; Perret, E.; Bonin, O.; Picard, A.; Caput, D.

submitted to the EMBL Data Library, October 1997

A:Description: TRX2, a fission yeast stress protein.

A:Reference number: Z23075

A:Accession: T46567

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-103 <LEN>

A:Cross-references: UNIPARC:UPI000016205F; EMBL:AJ003819; PIDN:CAA06033.1

A:Experimental source: strain 972(-)

C:Genetics:

A:Gene: trx2; SPAC7D4.07c

A:Map position: 1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 8

A28086

thioredoxin - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 30-Jun-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A28086

R:Johnson, R.S.; Mathews, W.R.; Biemann, K.; Hopper, S.

J. Biol. Chem. 263, 9589-9597, 1988

A:Title: Amino acid sequence of thioredoxin isolated from rabbit bone marrow determined

A:Reference number: A28086; MUID:86257078; PMID:3164311

A:Accession: A28086

A.Molecule type: protein
 A:Residues: 1-104 <JON>
 C:Species: Bacillus subtilis
 C:Date: 31-Jan-1992 #sequence revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: B37192; H69726
 C:Keywords: redox-active disulfide
 F:8-91/Domain: thioresoxin homology <THR>
 F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 9

B37192 thioresoxin - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 31-Jan-1992 #sequence revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: B37192; H69726

R:Chen, N.Y.; Zhang, U.J.; Paulus, H.

J. Gen. Microbiol. 135, 2931-2940, 1989

A:Title: Chromosomal location of the Bacillus subtilis aspartokinase II gene and nucleos

A:Reference number: A37192; PMID:90132525; PMID:2559145

A:Accession: B37192

A:Molecule type: DNA

A:Residues: 1-104 <CHE>

A:Cross-references: UNIPROT:P14949; UNIPARC:UPI000006087B; GB:U03294; GB:M26384; NID:914

R:Kumai, T.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emerson, P.T.; Eutlian, K.D.; Errington, J.; Fabret, C.; Ferrari, B.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall

leth, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koester, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maeda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, R.; Scorfone, F.; Sekiguchi, J.; Sekowska, A.; Ser

ateuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; PMID:98044033; PMID:9384377

A:Accession: H69726

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-104 <KUN>

A:Cross-references: UNIPARC:UPI000006087B; GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CA

A:Experimental source: strain 168

C:Genetics:

A:Gene: trxA

A:Map position: 70 min

C:Superfamily: thioresoxin; thioresoxin homology

C:Keywords: redox-active disulfide

F:8-90/Domain: thioresoxin homology <THR>

F:29-32/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 28 WCGPCK 33

RESULT 10
 T8Y1
 thioresoxin I - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein G7746; protein YGR209C; thioresoxin 2
 C:Species: Saccharomyces cerevisiae
 C:Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 05-Oct-2004
 C:Accession: S15049; B39847; S05793; S53932; S61947; S64531; S63858; A38669
 R:Gan, Z. R.

J. Biol. Chem. 266, 1692-1696, 1991

A:Title: Yeast thioresoxin genes.

A:Reference number: A38669; PMID:91107668; PMID:1988444

A:Accession: S15049

A:Molecule type: DNA

A:Residues: 1-104 <GAN>

A:Cross-references: UNIPROT:P22803; UNIPARC:UPI000004F91C; GB:M59168; NID:g173025; PIDN:

R:Miller, E.G.D.

J. Biol. Chem. 266, 9194-9202, 1991

A:Title: Thioresoxin deficiency in yeast prolongs S phase and shortens the G1 interval o

A:Reference number: A39847; PMID:9125027; PMID:2026619

A:Accession: B39847

A:Molecule type: DNA

A:Residues: 1-104 <MUL>

A:Cross-references: UNIPARC:UPI000004F91C; GB:M62648; NID:g173049; PIDN:AAA5178.1; PID:

R:Hall, D.E.; Baldesten, A.; Holmgren, A.; Reichard, P.

Eur. J. Biochem. 23, 328-335, 1971

A:Title: Yeast thioresoxin. Amino-acid sequence around the active-center disulfide of th

A:Reference number: S05793; PMID:72100583; PMID:4945270

A:Accession: S05793

A:Molecule type: protein

A:Residues: 2:27-43;98-104 <NAL>

A:Cross-references: UNIPARC:UPI000111EC95; UNIPARC:UPI000171E1F; UNIPARC:UPI000171E20

A:Note: the sequence from the summary and from Fig. 5 is inconsistent with that from pag

R:Guerrero, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pousa

submitted to the EMBL Data Library, April 1995

A:Description: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII

es, of the human.

A:Reference number: S53932

A:Accession: S53932

A:Molecule type: DNA

A:Residues: 1-104 <GUE>

A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; P

A:Experimental source: strain S288C

R:Song, J.M.; Cheung, B.; Rabinowitz, J.C.

submitted to the EMBL Data Library, November 1995

A:Description: Analysis of the 15.6-kb fragment encompassing the ADE3 gene.

A:Reference number: S61947

A:Accession: S61947

A:Molecule type: DNA

A:Residues: 1-104 <SON>

A:Cross-references: UNIPARC:UPI000004F91C; EMBL:U40843; NID:g1165213; PIDN:AAA85584.1; I

A:Experimental source: strain GRP88

R:Guerrero, P.; Barreiro, T.; Cyrne, L.; Soares, H.; Maia e Silva, A.; Rodrigues-Pous

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64531

A:Accession: S64531

A:Molecule type: DNA

A:Residues: 1-104 <GUM>

A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z72994; NID:g1323374; PIDN:CAA97236.1;

A:Experimental source: strain S288C

R:Guerrero, P.; Barreiro, T.; Soares, H.; Cyrne, L.; Maia e Silva, A.; Rodrigues-Pous

Yeast 12, 273-280, 1996

A:Title: Sequencing of a 17.6 kb segment on the right arm of yeast chromosome VII revea

terial electron-transferring flavoproteins (beta-chain) and of the Escherichia coli pho

A:Reference number: S63848; PMID:97060019; PMID:8904340

A:Accession: S63848

A:Molecule type: DNA

A:Residues: 1-104 <GUP>

A:Cross-references: UNIPARC:UPI000004F91C; EMBL:Z49133; NID:g790489; PIDN:CAA89002.1; P

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995

A:Gene: SGD:TRX2; TR-1; MIPS:YGR209C

A:Cross-references: SGD:S0003441; MIPS:YGR209C

A:Map position: 7R

C:Superfamily: thioresoxin; thioresoxin homology

C:Keywords: redox-active disulfide

F:2-104/Product: thioredoxin I #status experimental <MAT>
F:9-91/Domain: thioredoxin homology <THR>
F:31-34/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 11

S77780
thioredoxin - Mycoplasma capricolum (fragment)

N:Alternate names: protein WC064

C:Species: Mycoplasma capricolum

C:Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004

C:Accession: S77780; S46921

R:Bork, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.

Mol. Microbiol. 16, 955-967, 1995

A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology

A:Reference number: S77739; MUID:96059641; PMID:7476192

A:Accession: S77780

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-104 <BOR>

A:Cross-references: UNIPROT:Q48985; UNIPARC:UPI00000B3213; EMBL:Z33053; NID:9514449; PID

A:Experimental source: ATCC 27343

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994

C:Genetics:

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:13-93/Domain: thioredoxin homology <THR>

F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 12

A59394
thioredoxin - Clostridium pasteurianum

C:Species: Clostridium pasteurianum

C:Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 05-Oct-2004

C:Accession: B59394; A59394

R:Reynolds, C.M.; Meyer, J.; Poole, L.B.

Biochemistry 41, 1990-2001, 2002

A:Title: NADH-dependent bacterial thioredoxin reductase-like protein, in conjunction with

A:Reference number: B59394

A:Accession: B59394

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <REI>

A:Cross-references: UNIPARC:UPI0000174DEF

R:Reynolds, C.M.; Poole, L.B.; Hammett, K.E.; Made, K.; Buchanan, B.B.

submitted to the Protein Sequence Database, September 2001

A:Reference number: A59394

A:Accession: A59394

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <RE2>

A:Cross-references: UNIPARC:UPI0000174DEF

R:Hammett, K.E.; Cornwell, K.L.; Buchanan, B.B.

Proc. Natl. Acad. Sci. USA 80, 3681-3685, 1983

A:Title: Ferredoxin/flavoprotein-linked pathway for the reduction of thioredoxin.

A:Reference number: A59432
A:Contents: annotation; purification and characterization of the protein

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 13

B84037
thioredoxin trxA [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004

C:Accession: B84037

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hirai

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: B84037

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STO>

A:Cross-references: UNIPROT:Q9K8A8; UNIPARC:UPI00000C40CD; GB:AP001517; GB:BA000004; NIT

A:Experimental source: strain C-125

C:Genetics:

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 14

B89885
thioredoxin [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004

C:Accession: B89885

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratake, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: B89885

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <KUR>

A:Cross-references: UNIPROT:Q9ZEH4; UNIPARC:UPI00000D78B6; GB:BA000018; PID:G13700945; P

A:Experimental source: strain N315

C:Genetics:

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 15

A30006
 A:Species: Gallus gallus (chicken)
 C:Date: 31-Mar-1989 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: A30006
 R:Jones, S.W.; Luk, K.C.
 J:J Biol. Chem. 263, 9607-9611, 1988
 A:Title: Isolation of a chicken thioredoxin cDNA clone: thioredoxin mRNA is differential
 A:Reference number: A30006; MUID:88257080; PMID:2838473
 A:Accession: A30006
 A:Molecule type: mRNA
 A:Residues: 1-105 <ON>
 A:Cross-references: UNIPROT:P08629; UNIPARC:UPI00001713BC; GB:J03882; NID:g212765; PIDN:
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:9-92/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 16

JH0568
 A:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: JH0568; S04106; S44375; A31993; PT0079; A60749; A38922; S53453; A60870
 R:Tonissen, K.F.; Wells, J.R.E.
 Gene 102, 221-228, 1991
 A:Title: Isolation and characterization of human thioredoxin-encoding genes.
 A:Reference number: JH0568; MUID:91340156; PMID:1874447
 A:Accession: JH0568
 A:Molecule type: DNA
 A:Residues: 1-105 <TON>
 A:Cross-references: UNIPROT:P10599; UNIPARC:UPI000011065C; EMBL:X54539; NID:g37455; PIDN:
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 8, 757-764, 1989
 A:Title: ATL-derived factor (ADF), an II-2 receptor/TrAc inducer homologous to thioredoxin
 A:Reference number: S04106; MUID:89251607; PMID:2785919
 A:Accession: S04106
 A:Molecule type: mRNA
 A:Residues: 1-105 <TAG1>
 A:Cross-references: UNIPARC:UPI000011065C; GB:X77584; NID:g453963; PIDN:CA54687.1; PID:
 A:Note: this sequence has been revised in reference S44375
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMO J. 13, 2244, 1994
 A:Reference number: S44375; MUID:94244626; PMID:8187776
 A:Accession: S44375
 A:Contents: erratum
 A:Molecule type: mRNA
 A:Residues: 1-105 <TAG2>
 A:Cross-references: UNIPARC:UPI000011065C; EMBL:X77584; NID:g453963; PIDN:CA54687.1; PID:
 R:Wollman, E.E.; d'Amico, L.; Rimsky, L.; Shaw, A.; Jacquot, J.P.; Wingfield, P.; Grabe
 J. Biol. Chem. 263, 15506-15512, 1988
 A:Title: Cloning and expression of a cDNA for human thioredoxin.
 A:Reference number: A31993; MUID:89008454; PMID:3170555
 A:Accession: A31993
 A:Molecule type: mRNA
 A:Residues: 1-38, 'N', '40-73', 'T', '75-105 <MOD>
 A:Cross-references: UNIPARC:UPI000003066B; GB:J04026; NID:g339648; PIDN:AAA74596.1; PID:
 R:Martin, H.; Dean, M.
 Biochem. Biophys. Res. Commun. 175, 123-128, 1991
 A:Title: Identification of a thioredoxin-related protein associated with plasma membrane
 A:Reference number: PT0079; MUID:9115137; PMID:1998498
 A:Accession: PT0079

A:Molecule type: protein
 A:Residues: 2-13, 'X', '15 <MAR>
 A:Cross-references: UNIPARC:UPI0000171E19
 R:Silberstein, D.S.; Ali, M.H.; Baker, S.L.; David, J.R.
 J. Immunol. 143, 979-983, 1989
 A:Title: Human eosinophil cytotoxicity-enhancing factor. Purification, physical character
 A:Reference number: A60749; MUID:89309777; PMID:2745979
 A:Accession: A60749
 A:Molecule type: protein
 A:Residues: 2-12, 'K', '14-15', 'XX', '18-19', 'X', '21-22 <STL>
 A:Cross-references: UNIPARC:UPI0000171E1A
 A:Note: the abstract is inconsistent with figure 4 in having one undetermined residue at
 R:Rimsky, L.; Wakasugi, H.; Ferreira, P.; Robin, P.; Capdevielle, J.; Turaz, T.; Fradelizi
 J. Immunol. 136, 3304-3310, 1986
 A:Title: Purification to homogeneity and NH-2-terminal amino acid sequence of a novel in
 A:Reference number: A38922; MUID:86169664; PMID:3485686
 A:Accession: A38922
 A:Molecule type: protein
 A:Residues: 2-16 <WAK>
 A:Cross-references: UNIPARC:UPI0000171E1B
 R:Dean, M.F.; Martin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A:Title: Characterization of a thioredoxin-related surface protein.
 A:Reference number: S53453; MUID:95118305; PMID:7818492
 A:Accession: S53453
 A:Molecule type: protein
 A:Residues: 1-21, '38-57 <DEA>
 A:Cross-references: UNIPARC:UPI00000353C5; UNIPARC:UPI0000171E1C
 A:Note: described to be a surface-associated thioredoxin
 R:Wakasugi, H.; Rimsky, L.; Mahe, Y.; Kamel, A.M.; Fradelizi, D.; Turaz, T.; Bertoglio,
 Proc. Natl. Acad. Sci. U.S.A. 84, 804-808, 1987
 A:Title: Epstein-Barr virus-containing B-cell line produces an interleukin 1 that it use
 A:Reference number: A60870; MUID:87118252; PMID:3027706
 A:Contents: annotation
 R:Reichsel, A.; Gadsdaka, J.R.; Powis, G.; Montfort, W.R.
 submitted to the Brookhaven Protein Data Bank, February 1996
 A:Reference number: A65533; PDB:1ERT
 A:Contents: annotation; X-ray crystallography, 1.7 angstroms, reduced form, residues 1-1
 R:Reichsel, A.; Gadsdaka, J.R.; Powis, G.; Montfort, W.R.
 submitted to the Brookhaven Protein Data Bank, December 1990
 A:Reference number: A50924; PDB:4TRX
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-73, 'T', '75-105
 R:Forman-Kay, J.D.; Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M.
 Biochemistry 30, 2685-2698, 1991
 A:Title: High-resolution three-dimensional structure of reduced recombinant human thior
 A:Reference number: A38953; MUID:91159399; PMID:2001356
 A:Contents: annotation; conformation by (1)H- and (15)N-NMR
 C:Comment: This small ubiquitous protein functions in many intracellular biological pati

A:Gene: GDB:TXN
 A:Cross-references: GDB:120475; OMIM:187700
 A:Map position: 9q31-9q31
 A:Introns: 8/3; 43/3; 63/3; 85/3
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:2-105/Product: thioredoxin #status experimental <MAT>
 F:9-92/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 31 WCGPCK 36

RESULT 17

JS0667
 C:Species: rhesus macaque
 C:Date: 30-Jun-1992 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: JS0667
 R:An, G.; Wu, R.
 Biochem. Biophys. Res. Commun. 183, 170-175, 1992
 A:Title: Thioredoxin gene expression is transcriptionally up-regulated by retinol in mor
 A:Reference number: JS0667; MUID:92181438; PMID:1543487
 A:Accession: JS0667
 A:Molecule type: mRNA
 A:Residues: 1-105 <ANG>
 A:Cross-references: UNIPROT:P29451; UNIPARC:UPI000016C493; GB:M84643; NID:g342338; PIDN:
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 18

S04107
 C:Species: mouse
 N:Alternate names: ATL-derived factor (ADF)
 C:Date: 21-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 05-Oct-2004
 C:Accession: J04068; S04107
 R:Matsumi, M.; Taniguchi, Y.; Hirota, K.; Takeko, M.; Yodoi, J.
 Gene 152, 165-171, 1995
 A:Title: Structure of the mouse thioredoxin-encoding gene and its processed pseudogene.
 A:Reference number: J04068; MUID:95137382; PMID:7835695
 A:Accession: J04068
 A:Molecule type: DNA
 A:Residues: 1-105 <MAT>
 A:Cross-references: UNIPROT:P10639; UNIPARC:UPI0000163891; DDBJ:D21855; NID:g517128
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kando, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMBO J. 13, 2244, 1994
 A:Reference number: S44375; MUID:94244626; PMID:8187776
 A:Contents: erratum
 A:Accession: S44376
 A:Molecule type: mRNA
 A:Residues: 1-105 <TAGI>
 A:Cross-references: UNIPARC:UPI0000163891; EMBL:X77585; NID:g453971; PIDN:GAA54688.1; PI
 R:Tagaya, Y.; Maeda, Y.; Mitsui, A.; Kondo, N.; Matsui, H.; Hamuro, J.; Brown, N.; Arai,
 EMBO J. 8, 757-764, 1989
 A:Title: ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to thioredoxi
 A:Reference number: S04106; MUID:89251607; PMID:2785919
 A:Accession: S04107
 A:Molecule type: mRNA
 A:Residues: 1-93, 'N', '94-96, 'ALT', '100-104, 'S' <TAG2>
 A:Cross-references: UNIPARC:UPI000017181E; GB:X77585
 C:Comment: This small ubiquitous protein functions in many intracellular biological path
 C:Genetics:
 A:Gene: MGI:Txn
 A:Cross-references: MGI:36258
 A:Map position: 4:24.6
 A:Introns: 29/2; 44/1; 84/2
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 19

S04352
 C:Species: rat
 N:Alternate names: thioredoxin-related surface protein SASP
 C:Date: 31-Mar-1990 #sequence_revision 26-May-1994 #text_change 05-Oct-2004
 C:Accession: S04352; S66372
 R:Tonissen, K.F.; Robins, A.J.; Wells, J.R.E.
 Nucleic Acids Res. 17, 3973, 1989
 A:Title: Nucleotide sequence of a cDNA encoding rat thioredoxin.
 A:Reference number: S04352; MUID:89282399; PMID:2734107
 A:Accession: S04352
 A:Molecule type: mRNA
 A:Residues: 1-105 <TON>
 A:Cross-references: UNIPROT:P11232; UNIPARC:UPI000003066A; EMBL:X14878; NID:g57385; PIDN
 R:Dean, M.F.; Martin, H.; Sansom, P.A.
 Biochem. J. 304, 861-867, 1994
 A:Title: Characterization of a thioredoxin-related surface protein.
 A:Reference number: S53453; MUID:95118305; PMID:7818492
 A:Accession: S66372
 A:Molecule type: protein
 A:Residues: 2-21 <DBA>
 A:Cross-references: UNIPARC:UPI000017181D
 A:Note: 12-Lys, 15-Gly, 16-Leu, 17-Gln, and 18-Leu were also found
 A:Note: described to be a surface-associated thioredoxin
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:9-32/Domain: thioredoxin homology <THR>
 F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 31 WCGPCK 36

RESULT 20

TXFX
 C:Species: corynebacterium ATCC11425
 C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
 C:Accession: A00281
 R:Meng, M.; Hogenkamp, H.P.C.
 J. Biol. Chem. 256, 9174-9182, 1981
 A:Title: Purification, characterization, and amino acid sequence of thioredoxin from Co.
 A:Reference number: A00281; MUID:81264365; PMID:7021558
 A:Accession: A00281
 A:Molecule type: protein
 A:Residues: 1-105 <MEN>
 A:Cross-references: UNIPROT:P00275; UNIPARC:UPI0000136069
 A:Note: The source was designated as Corynebacterium nephridii
 C:Comment: Thioredoxins are ubiquitous small hydrogen carrier proteins that participate
 C:Superfamily: thioredoxin; thioredoxin homology
 C:Keywords: redox-active disulfide
 F:8-91/Domain: thioredoxin homology <THR>
 F:30-33/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 21

B97700
thioredoxin [imported] - Rickettsia conorii (strain Malish 7)

C:Species: Rickettsia conorii

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

C:Accession: B97700

R:Ogata, H.; Audic, S.; Renezo-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R

Science 293, 2093-2098, 2001

A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A:Reference number: A97700; PMID:21442074; PMID:1157893

A:Accession: B97700

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <NR>

A:Cross-references: UNIPROT:Q92JUR5; UNIPARC:UP10000136E9A; GB:AE006914; P1DN:ALU02540.1;

C:Genetics:

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 29 WCGPCK 34

RESULT 22

D97279
thioredoxin [imported] - Clostridium acetobutylicum

C:Species: Clostridium acetobutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004

C:Accession: D97279

R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,

J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1C

A:Reference number: A96900; PMID:21359325; PMID:21359325

A:Accession: D97279

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-105 <NR>

A:Cross-references: UNIPROT:Q97EM7; UNIPARC:UP100000CA715; GB:AE001437; P1DN:AK81023.1;

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3083

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 105;
Best Local Similarity 100.0%; Pred. No. 1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 29 WCGPCK 34

RESULT 23

S33357
thioredoxin - Streptomyces aureofaciens (fragment)

C:Species: Streptomyces aureofaciens

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33357

R:Labudova, O.; Nemethova, M.; Turna, J.; Kollárova, M.

submitted to the EMBL Data Library, April 1993

A:Description: PCR cloning of a protein-coding part of the thioredoxin gene from Strept

A:Reference number: S33357

A:Accession: S33357

A:Molecule type: DNA

A:Residues: 1-106 <LAB>

A:Cross-references: UNIPROT:P3J391; UNIPARC:UP10000136E9D; EMBL:X72799; NID:G297872; P1D
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:9-92/Domain: thioredoxin homology <THR>
F:31-34/Disulfide Bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 30 WCGPCK 35

RESULT 24

H64622
thioredoxin - Helicobacter pylori

C:Species: Helicobacter pylori

A:Variety: strains J99, 26695

C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C:Accession: H64622; C71890

R:Tomb, J.F.; White, O.; Kariavase, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Petersen, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khatal, H.G.; Glodex, A.; McKenne

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Wathey, L

Nature 388, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C

A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A:Reference number: A64520; PMID:97394467; PMID:9252185

A:Accession: H64622

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-106 <ROM>

A:Cross-references: UNIPROT:P56430; UNIPARC:UP10000136E82; GB:AE000594; GB:AE000511; NIT

A:Experimental source: strain 26695

R:Ives, R.A.; Ling, L.S.L.; Mott, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.,

J. Biol. Chem. 269, 176-180, 1999

A:Title: Genetic sequence comparison of two unrelated isolates of the human gastric pat

A:Reference number: A71800; PMID:99120557; PMID:9923682

A:Accession: C71890

A:Molecule type: DNA

A:Residues: 1-106 <ARN>

A:Cross-references: UNIPARC:UP10000136E82; GB:AE001507; GB:AE001439; NID:G4155326; P1DN

A:Experimental source: strain J99

C:Genetics:

A:Gene: trxA; HP0824

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 29 WCGPCK 34

RESULT 25

A49888
thioredoxin - Penicillium chrysogenum

C:Species: Penicillium chrysogenum

C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 05-Oct-2004

C:Accession: A49888; S38886

R:Cohen, G.; Argaman, A.; Schneider, R.; Mislavati, M.; Aharonowitz, Y.

J. Bacteriol. 176, 973-984, 1994

A:Title: The thioredoxin system of Penicillium chrysogenum and its possible role in pen

A:Reference number: A49888; PMID:94148789; PMID:8106340

A:Accession: A49888

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <COH>

A:Cross-references: UNIPROT:P3J4723; UNIPARC:UP10000136E91; EMBL:X76120; NID:G426468; P1D

C:Genetics:
A:Gene: trxa
A:Introns: 8/2
C:Superfamily: thioredoxin; thioredoxin homology
F:10-92/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 26

AG2579
thioredoxin C-1 trxa [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 05-Oct-2004

C:Accession: AG2579

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavyn, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AG2579

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-106 <KUR>

A:Cross-references: UNIPROT:Q8U46; UNIPARC:UPI0000164451; GB:AE008668; PIDD:AA141053.1;

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: trxa

A:Map position: circular chromosome

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 27

A26622
thioredoxin - Chromatium vinosum

C:Species: Chromatium vinosum

C:Date: 31-Mar-1988 #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: A26622

R:Johnson, R.S.; Biemann, K.

Biochemistry 26, 1209-1214, 1987

A:Title: The primary structure of thioredoxin from Chromatium vinosum determined by high

A:Reference number: A26622; MUID:87185419; PMID:3567166

A:Accession: A26622

A:Molecule type: protein

A:Residues: 1-107 <JOH>

A:Cross-references: UNIPROT:P09857; UNIPARC:UPI0000136E76

A>Note: unidentified residues are Ile or Leu

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: heat-stable protein; redox-active disulfide

F:10-93/Domain: thioredoxin homology <THR>

F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 28

S47867

thioredoxin-like protein - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: S47867

R:Salz, H.K.; Flickinger, T.W.; Mittenfior, E.; Pellicena-Palle, A.; Perschek, J.P.; Br

Genetics 136, 1075-1086, 1994

A:Title: The Drosophila maternal effect locus deadhead encodes a thioredoxin homolog re

A:Reference number: S47867; MUID:94274010; PMID:7516301

A:Accession: S47867

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-107 <SAL>

A:Cross-references: UNIPROT:P47938; UNIPARC:UPI0000124A52; EMBL:L27072; NID:G435591; PII

C:Genetics:

A:Gene: FlyBase:dhd

A:Cross-references: FlyBase:FBgn0011761

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:8-97/Domain: thioredoxin homology <THR>

F:31-34/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 29

T02814

thioredoxin TRXRPI [imported] - Leishmania major (strain Friedlin)

C:Species: Leishmania major

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C:Accession: B81458; T02814

R:Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;

Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999

A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c

A:Reference number: A81455; MUID:99178987; PMID:10077609

A:Accession: B81458

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-107 <PYL>

A:Cross-references: UNIPROT:Q25345; UNIPARC:UPI000007DDA; GB:AE001274; NID:G3264850; PI

A:Experimental source: strain MHOM/IL/81/Friedlin

C:Genetics:

A:Gene: TRXRPI

A:Map position: 1

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 30

AH3504

thioredoxin C-1 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 05-Oct-2004

C:Accession: AH3504

R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivanova, M.; Goldstein, E.; Selkov, E.; Elser, P.H.; Hagius, S.; O'Callaghan, D.; Letess, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*
A:Reference number: AD25252; PMID:11756688
A:Accession: AH3504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <KUR>
A:Cross-references: UNIPROT:Q8F566; UNIPARC:UPI00000582C9; GB:AE008917;
A:Experimental source: strain 16M
A:Gene: BME12022
A:Map position: 1
C:Superfamily: thioredoxin, thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 31
E64047
thioredoxin - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C:Accession: E64047
R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A:Reference number: A64000; PMID:95350630; PMID:7542800
A:Accession: E64047
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-107 <TIGR>
A:Cross-references: UNIPROT:PA3785; UNIPARC:UPI0000136E81; GB:U32693; GB:L42023; NID:915
A:Note: named as homolog to a protein from *Anacystis nidulans*
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:10-33/Domain: thioredoxin homology <THR>
F:32-35/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 32
G82991
thioredoxin PA5240 [imported] - *Pseudomonas aeruginosa* (strain PA01)
C:Species: *Pseudomonas aeruginosa*
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: G82991
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mircoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.V.; Coulter, S.N.; Folger, K.R.; Kas, A.; Hardig, K.; Lim, N.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: A82950; PMID:20437337; PMID:10984043
A:Accession: G82991
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-108 <STO>
A:Cross-references: UNIPROT:Q9X2T1; UNIPARC:UPI0000136E95; GB:AE004936; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetics:
A:Gene: trxA, PA5240
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 33
AD0471
thioredoxin 1 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C:Accession: AD0471
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skellern, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: AD0471
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <KUR>
A:Cross-references: UNIPROT:Q8ZAD9; UNIPARC:UPI00000DC68C; GB:AL590842; PIDN:CAC93336.1, C:Genetics:
A:Gene: trxA
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 34
D82338
thioredoxin VC0306 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: D82338
R:Reidberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, I.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; PMID:20406833; PMID:10953301
A:Accession: D82338
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-108 <HEI>
A:Cross-references: UNIPROT:Q9KV51; UNIPARC:UPI00000CC2CE; GB:AE004119; GB:AE003852; NID
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0306
A:Map position: 1
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 35

S35497

thioredoxin - Salmonella typhimurium

C:Species: Salmonella typhimurium

C:Accession: S35497; #sequence_revision 26-May-1994 #text_change 05-Oct-2004

C:Accession: S35497; A9917; S31928

R:Kotani, H.; Nakajima, K.

Nucleic Acids Res. 20, 1424, 1992

A:Title: Cloning and sequence of thioredoxin gene of Salmonella typhimurium LT2.

A:Reference number: S35497; MUID:92220625; PMID:1561103

A:Accession: S35497

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-109 <KOT>

A:Cross-references: UNIPARC:UP000003112A; EMBL:DJ10015; NID:G217084; PID

A:Experimental source: strain LT2

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1992

R:Miloslo, M.; Limauro, D.; Alfano, P.; Ravellini, F.; Lavitola, A.; Guilleta, E.; Bruni

J. Bacteriol. 175, 8030-8037, 1993

A:Title: Characterization of the rho genes of *Neisseria gonorrhoeae* and *Salmonella typhi*

A:Reference number: A49917; MUID:94075245; PMID:8253691

A:Accession: A49917

A:Molecule type: DNA

A:Residues: 1-109 <MLT>

A:Cross-references: UNIPARC:UP000003112A; GB:Z21789; NID:G49361; PIDN:CAA79851.1; PID:G

A:Note: submitted to the EMBL Data Library, February 1993

C:Genetics:

A:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:11-94/Domain: thioredoxin homology <THR>

F:33-36/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 36

TXEC thioredoxin [validated] - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 24-Apr-1984 #sequence_revision 01-Sep-1995 #text_change 05-Oct-2004

C:Accession: A91519; H65181; S30676; I54863; A91802; I52550; A91236; A00280; A22425; A24

R:Wallace, B.J.; Kushner, S.R.

Gene 32, 399-408, 1984

A:Title: Genetic and physical analysis of the thioredoxin (trxA) gene of *Escherichia coli*

A:Reference number: A91519; MUID:85155506; PMID:6099324

A:Accession: A91519

A:Molecule type: DNA

A:Residues: 'MLHQQRQHARLIPVELY', 1-109 <MAL>

A:Cross-references: UNIPARC:UP0000165538; GB:K02845; NID:G147610; PIDN:

A:Note: The sequence represents translation from an upstream ATG triplet that seems not

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H65181

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 'MLHQQRQHARLIPVELY', 1-109 <BLAT>

A:Cross-references: UNIPARC:UP0000165538; GB:AE000454; GB:U00096; NID:G2367278; PIDN:AA

A:Experimental source: strain K-12, substrain MG1655

A:Note: the sequence represents translation from an upstream ATG triplet that seems not

R:Danielis, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.

Science 257, 771-778, 1992

A:Title: Analysis of the *Escherichia coli* genome. DNA sequence of the region from 84.5 t

A:Reference number: S30676; MUID:92358234; PMID:1379743

A:Accession: S30676

A:Molecule type: DNA

A:Residues: 'MLHQQRQHARLIPVELY', 1-109 <DNAN>

A:Cross-references: UNIPARC:UP0000165538; EMBL:M87049; NID:G836656; PIDN:AAA67582.1; P

A:Note: the sequence represents translation from an upstream ATG triplet that seems not

R:Matsumoto, Y.; Shigesada, K.; Hirano, M.; Imai, M.

J. Bacteriol. 166, 945-958, 1986

A:Title: Autogenous regulation of the gene for transcription termination factor rho in p

A:Reference number: 154863; MUID:86223816; PMID:2423505

A:Accession: 154863

A:Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-109 <MAS>

A:Cross-references: UNIPARC:UP000003112A; GB:M12779; NID:G148067; PIDN:AAA24694.1; PID:

R:Lim, C.J.; Geraghty, D.; Fuchs, J.A.

J. Bacteriol. 163, 311-316, 1985

A:Title: Cloning and nucleotide sequence of the trxA gene of *Escherichia coli* K-12.

A:Reference number: A91802; MUID:85234377; PMID:3891733

A:Accession: A91802

A:Molecule type: DNA

A:Residues: 1-109 <LIM>

A:Cross-references: UNIPARC:UP000003112A; GB:M10424; NID:G147608; PIDN:AAA24533.1; PID

A:Experimental source: strain K12

R:Hoecog, J.

Biochem. Rep. 4, 917-923, 1984

A:Title: Nucleotide sequence of the thioredoxin gene from *Escherichia coli*.

A:Reference number: 152550; MUID:85123150; PMID:6098320

A:Accession: 152550

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-109 <HOE>

A:Cross-references: UNIPARC:UP000003112A; GB:M26133; NID:G148065; PIDN:AAA24693.1; PID

R:Holmgren, A.

Eur. J. Biochem. 6, 475-484, 1968

A:Title: Thioredoxin. 6. The amino acid sequence of the protein from *Escherichia coli* B

A:Reference number: A91236; MUID:69079993; PMID:4883076

A:Accession: A91236

A:Molecule type: protein

A:Residues: 2-16, 'LV', 19-71, 'IG', 74-109 <HOL>

A:Cross-references: UNIPARC:UP0000171E22

A:Experimental source: strain B

R:Haeblerlein, I.

Eur. J. Biochem. 223, 473-479, 1994

A:Title: Structure requirements for disulfide bridge sulfolysis of oxidized *Escherichia*

A:Reference number: S45671; MUID:94333336; PMID:8055916

A:Contents: annotation; chemical activity of wild type and engineered sequence

R:Kattil, S.K.; Lemster, D.M.; Eklund, H.

submitted to the Brookhaven Protein Data Bank, March 1990

A:Reference number: A50900; PDB:2TRX

A:Contents: annotation; X-ray crystallography, 1.68 angstroms, residues 2-109

R:Kattil, S.K.; Lemster, D.M.; Eklund, H.

J. Mol. Biol. 212, 167-184, 1990

A:Title: Crystal structure of thioredoxin from *Escherichia coli* at 1.68 Angstroms resolu

A:Reference number: A58630; MUID:90204538; PMID:2181145

A:Contents: annotation; X-ray crystallography, 1.68 angstroms

R:Holmgren, A.; Soderberg, B.O.; Eklund, H.; Branden, C.I.

Proc. Natl. Acad. Sci. U.S.A. 72, 2305-2309, 1975

A:Title: Three-dimensional structure of *Escherichia coli* thioredoxin-S-2 to 2.8 angstrom

A:Reference number: A93800; MUID:75176930; PMID:1094461

A:Contents: annotation; X-ray crystallography, 2.8 angstroms

R:Dyson, H.J.; Gipeert, G.P.; Case, D.A.; Holmgren, A.; Wright, P.E.

submitted to the Brookhaven Protein Data Bank, January 1990

A:Reference number: A50871; PDB:1TRX

A:Contents: annotation; conformation by (1)H-NMR, reduced form, residues 2-109

R:Dyson, H.J.; Gipeert, G.P.; Case, D.A.; Holmgren, A.; Wright, P.E.

Biochemistry 29, 4129-4136, 1990

A:Title: Three-dimensional solution structure of the reduced form of *Escherichia coli* th

A:Reference number: A58631; MUID:90298180; PMID:2193685

A:Contents: annotation, conformation by (1)H-NMR
 R.Jeng, M.F.; Campbell, A.P.; Begley, T.; Holmgren, A.; Case, D.A.; Wright, P.E.; Dyson, R.Jeng, M.F.; Campbell, A.P.; Begley, T.; Holmgren, A.; Case, D.A.; Wright, P.E.; Dyson, submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A66947; PDB:1XOA
 A:Contents: annotation, conformation by (1)H-, (15)N-NMR, oxidized form, residues 2-109
 R.Jeng, M.F.; Campbell, A.P.; Begley, T.; Holmgren, A.; Case, D.A.; Wright, P.E.; Dyson, submitted to the Brookhaven Protein Data Bank, November 1995
 A:Reference number: A66948; PDB:1XOB
 A:Contents: annotation, conformation by (1)H-, (15)N-NMR, reduced form, residues 2-109
 C:Genetics:
 A:Gene: trxA
 A:Map position: 85 min
 C:Function:
 A:Description: is reduced with NADPH by thioredoxin reductase (EC 1.6.4.5); the reduced
 o1-disulfide exchange reactions
 C:Superfamily: thioredoxin homology
 C:Keywords: redox-active disulfide
 F:2-109/Product: thioredoxin #status experimental <MAT>
 F:11-94/Domains: thioredoxin homology <THR>
 F:33-36/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 37
 S27053
 thioredoxin - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C:Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
 C:Accession: S27053
 R:Le Marchal, P.; Hoang, B.M.C.; Schmitter, J.M.; van Dorsselaer, A.; Decottignies, P.
 Eur. J. Biochem. 210, 421-429, 1992
 A:Title: Purification, properties and primary structure of thioredoxin from Aspergillus
 A:Reference number: S27053; PMID:93092975; PMID:1459127
 A:Accession: S27053
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <MAR>
 A:Cross-references: UNIPROT:P29429; UNIPARC:UPI0000136E7E
 C:Superfamily: thioredoxin; thioredoxin homology
 F:13-95/Domains: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 34 WCGPCK 39

RESULT 38
 AF0922
 thioredoxin [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AF0922
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Cornerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; PMID:21534947; PMID:11677608
 A:Accession: AF0922
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-109 <PAR>
 A:Cross-references: UNIPARC:UPI000003112A; GB:AL513382; PIDN:CAD09400.1; PID:g16504518;
 C:Genetics:
 A:Gene: STY3639
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 109;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 32 WCGPCK 37

RESULT 39
 AB7688
 thioredoxin [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
 C:Accession: AB7688
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; Desoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Kholmova, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: AB7249; PMID:21173698; PMID:11259647
 A:Accession: AB7688
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <STO>
 A:Cross-references: UNIPROT:Q9A2L8; UNIPARC:UPI00000C7AF9; GB:AE005673; NID:g13425273; F
 C:Genetics:
 A:Gene: CC3539
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 40
 CB1090
 thioredoxin NMB1366 [imported] - Neisseria meningitidis (strain MCS8 serogroup B)
 C:Species: Neisseria meningitidis
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
 C:Accession: CB1090
 R:Nettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
 Hickey, R.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
 et al.; H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizsa, M.
 Science 287, 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
 A:Reference number: AB1000; PMID:20175755; PMID:10710307
 A:Accession: CB1090
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <TET>
 A:Cross-references: UNIPROT:O9JYV9; UNIPARC:UPI00000C46C4; GB:AE002485; GB:AE002098; NI
 A:Experimental source: serogroup B, strain MCS8
 C:Genetics:
 A:Gene: NMB1366
 C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 33 WCGPCK 38

RESULT 41

E81850
 A:Chloreodoxin I NMA1578 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
 C:Species: Neisseria meningitidis
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
 A:Accession: E81850
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
 R.; Holtroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: E81850
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-110 <PAR>
 A:Cross-references: UNIPROT:O9JTV5; UNIPARC:UPI00000C4C16; GB:AL162756; GB:AL157959; NID
 C:Genetics:
 A:Gene: trxA, NMA1578
 C:Superfamily: thioresoxin; thioresoxin homology

Query Match 100.0%; Score 47; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 33 WCGPCK 38

RESULT 42

S57775
 A:Chloreodoxin h, cytosolic [validated] - Chlamydomonas reinhardtii
 C:Species: Chlamydomonas reinhardtii
 C>Date: 27-Oct-1995 #sequence_revision 21-Jan-1997 #text_change 05-Oct-2004
 A:Accession: S57775; S57799; S54868; S16090; S54870
 R:Stein, M.; Jacquot, J.P.; Jeanette, E.; Decottignies, P.; Hodges, M.; Lancelin, J.M.;
 Plant Mol. Biol. 28, 487-503, 1995
 A>Title: Chlamydomonas reinhardtii thioresoxins: structure of the genes coding for the c
 on and biochemical properties.
 A:Reference number: S57774; MUID:95359406; PMID:7632918
 A:Accession: S57775
 A:Molecule type: DNA
 A:Residues: 1-113 <STB>
 A:Cross-references: UNIPROT:P80028; UNIPARC:UPI000016DD37; EMBL:X80887; NID:9840742; PID
 A:Accession: S57799
 A:Molecule type: protein
 A:Residues: 2-15 <STW>
 A:Cross-references: UNIPARC:UPI0000171E26
 R:Stein, M.; Hodges, M.; Jeanette, E.; Lancelin, J.M.; Jacquot, J.P.
 submitted to the EMBL Data Library, April 1994
 A>Description: Chlamydomonas reinhardtii thioresoxins I : cDNA and amino acid deduced se
 A:Reference number: S54844
 A:Accession: S54868
 A:Molecule type: mRNA
 A:Residues: 1-113 <STP>
 A:Cross-references: UNIPARC:UPI000016DD37; EMBL:X78822; NID:9840740; PIND:CA55399.1; PI
 R:Decottignies, P.; Schmitter, J.M.; Dutka, S.; Jacquot, J.P.; Miginiac-Maslow, M.
 Eur. J. Biochem. 198, 505-512, 1991
 A>Title: Characterization and primary structure of a second thioresoxin from the green a
 A:Reference number: S16090; MUID:91249849; PMID:2040309
 A:Accession: S16090
 A:Molecule type: protein
 A:Residues: 2-112 <MG>
 A:Cross-references: UNIPARC:UPI0000171E27
 R:Mittard, V.; Blackledge, M.J.; Stein, M.; Jacquot, J.P.; Marion, D.; Lancelin, J.M.
 submitted to the Brookhaven Protein Data Bank, May 1996
 A:Reference number: A66748; PDB:1TOP

A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR, residues 2-113
 R:Mittard, V.; Morelle, N.; Brutscher, B.; Simorre, J.P.; Marion, D.; Stein, M.; Jacquot
 Eur. J. Biochem. 229, 473-485, 1995
 A>Title: (1)H, (13)C, (15)N-NMR, resonance assignments of oxidized thioresoxin h from th
 R spectroscopy and computer-assisted backbone assignment.
 A:Reference number: A58618; MUID:95262711; PMID:7744070
 A:Contents: annotation; conformation by (1)H, (13)C, (15)N-NMR
 C:Genetics:
 A:Introns: 27/3; 35/3; 69/3
 A:Superfamily: thioresoxin; thioresoxin homology

C:Keywords: redox-active disulfide
 F:2-113/Product: thioresoxin h #status experimental <MAT>
 F:15-98/Domain: thioresoxin homology <THR>
 F:37-40/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 36 WCGPCK 41

RESULT 43

T29044
 A:hypothetical protein B0228.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2004
 A:Accession: T29044
 R:Leinbach, D.
 submitted to the EMBL Data Library, March 1995
 A>Description: The sequence of C. elegans coamid B0228.
 A:Reference number: Z18324
 A:Accession: T29044
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-115 <LEI>
 A:Cross-references: UNIPROT:O09433; UNIPARC:UPI0000136067; EMBL:U23168; PIND:AA038808.1;
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:B0228.5
 A:Introns: 69/3; 93/3
 C:Superfamily: thioresoxin; thioresoxin homology

Query Match 100.0%; Score 47; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 38 WCGPCK 43

RESULT 44

B70851
 A:probable trxC protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004
 A:Accession: B70851
 R:Coile, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
 J.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: B70851
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-116 <COL>
 A:Cross-references: UNIPROT:P52229; UNIPARC:UPI0000165202; GB:AL021426; GB:AL123456; NID
 A:Experimental source: strain H37RV

C:Genetics:
A:Gene: trxC
C:Superfamily: thioredoxin; thioredoxin homology
F:15-98/Domain: thioredoxin homology <TR>

Query Match 100.0%; Score 47; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 36 WCGPCK 41

RESULT 45

E70107

thioredoxin (trxA) homolog - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004

C:Accession: E70107

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White
son, D.; Peterson, J.; Kexlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70107
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-117 <RUE>
A:Cross-references: UNIPROT:O51088; UNIPARC:UPI00005732A; GB:AE001119; GB:AE000783; NID
A:Experimental source: strain B31
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 39 WCGPCK 44

RESULT 46

S34812

thioredoxin h2 - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004

C:Accession: S34812

R:Brugidou, C.; Marty, I.; Chartier, Y.; Meyer, Y.

Mol. Gen. Genet. 238, 285-293, 1993

A:Title: The Nicotiana tabacum genome encodes two cytoplasmic thioredoxin genes which at

A:Reference number: S34812; MUID:93241165; PMID:8479434

A:Accession: S34812

A:Molecule type: DNA

A:Residues: 1-118 <BRU>

A:Cross-references: UNIPROT:Q07090; UNIPARC:UPI0000136D63; EMBL:Z11803; NID:G297518; PID

C:Genetics:

A:Introns: 29/3; 70/3

C:Superfamily: thioredoxin; thioredoxin homology

F:17-99/Domain: thioredoxin homology <THR>

Query Match 100.0%; Score 47; DB 1; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 38 WCGPCK 43

RESULT 47

T39387
thioredoxin ii - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T39387

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.

submitted to the EMBL Data Library, January 1999

A:Reference number: 221850

A:Accession: T39387

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-121 <LYN>

A:Cross-references: UNIPROT:O94504; UNIPARC:UPI000006BFB2; EMBL:AL035085; PTDN:CAA22681.

A:Experimental source: strain 972h-; cosmid c12D12

C:Genetics:

A:Gene: SPDB:SPBC12D12.07C

A:Map position: 2

A:Introns: 33/2

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 46 WCGPCK 51

RESULT 48

S19498

thioredoxin homolog YCR083w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C:Accession: S19498

R:Feldmann, H.; Mannhaupt, G.; Veltter, I.

submitted to the Protein Sequence Database, March 1992

A:Reference number: S19429

A:Accession: S19498

A:Molecule type: DNA

A:Residues: 1-127 <FEU>

A:Cross-references: UNIPROT:P25372; UNIPARC:UPI00001376B7; EMBL:X59720; NID:G1907116; P

C:Genetics:

A:Gene: SGD:TRX3; MIPS:YCR083W

A:Cross-references: SGD:S0000679

A:Map position: 3R

C:Superfamily: thioredoxin; thioredoxin homology

C:Keywords: redox-active disulfide

F:34-115/Domain: thioredoxin homology <THR>

F:55-58/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 1; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 54 WCGPCK 59

RESULT 49

B91218

thioredoxin 1 [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)

C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004

C:Accession: B91218

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gaesawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: B91218

A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-127 <HAV>
A:Cross-references: UNIPARC:UPI0000165538; GB:BA000007; PIDD:BAR38137.1; PJD:gl13364189;
A:Experimental source: strain 0157:H7, substrain RMD 0509552
A:Gene: ECs4714
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 50 WCGPCK 55

RESULT 50

Chlorodoxin 1 [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: C68064

R:Patel, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoculis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C68064

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-127 <STO>

A:Cross-references: UNIPARC:UPI0000165538; GB:AE005174; NID:gl12518641; PIDD:AAG58975.1;
A:Experimental source: strain 0157:H7, substrain EDL933

C:Gene: trxA

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 50 WCGPCK 55

RESULT 51

B96621
Chlorodoxin 1 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C:Accession: B96621

R:Thelander, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultar, L.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96621

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-129 <STO>

A:Cross-references: UNIPROT:Q9XIF4; UNIPARC:UPI0000008FOA; GB:AE005173; NID:gs080807; PI
C:Gene: F23H1.5

A:Map position: 1

C:Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 54 WCGPCK 59

RESULT 52

T08084
dynein light chain, 14K, outer arm - Chlamydomonas reinhardtii

N:Alternate names: thioredoxin homolog

C:Species: Chlamydomonas reinhardtii

C>Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 31-Dec-2004

C:Accession: T08084

R:Patel-King, R.S.; Benashaki, S.E.; Harrison, A.; King, S.M.

J. Biol. Chem. 271, 6283-6291, 1996

A:Title: Two functional thioredoxins containing redox-sensitive vicinal dithiols from the

A:Reference number: Z16342; MUID:96198089; PMID:8626422

A:Accession: T08084

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-129 <PAT>

A:Cross-references: UNIPROT:Q39591; UNIPARC:UPI0000129A19; EMBL:U43609; NID:gl163185; PI

A:Experimental source: strain 1132D

C:Comment: Seems to be associated with the intermediate chains at the base of the subunit

Query Match 100.0%; Score 47; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 33 WCGPCK 38

RESULT 53

D71707
thioredoxin (trxA) RP002 - Rickettsia prowazekii

C:Species: Rickettsia prowazekii

C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 05-Oct-2004

C:Accession: D71707

R:Anderson, S.G.R.; Zomorodipour, A.; Anderson, J.O.; Sichteritz-Ponten, T.; Alsmark, U.

Nature 396, 133-140, 1998

A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A:Reference number: A71630; MUID:99039499; PMID:9823893

A:Accession: D71707

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-130 <AND>

A:Cross-references: UNIPARC:UPI0000164C06; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDD:

A:Experimental source: strain Madrid E

C:Gene: trxA; RP002

C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 54 WCGPCK 59

RESULT 54

F97361
thioredoxin c-1 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004

C:Accession: F97361

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: F97361
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: UNIPROT:Q8UUA6; UNIPARC:UPI00000D1691; GB:AB007869; PIDN:AAK85847.1; C:Genetics: AGK_C_37
A:Gene: AGK_C_37
A:Map position: circular chromosome
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 57 WCGPCK 62

RESULT 55
S70356
thioredoxin C3 - coryneform bacterium
C:Species: coryneform bacterium
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 11-Jun-1999
C:Accession: S70356
R:Lim, C.J.; Sa, J.H.; Fuchs, J.A.
Biochim. Biophys. Acta 1307, 13-16, 1996
A:Title: Identification of a third thioredoxin gene from *Corynebacterium nephridii*.
A:Reference number: S70356; PMID:96254056; PMID:8652661
A:Accession: S70356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <LIM>
A:Cross-references: UNIPARC:UPI0000136D7A; EMBL:U43655; NID:G1165238; PIDN:AA06490.1; F
A:Note: the source is designated as *Corynebacterium nephridii*
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 64 WCGPCK 69

RESULT 56
B96721
probable thioredoxin T17F3.9 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: B96721
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anen, N.F.; Hughes, B.; Huizar, U.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; PMID:21016719; PMID:11130712
A:Accession: B96721
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <STO>
A:Cross-references: UNIPROT:Q9CASI; UNIPARC:UPI00000C0F3; GB:AE005173; NID:G6358805; PI

C:Genetics: T17F3.9
A:Gene: T17F3.9
A:Map position: 1
C:Superfamily: thioredoxin

Query Match 100.0%; Score 47; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 70 WCGPCK 75

RESULT 57
T08086
dynein light chain, 16K, outer arm - *Chlamydomonas reinhardtii*
N:Alternate names: thioredoxin homolog
C:Species: *Chlamydomonas reinhardtii*
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C:Accession: T08086
R:Patel-King, R.S.; Benashaki, S.E.; Harrison, A.; King, S.M.
J. Biol. Chem. 271, 6283-6291, 1996
A:Title: Two functional thioredoxins containing redox-sensitizing vicinal dithiols from the
A:Reference number: Z16342; PMID:96198089; PMID:8626422
A:Accession: T08086
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-156 <PAT>
A:Cross-references: UNIPROT:Q39592; UNIPARC:UPI0000129A1A; EMBL:U43610; NID:G1163187; PI
A:Experimental source: strain 1132D
C:Comment: Seems to interact directly with the a dynein heavy chain.
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 36 WCGPCK 41

RESULT 58
T09495
thioredoxin m - rape chloroplast
C:Species: chloroplast *Brassica napus* (rape)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T09495
R:Duek, P.D.; Mora Garcia, S.; Wolosinski, R.A.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z16696
A:Accession: T09495
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-177 <DUE>
A:Cross-references: UNIPROT:Q9XG80; UNIPARC:UPI000009E914; EMBL:U76831; NID:G1943719; PI
A:Genome: chloroplast
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:79-162/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 100 WCGPCK 105

RESULT 59

T00893
thioredoxin F21B7.7 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T00893
R:Shim, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Con-
eologs, A.; Ecker, J. R.
A:Description: Genomic sequence for Arabidopsis thaliana BAC F21B7.
A:Reference number: Z14208
A:Accession: T00893
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-179 <SH1>
A:Cross-references: UNIPROT:048737; UNIPARC:UPI000000C325; EMBL:AC002560; NID:92618677;
C:Genetics:
A:Gene: ATSP:F21B7.7
A:Map position: 1
A:Introns: 76/1
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide
F:82-165/Domain: thioredoxin homology <TXN>
F:104-107/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 179;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 103 WCGPCK 108

RESULT 60
TXSPM
thioredoxin m precursor - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 30-Sep-1988 #sequence_revision 13-Mar-1998 #text_change 05-Oct-2004
C:Accession: S20496; J00023; B20273
R:Wedel, N.; Clausmeyer, S.; Herrmann, R.G.; Gardet-Salvi, L.; Schuermann, P.
Plant Mol. Biol. 18, 527-533, 1992
A>Title: Nucleotide sequence of cDNAs encoding the entire precursor polypeptide for thio-
A:Reference number: S20496; MUID:92163017; PMID:1536927
A:Accession: S20496
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-181 <MED>
A:Cross-references: UNIPROT:P07591; UNIPARC:UPI0000136E67; GB:X51462; GB:S84848; NID:921
R:Maeda, K.; Tsugita, A.; Dalzoppo, D.; Vilbois, F.; Schurmann, P.
Eur. J. Biochem. 154, 197-203, 1986
A>Title: Further characterization and amino acid sequence of m-type thioredoxins from SF
A:Reference number: A91159; MUID:86108311; PMID:3510868
A:Accession: J00023
A:Molecule type: protein
A:Residues: 68-82; 'G', 84-89, 'Q', 91, 'SE', 94, 'S', 96-127, 'T', 129-164, 'D', 166, 'S', 168, 'YQ', 1
A:Cross-references: UNIPARC:UPI0000171E25
C:Comment: This enzyme has amino-terminal heterogeneity. Thioredoxin m activates malate
C:Comment: Arg-145 and Gly-164 are both essential for thioredoxin to interact with thior-
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:68-171/Product: thioredoxin mb #status experimental <PRB>
F:69-171/Product: thioredoxin mc #status experimental <PRC>
F:70-171/Product: thioredoxin md #status experimental <PRD>
F:82-165/Domain: thioredoxin homology <TXN>
F:104-107/Disulfide bonds: redox-active #status experimental

Query Match 100.0%; Score 47; DB 1; Length 181;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

DB 103 WCGPCK 108

RESULT 61
T07837
thioredoxin f precursor - rape
C:Species: Brassica napus (rape)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C:Accession: T07837
R:Moita-Garcia, S.E.F.; Rodriguez-Suarez, R.J.; Wolosinski, R.A.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z16164
A:Accession: T07837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-182 <MOR>
A:Cross-references: UNIPROT:048997; UNIPARC:UPI0000136DB6; EMBL:AF018174; NID:92921093;
A:Experimental source: 30-day old green leaves
C:Genetics:
A:Gene: TRXF
A:Genome: nuclear
C:Function:
A:Description: activates fructose 1,6-bisphosphatase during photosynthesis
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:79-163/Domain: thioredoxin homology <TXN>

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 101 WCGPCK 106

RESULT 62
S20929
thioredoxin f precursor - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: S20929
R:Leplanc, L.; Hodges, M.; Gadal, P.; Cretin, C.
Plant Mol. Biol. 18, 1023-1025, 1992
A>Title: Isolation, characterization and nucleotide sequence of a full-length pea cDNA e
A:Reference number: S20929; MUID:92256804; PMID:1581563
A:Accession: S20929
A:Molecule type: mRNA
A:Residues: 1-182 <LEP>
A:Cross-references: UNIPROT:P29450; UNIPARC:UPI0000136DB9; EMBL:X63537; NID:920906; PIDN
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-74/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:75-182/Product: thioredoxin f #status predicted <MAT>
F:83-167/Domain: thioredoxin homology <TXN>
F:106-109/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 105 WCGPCK 110

RESULT 63
E96539
hypothetical protein F1413.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: E96539
R:Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Author: Salzberrg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-182 <STO>
A:Cross-references: UNIPROT:Q9SX49; UNIPARC:UPI00000AC075; GB:AE005173; NID:95734774; PI
C:Genetics:
A:Gene: F1413.8
A:Map position: 1

Query Match 100.0%; Score 47; DB 2; Length 182;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 98 WCGPCK 103

RESULT 64
D95115
thioredoxin family protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: D95115
R:Retcelin, H.; Nelson, K.E.; Paulsen, I.T.; Eissen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberrg, S.L.; Lewis, M.R.; Radue, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: D95115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-185 <KUR>
A:Cross-references: UNIPROT:Q97R36; UNIPARC:UPI0000051693; GB:AE005672; PIDN:AAK75117.1;
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI000

Query Match 100.0%; Score 47; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 80 WCGPCK 85

RESULT 65
F85044
probable M-type thioredoxin [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: F85044
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: F85044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-186 <STO>

A:Cross-references: UNIPROT:Q9SEU8; UNIPARC:UPI0000001768; GB:NC_001268; NID:97270675; P
C:Genetics:
A:Gene: AT4G03520
A:Map position: 4
C:Superfamily: thioredoxin; thioredoxin homology

Query Match 100.0%; Score 47; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 109 WCGPCK 114

RESULT 66
S04661
thioredoxin f precursor - spinach
C:Species: *Spinacia oleracea* (spinach)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: S04661; A20273
R:Ramo, M.; Tsugita, A.; Wiesner, C.; Wedel, N.; Bartling, D.; Herrmann, R.G.; Aguilar,
Eur. J. Biochem. 182, 315-322, 1989
A:Title: Primary structure of spinach-chloroplast thioredoxin f. Protein sequencing and
A:Reference number: S04661; MUID:89289715; PMID:2737203
A:Accession: S04661
A:Molecule type: mRNA
A:Residues: 1-190 <KAM>
A:Cross-references: UNIPROT:P09856; UNIPARC:UPI0000136D8A; EMBL:X14959; NID:921343; PIDN
A:Note: part of this sequence was confirmed by protein sequencing
R:Tsugita, A.; Maeda, K.; Schnermann, P.
Biochem. Biophys. Res. Commun. 115, 1-7, 1983
A:Title: Spinach chloroplast thioredoxin in evolutionary drift.
A:Reference number: A20273; MUID:83308759; PMID:6351859

A:Accession: A20273
A:Molecule type: protein
A:Residues: 106-119, 'NGDKKATQHLGVQQA', 120 <TSU>
A:Cross-references: UNIPARC:UPI0000174DE8
A:Note: this sequence has been revised in reference S04661
C:Comment: thioredoxin f activates fructose 1,6-bisphosphatase during photosynthesis.
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: chloroplast; redox-active disulfide
F:1-77/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:78-190/Product: thioredoxin f #status predicted <MAT>
F:91-175/Domain: thioredoxin homology <THR>
F:114-117/Disulfide bonds: redox-active #status predicted

Query Match 100.0%; Score 47; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
|||||
Db 113 WCGPCK 118

RESULT 67
T12261
thioredoxin f precursor - common ice plant
C:Species: *Mesembryanthemum crystallinum* (common ice plant)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12261
R:Michalowski, C.B.; Bohner, H.J.,
submitted to the EMBL Data Library, June 1998
A:Description: A cDNA for thioredoxin F precursor from the common ice plant.
A:Reference number: Z17478
A:Accession: T12261
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-191 <MIC>
A:Cross-references: UNIPROT:O81332; UNIPARC:UPI0000136D88; EMBL:AF069314; NID:93202021;
C:Function:
A:Description: activates fructose 1,6-bisphosphatase during photosynthesis

C;Superfamily: thioredoxin, thioredoxin homology
C;Keywords: redox-active disulfide
F;92-176/Domain: thioredoxin homology <TXN>

```

Query Match      100.0%; Score 47; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY	1	WCGPCK	6
Db	114	WCGPCK	119

RESULT 68
H97984

conserved hypothetical protein spf0904 [imported] - Streptococcus pneumoniae (strain R6)
C/Species: Streptococcus pneumoniae
C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C/Accession: H97984
R/Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgitt, S.; DeHoff, B.S.; E
y, P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAnren, S.; M
J. Bacteriol. 183, 5709-5717, 2001
A/Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A/Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A/Reference number: A97872; MUID:21429245; PMID:11544234
A/Accession: H97984
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-191 <KIR>
A/Cross-references: UNIPROT:Q8D010; UNIPARC:UPI000000E3552; GB:AE007317; PIDD:AAK99708.1
/Genetics:
/Gene: spf0904

Query Match	100.0%;	Score 47;	DB 2;	Length 191;
Best Local Similarity	100.0%;	Pred. No. 1.6;		
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	1	WCGPCK	6
Db	86	WCGPCK	91

RESULT 69

T40552
thiodioxin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40552
R:Lyne, M.H.; Rajadream, M.A.; Barrell, B.G.; Xiang, Z.; Hunt, I.C.; Aves, S.J.
Submitted to the EMBL Data Library, September 1999
A:Reference number: Z11936
A:Accession: T40552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-290 <LYN>
A:Cross-references: UNIPROT:O9USR1; UNIPARC:UPI0000069A89; EMBL:AL110506; PIDD: CAB54816
A:Experimental source: strain 972h-, cosmid c577
C:Genetic8:
A:Gene: SPAC577.08c
A:Map position: 2
A:Introns: 75/2

Query Match	100.0%;	Score 47;	DB 2;	Length 290;
Best Local Similarity	100.0%;	Pred. No. 2.2;		
Matches	6;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

QY	1	WCGPCK	6
Db	30	WCGPCK	35

RESULT 70

АИЗ 011

```
thioredoxin trxa [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
CISpecies: Agrobacterium tumefaciens
CDate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
```

C/Accession: AH3011
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, E.; Giller, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClellan, J.; Karp, P.; Romero, P.; Zhang, S.

A/Authors: Yoo, H., Tao, Y., Biddle, P., Jung, M., Krespan, W., Perry, M., Gordon-Kamm, M., and E. W. Stein.

A; Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AH3011

A;Status: preliminary

A: Molecule type: DNA

A;Residues: 1-322 <KUR>

A; Cross-references: UNIPROT:Q8U9M8; UNIPARC:UPI0000164857; GB:AE008689; PIDN:AAL44510.1.

A; Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: trxA

A:Map position: linear chromosome

Query Match	100.0%	Score 47	DB 2	Length 322
Best Local Similarity	100.0%	Pred. No. 2,3		
Matches 6	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY 1 WCGPCK 6
|||
Db 63 WCGPCK 6

Search completed: February 23, 2006, 00:42:33
Job time : 32.5 secs

This Page Blank (us910)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:11:42 ; Search time 146.5 Seconds

(without alignments)
28.895 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Uniprot 05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	80	Q4T7B7_TETNG	Q4T7B7 tetrandon n
2	47	100.0	84	Q60744_HUMAN	Q60744 homo sapien
3	47	100.0	85	Q5T936_HUMAN	Q5T936 homo sapien
4	47	100.0	88	Q5V032_HALMA	Q5V032 halobacteri
5	47	100.0	89	Q9HMD0_HALMA	Q9HMD0 halobacteri
6	47	100.0	91	THIO_THIRO	P96132 thiocapsa r
7	47	100.0	95	Q4XKV3_PLACH	Q4XKV3 plasmodium
8	47	100.0	96	Q4Z518_PLABE	Q4Z518 plasmodium
9	47	100.0	98	Q5IB12_BACFN	Q5IB12 bacteroides
10	47	100.0	98	Q64R91_BACFR	Q64R91 bacteroides
11	47	100.0	99	Q8AB91_BACTN	Q8AB91 bacteroides
12	47	100.0	100	THIO_MYCGA	Q916P9 mycoplasma
13	47	100.0	100	Q9JNG4_MYCGA	Q9JNG4 mycoplasma
14	47	100.0	101	THIO1_CHLTR	Q8K644 chlorobium
15	47	100.0	101	Q6K1E7_MYCNO	Q6K1E7 mycoplasma
16	47	100.0	102	THIO_CHLTV	P52227 chlamydomon
17	47	100.0	102	THIO_CHLTV	Q9P1K3 chlamydia m
18	47	100.0	102	THIO_CHLTR	Q84544 chlamydia t
19	47	100.0	102	THIO_MYCGE	P47370 mycoplasma
20	47	100.0	102	THIO_MYCPY	P75512 mycoplasma
21	47	100.0	102	THIO_SCHPO	O14463 mycoplasma
22	47	100.0	102	TRX1_YEAST	P22217 schizosacch
23	47	100.0	102	Q5L731_CHLAB	Q5L731 saccharomyc
24	47	100.0	102	Q6F1T8_MESFL	Q6F1T8 mesoplasma
25	47	100.0	102	Q6MUG0_MYCMS	Q6MUG0 mycoplasma
26	47	100.0	103	THIO_BACSV	P14949 bacillus su
27	47	100.0	103	TRX2_YEAST	P22803 saccharomyc
28	47	100.0	103	Q75CQ0_ASHGO	Q75CQ0 ashbya gose
29	47	100.0	103	Q6FND5_CANGA	Q6FND5 candida gla
30	47	100.0	103	Q6BJ80_DEBHA	Q6BJ80 debaromyce
31	47	100.0	103	Q5ACN1_CANAL	Q5ACN1 candida alb

105	47	100.0	106	2	Q5VAN9_RHET	Q5van9_rhizobium e	178	47	100.0	110	2	Q4WV97_AS PFU	Q4wv97_aspergillus
106	47	100.0	106	2	Q4TMB6_9SPHN	Q4tmb6_erythrobact	179	47	100.0	110	2	Q6GUK5_PAXIN	Q6guk5_paxillus in
107	47	100.0	106	2	Q8KYV0_9PROT	Q8kyv0_uncultured	180	47	100.0	110	2	Q5BHL0_EMENT	Q5bhl0_aspergillus
108	47	100.0	106	2	Q8UJA6_AGR75	Q8uja6_agrobacteri	181	47	100.0	110	2	Q6ZYU0_9METZ	Q6zyu0_suberites f
109	47	100.0	106	2	Q8EWM2_MYCPB	Q8ewm2_mycoplasma	182	47	100.0	110	2	Q5FRV8_NETGI	Q5frv8_netseries g
110	47	100.0	106	2	Q5LLP8_SILPO	Q5llp8_silicibacte	183	47	100.0	110	2	Q9A2L8_CACRC	Q9a2l8_caulobacter
111	47	100.0	106	2	Q4SOR5_TETNG	Q4sor5_tetradion n	184	47	100.0	110	2	Q9UYV9_NEIMB	Q9uyv9_neisseria m
112	47	100.0	107	1	THIO1_DROME	P47938_drosophila	185	47	100.0	110	2	Q9JLY5_NEISB	Q9jly5_neisseria m
113	47	100.0	107	1	THIO1_DROYA	P60226_drosophila	186	47	100.0	110	2	Q88ZK9_LACPL	Q88zk9_lactobacill
114	47	100.0	107	1	THIO1_CHRVI	P09857_chromatium	187	47	100.0	110	2	Q5YMS6_NOCFA	Q5yms6_nocardia fa
115	47	100.0	107	1	THIO_EGHR	Q17486_ecthinococcu	188	47	100.0	111	2	Q5EUB4_9ENTR	Q5eub4_buchnera ap
116	47	100.0	107	1	THIO_HABIN	P43783_haemophilus	189	47	100.0	112	1	THIO_MYCSM	Q30974_mycobacteri
117	47	100.0	107	2	Q7RVX8_NEUCR	Q7rvx8_neutrospora	190	47	100.0	112	1	TRXH_CHLRE	P80028_chlamydomon
118	47	100.0	107	2	Q9C1L1_NEUCR	Q9c1l1_neutrospora	191	47	100.0	112	2	Q5YBBI_9CHLO	Q5ybbi_helicospori
119	47	100.0	107	2	Q7PMZ6_ANOGA	Q7pmz6_anophelies g	192	47	100.0	112	2	Q7MGPE_VIBVU	Q7mgpe_vibrio vuln
120	47	100.0	107	2	Q9NGZ1_ANOGA	Q9ngz1_anophelies g	193	47	100.0	112	2	Q6LLLE_PHOPR	Q6llle_photobacter
121	47	100.0	107	2	Q9NGZ3_TRYBB	Q9ngz3_trypanosoma	194	47	100.0	112	2	Q4UPY4_XANCP	Q4upy4_xanthomonas
122	47	100.0	107	2	Q25345_LEIWA	Q25345_leishmania	195	47	100.0	113	2	Q5GUR7_XANOR	Q5gur7_xanthomonas
123	47	100.0	107	2	Q6B343_TRYCR	Q6b343_trypanosoma	196	47	100.0	113	2	Q8PFZ2_XANAC	Q8pfz2_xanthomonas
124	47	100.0	107	2	Q5S1X7_IKOSC	Q5s1x7_ikodes scap	197	47	100.0	113	2	Q8PAD3_XANCP	Q8pad3_xanthomonas
125	47	100.0	107	2	Q57AF5_BRUAB	Q57af5_brucella ab	198	47	100.0	113	2	Q879Y5_XYLFT	Q879y5_xylella fas
126	47	100.0	107	2	Q5FGA3_EHRBG	Q5fga3_ehrlichia r	199	47	100.0	114	1	THIO2_DROME	Q9y429_drosophila
127	47	100.0	107	2	Q9AJR5_ACTAC	Q9ajr5_actinobacil	200	47	100.0	114	2	Q51FHE_ENTHI	Q51fhe_entamoeba h
128	47	100.0	107	2	Q6M1C7_CORGL	Q6m1c7_corynebacte	201	47	100.0	114	2	Q7YZF7_CABEL	Q7yzf7_caenothabdi
129	47	100.0	107	2	Q4QPG1_HAB18	Q4qpg1_haemophilus	202	47	100.0	115	2	THIO1_CABEL	Q09433_caenothabdi
130	47	100.0	107	2	Q6NEA2_CORDI	Q6nea2_corynebacte	203	47	100.0	115	1	THIO_MYCBO	P06617_mycobacteri
131	47	100.0	107	2	Q92ATC5_RHIME	Q92atc5_rhizobium m	204	47	100.0	115	1	THIO_MYCBO	P06616_mycobacteri
132	47	100.0	107	2	Q6G1B7_BAROU	Q6g1b7_bartonella	205	47	100.0	116	2	Q4WB53_AS PFU	Q4wb53_aspergilliu
133	47	100.0	107	2	Q6G5B8_BABRE	Q6g5b8_bartonella	206	47	100.0	116	2	Q6UB18_PABRR	Q6ub18_paracoccidi
134	47	100.0	107	2	Q8RXY9_BRUSU	Q8rxy9_brucella bu	207	47	100.0	116	2	Q4ZZP9_PESBY	Q4zzp9_pseudococc
135	47	100.0	107	2	Q98CM9_RHILU	Q98cm9_rhizobium l	208	47	100.0	117	1	THIO_BORBU	Q51088_borrella bu
136	47	100.0	107	2	Q73GQ5_WOLPM	Q73gq5_wolbachia p	209	47	100.0	117	2	Q662V3_BORGA	Q662v3_borrella ga
137	47	100.0	107	2	Q8YB56_BRUME	Q8yb56_brucella me	210	47	100.0	117	2	Q93AQ3_MYCPA	Q93aq3_mycobacteri
138	47	100.0	107	2	Q8RSMO_CORCF	Q8rsmo_corynebacte	211	47	100.0	118	1	TRXH2_TOBAC	Q07090_nicotiana t
139	47	100.0	107	2	Q5NPF9_FRTAT	Q5npf9_francisella	212	47	100.0	121	2	Q945D0_SCHPO	Q945d0_schizosach
140	47	100.0	107	2	Q5HAC8_EHRBW	Q5hac8_ehrlichia r	213	47	100.0	121	2	Q61CC9_CABBR	Q61cc9_caenothabdi
141	47	100.0	108	1	THIO_ECOLI	P00274_escherichia	214	47	100.0	123	2	Q4USG8_COKJK	Q4usg8_corynebacte
142	47	100.0	108	1	THIO_PSEAE	Q9x2t1_pseudomonas	215	47	100.0	124	2	Q8NL58_CORGL	Q8nl58_corynebacte
143	47	100.0	108	1	THIO_THIPE	P52233_thiobacillu	216	47	100.0	126	2	Q8RGH7_PODAN	Q8rgh7_podopora a
144	47	100.0	108	2	Q41OD7_9BIVA	Q41od7_chlamys far	217	47	100.0	126	2	Q685V8_9SCOR	Q685v8_mecobuthus
145	47	100.0	108	2	Q5TY47_ANOGA	Q5ty47_anophelies g	218	47	100.0	126	2	Q685V4_9SCOR	Q685v4_mecobuthus
146	47	100.0	108	2	Q61VR6_9GAMM	Q61vr6_uncultured	219	47	100.0	126	2	Q685X1_9SCOR	Q685x1_mecobuthus
147	47	100.0	108	2	Q7BAF7_PRR01	Q7baf7_gamma-prote	220	47	100.0	126	2	Q685X8_9SCOR	Q685x8_mecobuthus
148	47	100.0	108	2	Q4LH05_9BRUX	Q4lh05_burkholderi	221	47	100.0	126	2	Q685Y8_9SCOR	Q685y8_mecobuthus
149	47	100.0	108	2	Q4J018_AZCVI	Q4j018_azotobacter	222	47	100.0	126	2	Q685Y8_9SCOR	Q685y8_mecobuthus
150	47	100.0	108	2	Q6Q926_9GAMM	Q6q926_uncultured	223	47	100.0	126	2	Q685Y9_9SCOR	Q685y9_mecobuthus
151	47	100.0	108	2	Q5SBU4_VIRBFI	Q5ebu4_vibrio ficc	224	47	100.0	126	2	Q685Y9_9SCOR	Q685y9_mecobuthus
152	47	100.0	108	2	Q4FQ72_9GAMM	Q4fq72_psychrobact	225	47	100.0	126	2	Q685X3_9SCOR	Q685x3_mecobuthus
153	47	100.0	108	2	Q7MYL3_PHOLL	Q7myl3_photorhabd	226	47	100.0	126	2	Q685W5_9SCOR	Q685w5_mecobuthus
154	47	100.0	108	2	Q8ZAD9_YERPE	Q8zad9_yersinia pe	227	47	100.0	127	1	THIO_NEUCR	P43115_neutrospora
155	47	100.0	108	2	Q66G18_YERPS	Q66g18_yersinia ps	228	47	100.0	127	1	TRX3_YEAST	Q25372_saccharomyc
156	47	100.0	108	2	Q6CZB0_ERMCT	Q6czb0_erythria car	229	47	100.0	127	1	TXNDB_MOUSE	Q69621_rattus muscu
157	47	100.0	108	2	Q5FT93_GLUOX	Q5ft93_glucobact	230	47	100.0	127	1	TXNDB_MOUSE	Q69621_rattus muscu
158	47	100.0	108	2	Q9KVS1_VIRCH	Q9kvs1_vibrio chol	231	47	100.0	129	1	DY14_CHLRE	Q39591_chlamydomon
159	47	100.0	108	2	Q8Y056_RALSO	Q8y056_ralstonia s	232	47	100.0	129	2	Q9XIF4_ARATH	Q9xif4_arabidopsis
160	47	100.0	108	2	Q8BJO6_SHEON	Q8bj06_shewanella	233	47	100.0	130	2	Q8GUR6_PEA	Q8gur6_plum sativ
161	47	100.0	108	2	Q8BDN7_VIBVU	Q8bdn7_vibrio vuln	234	47	100.0	133	2	Q7D2B9_AGR75	Q7d2b9_agrobacteri
162	47	100.0	108	2	Q87KH6_VIRBA	Q87kh6_vibrio para	235	47	100.0	134	2	Q9RD25_STRCO	Q9rd25_streptomyce
163	47	100.0	108	2	Q7NKP2_CHRVO	Q7nkp2_chromobacte	236	47	100.0	135	2	Q6PV94_SOYBN	Q6pv94_glycine max
164	47	100.0	108	2	Q6A034_DESPS	Q6a034_desulfofotale	237	47	100.0	135	2	Q57HT5_SALCH	Q57ht5_halimella
165	47	100.0	108	2	Q63U09_BURPS	Q63u09_burkholderi	238	47	100.0	136	2	Q5UWAE_HALMA	Q5uwa_e_haloarcula
166	47	100.0	108	2	Q62JU6_BURMA	Q62ju6_burkholderi	239	47	100.0	137	2	Q4PLX7_IKOSC	Q4plx7_ikodes scap
167	47	100.0	108	2	Q5GYF9_IDILO	Q5gyf9_idiomarina	240	47	100.0	137	2	Q4NH78_9MICC	Q4nh78_agrobacte
168	47	100.0	108	2	Q5PIK8_AZOSE	Q5pik8_azotobacter	241	47	100.0	137	2	Q5UR29_MIMIV	Q5ur29_mimivirus
169	47	100.0	108	2	Q5NG78_FRAAT	Q5ng78_franziscella	242	47	100.0	138	2	Q6Z413_ORYSA	Q6z413_oryza sativ
170	47	100.0	109	1	THIO_EMENT	P29429_ementicella	243	47	100.0	139	2	Q6CK18_KULUA	Q6ck18_kluyveromyc
171	47	100.0	109	2	Q4W214_AS PFU	Q4w214_aspergillus	244	47	100.0	139	2	Q7NZ16_CHRVO	Q7nz16_chromobacte
172	47	100.0	109	2	Q4K3Z3_PSEFS	Q4k3z3_pseudomonas	245	47	100.0	140	2	Q9C9Y6_ARATH	Q9c9y6_arabidopsis
173	47	100.0	109	2	Q5PKK3_SALPA	Q5pkk3_salmonella	246	47	100.0	140	2	Q8BJL1_SHEON	Q8bjl1_shewanella
174	47	100.0	109	2	Q88CG6_PSBPX	Q88cg6_pseudomonas	247	47	100.0	140	2	Q5ZJY6_CHICK	Q5zjy6_gallus gall
175	47	100.0	109	2	Q87UQ3_PSSSM	Q87uq3_pseudomonas	248	47	100.0	141	2	Q6FRV1_CANGA	Q6frv1_candida gla
176	47	100.0	109	2	Q60CP8_METCA	Q60cp8_methylcocc	249	47	100.0	141	2	Q7MHH7_BORBR	Q7mhh7_bordecella
177	47	100.0	109	2	Q4SOR6_TETNG	Q4sor6_tetradion n	250	47	100.0	141	2	Q7W990_BORPA	Q7w990_bordecella

251	47	100.0	141	2	Q7VP8 BORPE	Q7VP8 bordecella	324	47	100.0	301	2	Q63W5 BURPS	Q63W5 burkholderi
252	47	100.0	141	2	Q6F74 ACIAD	Q6F74 acinetobact	325	47	100.0	304	2	Q51M9 SIJPO	Q51M9 silicibact
253	47	100.0	142	2	Q5ZFA4 PLAMJ	Q5ZFA4 plantago ma	326	47	100.0	305	2	Q4TRI0 98PHN	Q4TRI0 erythrobact
254	47	100.0	143	2	Q6VB16 IPDBA	Q6VB16 ipomoea bat	327	47	100.0	306	2	Q6ND42 RHOPA	Q6ND42 rhodospseudo
255	47	100.0	144	2	Q51010 ENTHI	Q51010 entamoeba h	328	47	100.0	313	2	Q4INX3 GIBZE	Q4INX3 gibberella
256	47	100.0	144	2	Q41UJ1 AZOVH	Q41UJ1 azotobacter	329	47	100.0	313	2	Q89WT4 BRUJA	Q89WT4 bradyrhizob
257	47	100.0	144	2	Q4KJF7 PSERF5	Q4KJF7 pseudomonas	330	47	100.0	317	2	Q5FSW0 GIUOX	Q5FSW0 gluconobact
258	47	100.0	144	2	Q88CWL PSERK	Q88CWL pseudomonas	331	47	100.0	322	2	Q8U9M8 AGRTS	Q8U9M8 agrobacteri
259	47	100.0	145	1	THIO3 CORRE	P52228 corynebacte	332	47	100.0	324	2	Q6C3W5 YARLI	Q6C3W5 yarrowia li
260	47	100.0	145	2	Q84XR3 CHIRE	Q84XR3 chlamydomon	333	47	100.0	324	2	Q6FVFO BRUSU	Q6FVFO bruceella su
261	47	100.0	146	2	Q802D6 MELUD	Q802D6 melopsittac	334	47	100.0	326	2	Q5GX15 XANOR	Q5GX15 xanthomonas
262	47	100.0	147	2	Q58HK3 SCMA	Q58HK3 schistosoma	335	47	100.0	329	2	Q5Y9B4 BRUAB	Q5Y9B4 bruceella ab
263	47	100.0	148	2	Q9CASI ARATH	Q9CASI arabidopsis	336	47	100.0	329	2	Q8YCX7 BRUME	Q8YCX7 bruceella me
264	47	100.0	149	2	Q988U5 RHIL0	Q988U5 rhizobium l	337	47	100.0	330	1	TXNDS HUMAN	Q86XW9 homo sapien
265	47	100.0	150	2	Q5DPA0 SCJJA	Q5DPA0 schistosoma	338	47	100.0	330	2	Q92L96 RHIME	Q92L96 rhizobium m
266	47	100.0	152	2	Q4U0M0 NICAL	Q4U0M0 nicotiana a	339	47	100.0	331	2	Q7CT41 AGRTS	Q7CT41 agrobacteri
267	47	100.0	153	2	Q4UNK3 RICE	Q4UNK3 rickettsia	340	47	100.0	332	2	Q4NW9 98ELT	Q4NW9 anaeromyxob
268	47	100.0	156	1	DYLS CHIRE	Q39592 chlamydomon	341	47	100.0	333	2	Q4WPE6 ASPFU	Q4WPE6 aspergillus
269	47	100.0	157	1	THIO7 DROME	Q81F74 bacteroides	342	47	100.0	335	2	Q98B31 RHIL0	Q98B31 rhizobium l
270	47	100.0	157	2	Q8A7R8 BACTN	Q8A7R8 bacteroides	343	47	100.0	385	2	Q75RF6 ASHGO	Q75RF6 ashbya goss
271	47	100.0	160	2	Q64CW9 9ACCH	Q64CW9 uncultured	344	47	100.0	416	2	Q8A386 BACTN	Q8A386 bacteroides
272	47	100.0	160	2	Q4P051 USTMA	Q4P051 ustilago ma	345	47	100.0	458	1	TXXB MYCIE	P4843 mycobacteri
273	47	100.0	161	2	Q87G10 PODAN	Q87G10 podospira a	346	47	100.0	540	2	Q75JME DICDI	Q75JME dictyosteli
274	47	100.0	161	2	Q5LXB8 BACFN	Q5LXB8 bacteroides	347	47	100.0	586	1	TXNDS MOUSE	Q715T0 mus musculu
275	47	100.0	161	2	Q64SV7 BACFR	Q64SV7 bacteroides	348	47	100.0	587	1	Q4R719 MACPA	Q4R719 rattus norv
276	47	100.0	163	2	Q8D6F4 VIBVU	Q8D6F4 vibrio vuln	349	47	100.0	588	2	Q4R719 MACPA	Q4R719 macaca faec
277	47	100.0	163	2	Q7MDA8 VIBVY	Q7MDA8 vibrio vuln	350	47	100.0	601	2	Q4R5Y0 MACPA	Q4R5Y0 macaca faec
278	47	100.0	166	1	THIOM BOVIN	Q95108 bos taurus	351	47	100.0	625	2	Q6TRC5 XENLA	Q6TRC5 xenopus lae
279	47	100.0	166	1	THIOM HUMAN	Q99757 homo sapien	352	47	100.0	709	2	Q4HZP6 GIBZE	Q4HZP6 gibberella
280	47	100.0	166	1	THIOM MOUSE	P97493 mus musculu	353	47	100.0	870	2	Q8A213 BACTN	Q8A213 bacteroides
281	47	100.0	166	2	THIOM RAT	P97615 rattus norv	354	47	100.0	952	2	Q4P5N4 USTMA	Q4P5N4 ustilago ma
282	47	100.0	166	2	Q6FH60 HUMAN	Q6FH60 homo sapien	355	47	100.0	989	2	Q41011 GIBZE	Q41011 gibberella
283	47	100.0	166	2	Q5K553 9BACT	Q5K553 uncultured	356	47	100.0	999	2	Q5B4R0 9RRVP	Q5B4R0 trypanosoma
284	47	100.0	166	2	Q545D3 MOUSE	Q545D3 mus musculu	357	47	93.6	87	2	Q5C922 ARATH	Q5C922 arabidopsi
285	47	100.0	166	2	Q6P131 BRARE	Q6P131 brachydanio	358	47	93.6	88	1	THIO2 DICDI	P2446 dictyosteli
286	47	100.0	170	2	Q7ZYG6 XENLA	Q7ZYG6 xenopus lae	359	47	93.6	88	2	Q8PZ06 METAC	Q8PZ06 methanosarc
287	47	100.0	170	2	Q641J6 XENTR	Q641J6 xenopus tro	360	47	93.6	93	2	Q8TL30 METAC	Q8TL30 methanosarc
288	47	100.0	173	2	Q84XR8 CHIRE	Q84XR8 chlamydomon	361	47	93.6	96	2	Q8GM51 ARATH	Q8GM51 arabidopsi
289	47	100.0	173	2	Q6H7B4 ORYSA	Q6H7B4 oryza sativ	362	47	93.6	100	2	Q6K1E8 MYCWO	Q6K1E8 mycoplasma
290	47	100.0	177	1	TRXM BRANA	Q9X980 brasilia na	363	47	93.6	101	2	Q22031 CYACA	Q22031 cyanidium c
291	47	100.0	178	1	TRXF1 ARATH	Q9X980 brasilia na	364	47	93.6	102	1	THIO CHLPN	Q9X7P5 chlamydia p
292	47	100.0	179	1	TRXM1 ARATH	Q48737 arabidopsi	365	47	93.6	102	1	THIO CYAME	Q22022 cyanidiosc
293	47	100.0	180	2	Q7X8R5 ORYSA	Q7X8R5 oryza sativ	366	47	93.6	103	1	THIO LISIN	P04413 listeria in
294	47	100.0	181	1	TRXM SPICL	P07591 spinacia ol	367	47	93.6	103	1	THIO LISMO	P04413 listeria mo
295	47	100.0	182	1	TRXF BRANA	Q48897 brasilia na	368	47	93.6	103	2	Q51E84 ENTHI	Q51E84 entamoeba h
296	47	100.0	182	1	TRXF PEA	P29450 pisum sativ	369	47	93.6	103	2	Q88V17 LACPL	Q88V17 lactobacilli
297	47	100.0	185	1	TRXX ARATH	Q81D49 arabidopsi	370	47	93.6	104	1	THIO3 DICDI	P23447 dictyosteli
298	47	100.0	185	2	Q97R36 STRPN	Q9X739 arabidopsi	371	47	93.6	104	1	THIO RHORU	P10473 rhodospirill
299	47	100.0	186	1	TRXM2 ARATH	Q98608 arabidopsi	372	47	93.6	104	2	Q9ULG7 PASHE	Q9ULG7 fasciola he
300	47	100.0	186	2	Q81G26 ARATH	Q81G26 arabidopsi	373	47	93.6	104	2	Q9U544 PASHE	Q9U544 fasciola he
301	47	100.0	186	2	Q56YG4 ARATH	Q56YG4 arabidopsi	374	47	93.6	104	2	Q962B7 BRABE	Q962B7 brachyosco
302	47	100.0	187	2	Q88091 ORYSA	P09856 spinacia ol	375	47	93.6	104	2	Q4HFK4 CAMCO	Q4HFK4 campylobact
303	47	100.0	190	1	TRXF SPICL	Q81332 mesembryant	376	47	93.6	104	2	Q4HJN3 CAMLA	Q4HJN3 campylobact
304	47	100.0	191	1	TRXF MESCR	Q84D10 streptococc	377	47	93.6	104	2	Q8DNP9 STRRP	Q8DNP9 streptococc
305	47	100.0	191	2	Q8D010 STRRP6	Q84D10 streptococc	378	47	93.6	104	2	Q9PIYO CAMJE	Q9PIYO campylobact
306	47	100.0	195	2	Q5YUQ5 9ASPA	Q5YUQ5 hyacinthus	379	47	93.6	104	2	Q9CR37 LACIA	Q9CR37 lactococcus
307	47	100.0	199	2	Q6C4U8 YARLI	Q6C4U8 yarrowia li	380	47	93.6	104	2	Q97P68 STRPN	Q97P68 streptococc
308	47	100.0	211	2	Q4HX91 GIBZE	Q4HX91 gibberella	381	47	93.6	104	2	Q8NZ17 STRP8	Q8NZ17 streptococc
309	47	100.0	219	2	Q5AT09 EMEHI	Q5AT09 aspergillus	382	47	93.6	104	2	Q99Y75 STRRP	Q99Y75 streptococc
310	47	100.0	217	2	Q7S153 NEUCR	Q7S153 neurospora	383	47	93.6	104	2	Q8E3J7 STRRP3	Q8E3J7 streptococc
311	47	100.0	222	2	Q64E03 9ARCH	Q64E03 uncultured	384	47	93.6	104	2	Q8DXX8 STRRP5	Q8DXX8 streptococc
312	47	100.0	232	2	Q4V8P5 RAT	Q4V8P5 rattus norv	385	47	93.6	104	2	Q835H2 ENTPA	Q835H2 enterococcu
313	47	100.0	254	2	Q61MM2 CABBR	Q61MM2 caenorhabdi	386	47	93.6	104	2	Q7MKW5 FORGI	Q7MKW5 porphyromon
314	47	100.0	282	2	Q4LIU3 9BURK	Q4LIU3 burkholderi	387	47	93.6	104	2	Q7CET1 STRP3	Q7CET1 streptococc
315	47	100.0	283	2	Q617G4 CABBR	Q617G4 caenorhabdi	388	47	93.6	104	2	Q720Y0 LEPIC	Q720Y0 leptospira
316	47	100.0	284	2	Q9NZK6 CABEL	Q9NZK6 caenorhabdi	389	47	93.6	104	2	Q5HX18 CAMUR	Q5HX18 campylobact
317	47	100.0	285	2	Q4UML0 XANCP	Q4UML0 xanthomonas	390	47	93.6	104	2	THIO1 DICDI	THIO1 dictyosteli
318	47	100.0	285	2	Q8P7I9 XANCP	Q8P7I9 xanthomonas	391	47	93.6	105	1	THIO RHOSH	THIO rhodospirill
319	47	100.0	286	2	Q8P1W2 XANCP	Q8P1W2 xanthomonas	392	47	93.6	105	1	THIO RHOSH	THIO rhodospirill
320	47	100.0	287	2	Q7KMR7 DROME	Q7KMR7 dirosophila	393	47	93.6	105	1	Q519H9 ENTHI	Q519H9 entamoeba h
321	47	100.0	287	2	Q9VWR3 DROME	Q9VWR3 dirosophila	394	47	93.6	105	2	Q54KN7 DICDI	Q54KN7 dictyosteli
322	47	100.0	290	2	Q9USR1 SCHPO	Q9USR1 schizosacch	395	47	93.6	105	2	Q890T2 CIOTE	Q890T2 clostridium
323	47	100.0	290	2			396	47	93.6	105	2		

397	44	93.6	105	2	Q7YKR2_HABDU	Q7VKI2_haemophilus	470	44	93.6	120	2	Q6SKK3_ARTAU	Q6KEJ3_arthrobacte
398	44	93.6	105	2	Q7US34_SYMPX	Q7US34_synchococc	471	44	93.6	121	2	Q6FRF3_ORYSA	Q6FRF3_oryza sativ
399	44	93.6	105	2	Q5KMG6_GEOKA	Q5KMG6_geobacillus	472	44	93.6	121	2	Q6L4X5_ORYSA	Q6L4X5_oryza sativ
400	44	93.6	106	1	THIO1_AMABO	P0A112_anabaena sp	473	44	93.6	122	1	TRXH_ORYSA	Q42443_oryza sativ
401	44	93.6	106	1	THIO1_AMASP	P0A111_anabaena sp	474	44	93.6	122	2	Q7EZK7_ORYSA	Q7EXX7_oryza sativ
402	44	93.6	106	1	THIO1_SYNP7	P12243_synchococc	475	44	93.6	122	2	Q7XZK2_HORVD	Q7XZK2_hordeum vul
403	44	93.6	106	1	THIO_COPCM	Q9UW02_coplinus co	476	44	93.6	122	2	Q4WIF6_MAIZE	Q4WIF6_zea mays (m
404	44	93.6	106	1	THIO_PASMU	Q9CM49_pasteurella	477	44	93.6	123	2	Q7XJG3_ARATH	Q7XJG3_arabidopsis
405	44	93.6	106	1	THIO_PASNY3	P52231_synchocyst	478	44	93.6	123	2	Q6VB14_IPOBA	Q6VB14_ipomoea bat
406	44	93.6	106	2	Q5NNI9_ZYMMO	Q5NNI9_zymomonas m	479	44	93.6	123	2	Q7U005_MYCOB	Q7U005_mycobacteri
407	44	93.6	106	2	Q6NDN2_RHOPA	Q6NDN2_rhodopseudo	480	44	93.6	123	2	Q7DBE1_MYCTU	Q7DBE1_mycobacteri
408	44	93.6	106	2	Q8WMD9_BRALJ	Q8WMD9_bradynizob	481	44	93.6	123	2	Q6G4Z3_BIFLO	Q6G4Z3_bifidobacte
409	44	93.6	106	2	Q8DGN0_SYNEL	Q8DGN0_synchococc	482	44	93.6	124	2	Q6KJZ7_CAPAN	Q6KJZ7_capsicum an
410	44	93.6	106	2	Q7MSG6_WOLSU	Q7MSG6_wolinnella s	483	44	93.6	124	2	Q6M1N0_CORGL	Q6M1N0_corynebacte
411	44	93.6	106	2	Q6MEG6_PARUM	Q6MEG6_parachlamyd	484	44	93.6	124	2	Q6EYLL_NOCFA	Q6EYLL_nocardia fa
412	44	93.6	107	1	THIO_CTACA	P37395_cyanidium c	485	44	93.6	125	1	TRXH_PICMA	Q65049_picea maria
413	44	93.6	107	1	THIO_PORPU	P51225_porphyras pu	486	44	93.6	125	1	Q9LUD4_WHEAT	Q9LUD4_triticum ae
414	44	93.6	107	1	THIO_PORYE	P50254_porphyras ye	487	44	93.6	126	1	TRXH1_TOBAC	P29449_nicotiana t
415	44	93.6	107	1	THIO_SYRCL	Q05739_streptomyce	488	44	93.6	126	1	TRXH_WHEAT	Q64394_triticum ae
416	44	93.6	107	1	Q5EN23_MAGGR	Q5EN23_magnaporthe	489	44	93.6	127	2	Q6NEB0_CORDI	Q6NEJ0_corynebacte
417	44	93.6	107	2	Q51V99_MAGGR	Q51V99_magnaporthe	490	44	93.6	127	2	Q7W131_BORBR	Q7W131_bordecella
418	44	93.6	107	2	Q79M44_SYNP7	Q79M44_synchococc	491	44	93.6	127	2	Q7W665_BORPA	Q7W665_bordecella
419	44	93.6	107	2	Q8DKP7_SYNEL	Q8DKP7_synchococc	492	44	93.6	127	2	Q7YXN6_BORPE	Q7YXN6_bordecella
420	44	93.6	107	2	Q7VBF6_PROMA	Q7VBF6_prochloroco	493	44	93.6	129	2	Q82SV1_STRAW	Q82SV1_streptomyce
421	44	93.6	107	2	Q7V6M6_PROMM	Q7V6M6_prochloroco	494	44	93.6	130	2	Q64395_TRITU	Q64395_triticum ae
422	44	93.6	107	2	Q7V126_PROMP	Q7V126_prochloroco	495	44	93.6	130	2	Q7PT21_WHEAT	Q7PT21_triticum ae
423	44	93.6	107	2	Q7U898_SYNPX	Q7U898_synchococc	496	44	93.6	131	2	Q9SMG5_SECCB	Q9SMG5_secale cere
424	44	93.6	107	2	Q72B01_DESVH	Q72B01_desulfovibr	497	44	93.6	131	2	Q9SMG4_LOLPR	Q9SMG4_lolium pere
425	44	93.6	107	2	Q6SS27_MANSM	Q6SS27_mannheimia	498	44	93.6	131	2	Q9SMG6_HORBU	Q9SMG6_hordeum bul
426	44	93.6	107	2	Q5MZK6_SYNP6	Q5MZK6_synchococc	499	44	93.6	131	2	Q8H6X0_WHEAT	Q8H6X0_triticum ae
427	44	93.6	108	2	Q4WMD4_ASPPU	Q4WMD4_aspergillus	500	44	93.6	131	2	Q8GZK4_HORVD	Q8GZK4_hordeum vul
428	44	93.6	108	2	Q5JRY2_HUMAN	Q5JRY2_homo sapien	501	44	93.6	131	2	Q84X91_YEPOAL	Q84X91_leymus chin
429	44	93.6	108	2	Q6VB15_IPOBA	Q6VB15_ipomoea bat	502	44	93.6	131	2	Q9AS75_ORYSA	Q9AS75_oryza sativ
430	44	93.6	108	2	Q4NK10_9M1CC	Q4NK10_arthrobacte	503	44	93.6	131	2	Q9S753_9POAL	Q9S753_phalaris co
431	44	93.6	108	2	Q8YVH9_ANASP	Q8YVH9_anabaena sp	504	44	93.6	131	2	Q4NT79_9DELT	Q4NT79_aeromonas
432	44	93.6	108	2	Q82VNA_NITBU	Q82VNA_nitrosomonas	505	44	93.6	132	2	Q8H6K4_ORYSA	Q8H6K4_oryza sativ
433	44	93.6	108	2	Q7UJ35_RHOPA	Q7UJ35_rhodopirell	506	44	93.6	133	1	TRXH2_ARATH	Q38679_arabidopsis
434	44	93.6	108	2	Q6MMD2_BDEBA	Q6MMD2_bdellovibrio	507	44	93.6	133	2	Q8H6X5_MAIZE	Q8H6X5_zea mays (m
435	44	93.6	108	2	Q6ABW1_LEIXX	Q6ABW1_leifsonia x	508	44	93.6	133	2	Q8GZT3_BRACM	Q8GZT3_brasileia ca
436	44	93.6	108	2	Q5ZRE7_LEGPH	Q5ZRE7_legionella	509	44	93.6	134	2	Q8L9A6_ARATH	Q8L9A6_arabidopsis
437	44	93.6	108	2	Q5XOU3_LEGPA	Q5XOU3_legionella	510	44	93.6	134	2	Q851R5_ORYSA	Q851R5_oryza sativ
438	44	93.6	108	2	Q5MSL4_LEGPL	Q5MSL4_legionella	511	44	93.6	136	2	Q93WZ3_PRUPE	Q93WZ3_prunus pers
439	44	93.6	109	1	THIO2_SYNY3	P73163_synchocyst	512	44	93.6	139	1	THIO2_ECOLI	P33636_escherichia
440	44	93.6	109	1	THIO_CHIAU	P73169_chloroflexu	513	44	93.6	139	2	Q57L52_SALCH	Q57L52_salmonella
441	44	93.6	109	1	THIO_GRIPA	P50338_griffithsia	514	44	93.6	139	2	Q5LBI1_BACFN	Q5LBI1_bacteroides
442	44	93.6	110	1	THIO_STRGO	P52230_streptomyce	515	44	93.6	139	2	Q8Z4J6_SALTI	Q8Z4J6_salmonella
443	44	93.6	110	2	Q4H9D7_9DEIO	Q4H9D7_deinococcus	516	44	93.6	139	2	Q8ZMX4_SALTY	Q8ZMX4_salmonella
444	44	93.6	110	2	Q879K6_STREP3	Q879K6_streptococc	517	44	93.6	139	2	Q5P1D7_SALPA	Q5P1D7_salmonella
445	44	93.6	110	2	Q8YVY7_ANASP	Q8YVY7_anabaena sp	518	44	93.6	139	2	Q67747_AQUAE	Q67747_aquifex aeo
446	44	93.6	110	2	Q82FE7_STRAW	Q82FE7_streptomyce	519	44	93.6	140	1	Q605Y8_METCA	Q605Y8_methylococc
447	44	93.6	110	2	Q7NM87_GLOVI	Q7NM87_gloeobacter	520	44	93.6	140	1	TRXM_CHLRE	P23400_chlamydomon
448	44	93.6	111	2	Q9ALA7_SYNP7	Q9ALA7_synchococc	521	44	93.6	140	2	Q721L5_THET2	Q721L5_thermus the
449	44	93.6	111	2	Q5N062_SYNP6	Q5N062_synchococc	522	44	93.6	140	2	Q5S193_THET8	Q5S193_thermus the
450	44	93.6	112	2	Q67LQ7_SYMTH	Q67LQ7_synbiobacte	523	44	93.6	141	2	Q4H6T8_9DEIO	Q4H6T8_deinococcus
451	44	93.6	113	2	Q68BP1_GRAUL	Q68BP1_gracilaria	524	44	93.6	141	2	Q5LMA0_SILPO	Q5LMA0_silicibacte
452	44	93.6	113	2	Q68GP9_PEA	Q68GP9_pisum sativ	525	44	93.6	142	1	Q9RV58_DEIRA	Q9RV58_deinococcus
453	44	93.6	114	1	TRXH1_ARATH	P29448_arabidopsis	526	44	93.6	142	2	Q61985_CABEL	Q61985_cannorhabdi
454	44	93.6	114	1	Q67SM1_SYMTH	Q67SM1_synbiobacte	527	44	93.6	142	2	Q9RYY9_DEIRA	Q9RYY9_deinococcus
455	44	93.6	115	2	Q751D5_ASHGO	Q751D5_ashbya goss	528	44	93.6	143	2	Q8S312_9ROSI	Q8S312_populus tre
456	44	93.6	115	2	Q5MZN0_SYNP6	Q5MZN0_synchococc	529	44	93.6	144	2	Q7UFP31_RHOPA	Q7UFP31_rhodopirell
457	44	93.6	116	1	TRXH_FAGES	Q96419_fagopyrum e	530	44	93.6	145	2	Q6NCU6_RHOPA	Q6NCU6_rhodopseudo
458	44	93.6	117	2	Q740Z6_MYCPA	Q740Z6_mycobacteri	531	44	93.6	145	2	Q8ZBM4_YERPE	Q8ZBM4_yersinia ps
459	44	93.6	118	1	TRXH_RICCO	Q43636_ricinus com	532	44	93.6	145	2	Q6E640_YERPS	Q6E640_yersinia pe
460	44	93.6	118	2	Q93XZ4_PEA	Q93XZ4_pisum sativ	533	44	93.6	145	2	Q7NOC6_CHRVO	Q7NOC6_chromobacte
461	44	93.6	118	2	Q8GVD3_WHEAT	Q8GVD3_triticum ae	534	44	93.6	145	2	Q5P2H5_AZOSE	Q5P2H5_azorhizob
462	44	93.6	118	2	Q7XZK3_HORVD	Q7XZK3_hordeum vul	535	44	93.6	147	2	Q8J164_BRALJ	Q8J164_bradynizob
463	44	93.6	118	2	Q5XAS7_STRP6	Q5XAS7_streptococc	536	44	93.6	148	2	Q5M1S6_AEDAL	Q5M1S6_aedes albop
464	44	93.6	119	2	Q9SP36_SECCB	Q9SP36_secale cere	537	44	93.6	149	2	Q8N1G6_CORGL	Q8N1G6_corynebacte
465	44	93.6	119	2	Q5ZP48_P1AMU	Q5ZP48_plantago ma	538	44	93.6	150	2	Q84XS0_CHLRE	Q84XS0_chlamydomon
466	44	93.6	119	2	Q8FAW0_LEPIN	Q8FAW0_lepocspira	539	44	93.6	151	2	Q8Z6P1_STRAW	Q8Z6P1_streptomyce
467	44	93.6	120	2	Q5URY3_HUMAN	Q5URY3_homo sapien	540	44	93.6	152	2	Q8H6K3_TOBAC	Q8H6K3_nicotiana t
468	44	93.6	120	2	Q9AR82_PEA	Q9AR82_pisum sativ	541	44	93.6	153	2	Q7XY47_GRIUA	Q7XY47_griffithsia
469	44	93.6	120	2	Q4NLS3_9M1CC	Q4NLS3_arthrobacte	542	44	93.6	153	2	Q9FVJ3_ARATH	Q9FYJ3_arabidopsis

543	44	93.6	154	2	Q4K890_PSEF5	Q4K890_pseudomonas	616	44	93.6	512	2	Q4SEJ5_TETNG	Q4sej5_tetradon n
544	44	93.6	154	2	Q88MC_PSEPK	Q88mc_pseudomonas	617	44	93.6	515	1	TXND2_MOUSE	Q56902 mus musculus
545	44	93.6	154	2	Q8AB92_BACTN	Q8ab92_bacteroides	618	44	93.6	543	1	OSLAW9_BACFN	OSlaw9_bacteroides
546	44	93.6	155	2	Q4ZQ3_PSESY	Q4zq3_pseudomonas	619	44	93.6	543	2	Q4RB6_BACFR	Q4rb6_bacteroides
547	44	93.6	155	2	Q8EF86_SHEON	Q8ef86_shewanella	620	44	93.6	550	1	TXND2_RAT	Q5hxk6 ratuus norv
548	44	93.6	155	2	Q88523_PSESM	Q88523_pseudomonas	621	44	93.6	553	1	TXND2_HUMAN	Q86vq3 homo sapien
549	44	93.6	155	2	Q6ARG0_BACFR	Q6arg0_bacteroides	622	44	93.6	569	2	Q7OEB8_ORYSA	Q70eb8 oryza sativ
550	44	93.6	157	2	Q4NJ4_9MICC	Q4nj4_arthrobacter	623	44	93.6	581	2	Q4RON5_TETNG	Q4rns tetradon n
551	44	93.6	158	2	Q94282_CABEL	Q94282_caenorhabdi	624	44	93.6	588	1	TXND2_HUMAN	Q84227 homo sapien
552	44	93.6	159	2	Q93VQ9_ARATH	Q93vq9_arabidopsis	625	44	93.6	596	2	Q6FW4_HUMAN	Q6fw4 homo sapien
553	44	93.6	160	2	P95355_NEIGO	P95355_neisseria g	626	44	93.6	602	2	Q5WNE3_CABER	Q5wne3 caenorhabdi
554	44	93.6	160	2	Q5FPK1_NEIG1	Q5fPk1_neisseria g	627	44	93.6	605	2	Q7IG53_BRARE	Q71g53 brachydanto
555	44	93.6	160	2	Q9KLR4_NEIMB	Q9kLr4_neisseria m	628	44	93.6	606	2	Q9TW67_CABEL	Q9tw67 caenorhabdi
556	44	93.6	167	1	TXMX8_MAIZE	TXmx8_zea mays (m	629	44	93.6	610	2	Q71G52_BRARE	Q71g52 brachydanto
557	44	93.6	169	2	Q7MXC8_PORGI	Q7mx8_porphyromon	630	44	93.6	619	1	TFP12_HUMAN	Q9qdb0 homo sapien
558	44	93.6	170	2	Q8KDH8_CHLTE	Q8kdh8_chlorobium	631	44	93.6	633	2	Q5L8Y4_BACFN	Q5l8y4 bacteroides
559	44	93.6	172	1	TXMX_ORYSA	TXmx_oryza sativ	632	44	93.6	633	2	Q64P47_BACFR	Q64p47 bacteroides
560	44	93.6	172	1	TXMX_ORYSA	P48384 plium sativ	633	44	93.6	634	2	Q8A0X4_BACTN	Q8a0x4 bacteroides
561	44	93.6	173	1	TXMX_ARATH	Q9seu7_arabidopsis	634	44	91.5	98	2	Q25549_NAEFO	Q25549 naegleria f
562	44	93.6	173	2	Q681Y9_ARATH	Q681y9_arabidopsis	635	44	91.5	105	1	THIO1_SYNY3	P52232 synecocyst
563	44	93.6	173	2	Q67ZH7_ARATH	Q67zh7_arabidopsis	636	44	91.5	105	2	Q5XGB5_XENTR	Q5xgb5 xenopus tro
564	44	93.6	173	2	Q67XN4_ARATH	Q67xn4_arabidopsis	637	44	91.5	105	2	Q5U566_XENLA	Q5u566 xenopus lae
565	44	93.6	173	2	Q4NX02_9BELT	Q4nx02_aeaeomyxob	638	44	91.5	105	2	Q5U566_XENLA	Q5u566 xenopus lae
566	44	93.6	174	2	Q623W5_CABER	Q623w5_caenorhabdi	639	44	91.5	106	1	THIO1_GEOCY	Q96952 geodia cydo
567	44	93.6	175	1	TXMX_WHEAT	Q9zpz21 triticum ae	640	44	91.5	107	1	THIO1_ICTPU	Q9dgl3 ictalurus p
568	44	93.6	175	2	Q9LV12_ARATH	Q9lv12_arabidopsis	641	44	91.5	107	2	Q9TXH8_CABEL	Q9txh8 caenorhabdi
569	44	93.6	175	2	Q5NDA6_TRTTU	Q5nda6_triticum tu	642	44	91.5	107	2	Q617H0_CABER	Q617h0 caenorhabdi
570	44	93.6	177	2	Q7MS25_BRECH	Q7ms25_brevibacill	643	44	91.5	107	2	Q6DG16_BRARE	Q6dgi6 brachydanto
571	44	93.6	180	2	Q7XKD0_ORYSA	Q7xkd0_oryza sativ	644	44	91.5	108	2	Q7ZU14_BRARE	Q7zu14 brachydanto
572	44	93.6	180	2	Q95AH9_PEA	Q95ah9_plium sativ	645	44	91.5	109	2	Q84XS1_CHLRE	Q84xs1 chlamydomon
573	44	93.6	184	2	Q8FLQ6_CORER	Q8flq6_corynebacte	646	44	91.5	110	1	THIO2_ANASP	P20857 anabaena sp
574	44	93.6	185	2	Q65XW6_DEIRA	Q65xw6_deinococcus	647	44	91.5	112	2	Q81EV4_TRIVA	Q81ev4 trichomonas
575	44	93.6	189	2	Q655X0_ORYSA	Q655x0_oryza sativ	648	44	91.5	112	2	Q6IVS9_TRIVA	Q6ivs9 trichomonas
576	44	93.6	192	2	Q4HB83_9DEIO	Q4hb83_deinococcus	649	44	91.5	112	2	Q6IVS8_TRIVA	Q6ivs8 trichomonas
577	44	93.6	193	1	TXMX4_ARATH	Q9seu6_arabidopsis	650	44	91.5	119	1	THIO2_CABEL	Q17424 caenorhabdi
578	44	93.6	194	2	Q64764_ARATH	Q64764_arabidopsis	651	44	91.5	119	1	Q5V6K7_HALMA	Q5v6k7 haloarcula
579	44	93.6	194	2	Q6ZN00_HUMAN	Q6zn00_homo sapien	652	44	91.5	119	2	Q64709_HALMA	Q64709 haloarcula
580	44	93.6	197	2	Q73S01_MYCJA	Q73s01_mycobacteri	653	44	91.5	121	2	Q6A4H7_PROAC	Q6a4h7 propionibac
581	44	93.6	202	2	Q4J5Y3_CORJX	Q4j5y3_mycobacteri	654	44	91.5	123	2	Q5JMR9_ORYSA	Q5jmr9 oryza sativ
582	44	93.6	207	2	Q5UR15_HUMAN	Q5ur15_homo sapien	655	44	91.5	142	2	Q5QZV7_IDILO	Q5qzv7 idiomarina
583	44	93.6	208	2	Q7OK47_9ACTO	Q7ok47_gordonia we	656	44	91.5	151	2	Q61JZ7_CABER	Q61jz7 caenorhabdi
584	44	93.6	211	2	Q67LA9_SYWTH	Q67la9_symbiodacte	657	44	91.5	151	2	Q6SRD7_ARATH	Q6srd7 arabidopsis
585	44	93.6	212	2	Q6XN29_RHOER	Q6xn29_rhodococcus	658	44	91.5	152	2	Q84XS2_CHLRE	Q84xs2 chlamydomon
586	44	93.6	212	2	Q5YP81_NOCPA	Q5yp81_nocardia fa	659	44	91.5	160	2	Q9JMT2_NEIMA	Q9jmt2 neisseria m
587	44	93.6	216	2	Q49816_MYCLB	Q49816_mycobacteri	660	44	91.5	161	2	Q8TIA1_METAC	Q8tia1 methanosarc
588	44	93.6	216	2	Q7UIU8_MYCBO	Q7uiu8_mycobacteri	661	44	91.5	165	2	Q8PY73_METMA	Q8py73 methanosarc
589	44	93.6	216	2	Q06392_MYCTU	Q06392_mycobacteri	662	44	91.5	167	2	Q8L7S9_ARATH	Q8l7s9 arabidopsis
590	44	93.6	220	2	Q5YMM0_NOCPA	Q5ymm0_nocardia fa	663	44	91.5	169	2	Q6MLM7_BDEBA	Q6mlm7 bdellovibri
591	44	93.6	222	2	Q9CB61_MYCLB	Q9cb61_mycobacteri	664	44	91.5	172	2	Q6NPF9_ARATH	Q6npf9 arabidopsis
592	44	93.6	266	2	Q7XQO2_ORYSA	Q7xqo2_oryza sativ	665	44	91.5	184	2	Q4MU10_BACCE	Q4mu10 bacteroides
593	44	93.6	268	2	Q8KD40_CHLTE	Q8kd40_chlorobium	666	44	91.5	184	2	Q73AC8_BACCI	Q73ac8 bacteroides
594	44	93.6	280	2	Q811B1_RALISO	Q8y1b1_ralstonia s	667	44	91.5	184	2	Q81F76_BACCR	Q81f76 bacteroides
595	44	93.6	286	2	Q7PNL3_ANGOA	Q7pnl3_anopheles g	668	44	91.5	184	2	Q81S90_BACAN	Q81s90 bacteroides
596	44	93.6	299	2	Q9ABW0_CAVCR	Q9abw0_caulobacter	669	44	91.5	184	2	Q6HKG7_BACCH	Q6hkg7 bacteroides
597	44	93.6	317	2	Q6ES52_ORYSA	Q6es52_oryza sativ	670	44	91.5	184	2	Q63D26_BACCE	Q63d26 bacteroides
598	44	93.6	328	2	Q7MUAO_PORGI	Q7muao_porphyromon	671	44	91.5	191	2	Q4MNH0_BACCE	Q4mnh0 bacteroides
599	44	93.6	333	2	Q5DBJ3_SCHUA	Q5dbj3_schistosoma	672	44	91.5	191	2	Q733M6_BACCI	Q733m6 bacteroides
600	44	93.6	340	2	Q91B43_CHICK	Q91b43_gallus gall	673	44	91.5	191	2	Q81AF8_BACCR	Q81af8 bacteroides
601	44	93.6	355	2	Q5PU93_BRARE	Q5pu93_birachydanto	674	44	91.5	191	2	Q81Y83_BACAN	Q81y83 bacteroides
602	44	93.6	358	2	Q7MWH7_PORGI	Q7mwh7_porphyromon	675	44	91.5	191	2	Q6HFI7_BACCH	Q6hfi7 bacteroides
603	44	93.6	361	2	Q5LAX1_BACFN	Q5lax1_bacteroides	676	44	91.5	191	2	Q637L5_BACCE	Q637l5 bacteroides
604	44	93.6	361	2	Q64RB8_BACFR	Q64rb8_bacteroides	677	44	91.5	242	2	Q9XIG4_ARATH	Q9xig4 arabidopsis
605	44	93.6	364	2	Q7T264_XENLA	Q7t264_xenopus lae	678	44	91.5	248	2	Q4N8K0_TREPA	Q4n8k0 theileria p
606	44	93.6	364	2	Q7T265_XENTR	Q7t265_xenopus tro	679	44	91.5	254	2	Q9N357_CABEL	Q9n357 caenorhabdi
607	44	93.6	366	2	Q8A882_BACTN	Q8a882_bacteroides	680	44	91.5	277	2	Q8NC82_HUMAN	Q8nc82 homo sapien
608	44	93.6	367	2	Q5LBT3_BACFN	Q5lbt3_bacteroides	681	44	91.5	327	2	Q5A915_CANAL	Q5a915 candida alb
609	44	93.6	367	2	Q64SOS_BACFR	Q64sos_bacteroides	682	44	91.5	336	2	Q6BRN9_DEBHA	Q6brn9 debaryomyce
610	44	93.6	380	2	Q81G82_ARATH	Q81g82_arabidopsis	683	44	91.5	444	2	Q4SP6_TETNG	Q4sp6 tetradon n
611	44	93.6	380	2	Q8WVG7_ARATH	Q8wvg7_arabidopsis	684	44	91.5	464	2	Q53OT7_HUMAN	Q53ot7 homo sapien
612	44	93.6	385	2	Q93X83_9ROST	Q93x83_vitis labru	685	44	91.5	464	2	Q9NSY6_HUMAN	Q9nsy6 homo sapien
613	44	93.6	386	2	Q8VZH4_TOBAC	Q8vzh4_nicotiana t	686	44	91.5	476	2	Q9JLV4_MOUSE	Q9jlv4 mus musculu
614	44	93.6	413	2	Q67T35_SYWTH	Q67t35_symbiodacte	687	44	91.5	578	2	Q81B68_ARATH	Q81b68 arabidopsis
615	44	93.6	433	2	Q4R6D4_MACFA	Q4r6d4_macaca fasc	688	44	91.5	578	2	Q80763_ARATH	Q80763 arabidopsis

689	43	91.5	612	2	Q96K36_HUMAN	Q96K36 homo sapien	762	42	89.4	460	2	Q7URF7_RHOBA	Q7URF7 rhodopirell
690	43	91.5	706	2	Q9VYR5_DROME	Q9VYR5 drosophila	763	42	89.4	473	2	Q5L9C4_BACFN	Q5L9C4 bacteroides
691	43	91.5	706	2	Q6NBP8_DROME	Q6NBP8 drosophila	764	42	89.4	473	2	Q64PK8_BACFN	Q64PK8 bacteroides
692	43	91.5	747	2	Q8TD87_HUMAN	Q8TD87 homo sapien	765	42	89.4	477	2	Q7IG54_BRARE	Q7IG54 brachydanio
693	43	91.5	747	2	Q6UWZ6_HUMAN	Q6UWZ6 homo sapien	766	42	89.4	491	2	Q7UI68_RHOBA	Q7UI68 rhodopirell
694	43	91.5	768	2	Q96K54_HUMAN	Q96K54 homo sapien	767	42	89.4	506	2	Q6UQO2_QUEBU	Q6UQO2 quercus sub
695	43	91.5	781	2	Q614U3_CABER	Q614U3 caenorhabdi	768	42	89.4	506	2	Q8GTC2_QUEBU	Q8GTC2 quercus sub
696	43	91.5	788	2	Q9XWE1_CABER	Q9XWE1 caenorhabdi	769	42	89.4	517	2	Q7Q063_QUEBU	Q7Q063 quercus sub
697	43	91.5	792	2	Q86F61_HUMAN	Q86F61 homo sapien	770	42	89.4	534	1	ENV_FSVST	ENV_FSVST
698	43	91.5	793	2	Q8IXB1_HUMAN	Q8IXB1 homo sapien	771	42	89.4	606	2	Q9VMF6_DROME	Q9VMF6 drosophila
699	43	91.5	793	2	Q96K38_HUMAN	Q96K38 homo sapien	772	42	89.4	653	1	TXND3_CIOIN	TXND3 ciona intes
700	43	91.5	793	2	Q96K44_HUMAN	Q96K44 homo sapien	773	42	89.4	662	1	ENV_FTVLB	ENV_FTVLB
701	43	91.5	793	2	Q5R5L3_PONPY	Q5R5L3 pongo pygma	774	42	89.4	662	1	ENV_FSVGA	ENV_FSVGA
702	43	91.5	793	2	Q8CIB0_MOUSE	Q8CIB0 mus musculu	775	42	89.4	662	2	Q7LYT7_FTV	Q7LYT7 flv
703	43	91.5	793	2	Q9DC23_MOUSE	Q9DC23 mus musculu	776	42	89.4	666	2	Q90AE9_FTV	Q90AE9 flv
704	43	91.5	793	2	Q7LS84_MOUSE	Q7LS84 mus musculu	777	42	89.4	668	1	ENV_FVVC6	ENV_FVVC6
705	43	91.5	795	2	Q8CH78_MOUSE	Q8CH78 mus musculu	778	42	89.4	837	1	TXND3_ANTCR	TXND3 antcr
706	43	91.5	796	2	Q6NRT6_XENLA	Q6NRT6 xenopus lae	779	42	89.4	1019	2	Q7UMF5_RHOBA	Q7UMF5 rhodoba
707	43	91.5	777	2	Q4Q7K2_LEIMA	Q4Q7K2 leishmania	780	42	89.4	1083	2	Q7UM78_RHOBA	Q7UM78 rhodoba
708	42	89.4	89	2	Q4HCJ2_GDEIO	Q4HCJ2 deionococcus	781	41	87.2	45	2	Q9VM82_DROME	Q9VM82 drosophila
709	42	89.4	89	2	Q4NZX5_THRPA	Q4NZX5 theileria p	782	41	87.2	100	2	Q4YUN1_PLABE	Q4YUN1 plasmodium
710	42	89.4	101	2	Q8BDS2_STRMU	Q8BDS2 streptococc	783	41	87.2	105	2	Q4FND3_9RICB	Q4FND3 9ricb
711	42	89.4	104	2	Q5M2L2_STR12	Q5M2L2 streptococc	784	41	87.2	105	2	Q7VK37_HELHP	Q7VK37 helicobact
712	42	89.4	104	2	Q5M2L2_STR12	Q5M2L2 streptococc	785	41	87.2	107	1	THIO2_CORRE	THIO2 corne
713	42	89.4	104	2	Q5LY08_STR11	Q5LY08 streptococc	786	41	87.2	108	1	THIO_BUCAL	THIO bucal
714	42	89.4	105	2	Q5CR91_CRYPV	Q5CR91 cryptospori	787	41	87.2	108	1	THIO_BUCAP	THIO bucap
715	42	89.4	108	1	THIO2_CHLTF	THIO2 chlorobium	788	41	87.2	109	1	Q747T5_GEOSL	Q747T5 geosli
716	42	89.4	108	1	THIO2_CHLTF	THIO2 chlorobium	789	41	87.2	109	2	Q8LI1NO_BUCPS	Q8LI1NO bucps
717	42	89.4	115	2	Q5PB59_ANAMM	Q5PB59 anaplasma m	790	41	87.2	110	2	Q6F877_ACTAD	Q6F877 actad
718	42	89.4	121	2	Q8IKL4_PLAFV	Q8IKL4 plasmodium	791	41	87.2	112	2	Q6F877_ACTAD	Q6F877 actad
719	42	89.4	121	2	Q7R8F6_PLAYO	Q7R8F6 plasmodium	792	41	87.2	113	2	Q9PA22_XYUFA	Q9PA22 xyufa
720	42	89.4	121	2	Q4YYF5_PLABE	Q4YYF5 plasmodium	793	41	87.2	113	2	Q7VRM1_CANFB	Q7VRM1 canfb
721	42	89.4	139	2	Q9VUG9_DROME	Q9VUG9 drosophila	794	41	87.2	117	2	Q812Q3_PLAF7	Q812Q3 plasmodium
722	42	89.4	139	2	Q6DID1_ERMCT	Q6DID1 erwinia car	795	41	87.2	120	2	Q5ZVM8_LBEPH	Q5ZVM8 lbeph
723	42	89.4	139	2	Q743D8_MYCPA	Q743D8 mycobacteri	796	41	87.2	120	2	Q5X5F3_LBSPN	Q5X5F3 legionella
724	42	89.4	140	2	Q9CB08_MYCLE	Q9CB08 mycobacteri	797	41	87.2	120	2	Q5WMT6_LBEPH	Q5WMT6 legionella
725	42	89.4	141	2	Q4UBR7_SULAC	Q4UBR7 sulfolobus	798	41	87.2	128	2	Q7IG48_PLAF7	Q7IG48 plasmodium
726	42	89.4	148	2	Q4US63_XANCP	Q4US63 xanthomonas	799	41	87.2	129	2	Q4HN70_CAMLA	Q4HN70 campylobact
727	42	89.4	148	2	Q5Z2A0_NOCFA	Q5Z2A0 nocardia fa	800	41	87.2	142	2	Q9W022_DROME	Q9W022 drosophila
728	42	89.4	148	2	Q8PMZ8_XANAC	Q8PMZ8 xanthomonas	801	41	87.2	159	2	Q6A5E3_PROAC	Q6A5E3 propionibac
729	42	89.4	148	2	Q8PBE2_XANAC	Q8PBE2 xanthomonas	802	41	87.2	184	2	Q4TRK5_ESPHN	Q4TRK5 erythrobact
730	42	89.4	160	2	Q6O4X8_METCA	Q6O4X8 methylococc	803	41	87.2	200	2	Q5CS14_CRYPV	Q5CS14 cryptospori
731	42	89.4	160	2	Q63QP3_BURPS	Q63QP3 burkholderi	804	41	87.2	200	2	Q5CKF3_CRYHO	Q5CKF3 cryptospori
732	42	89.4	172	2	Q50039_MYCLE	Q50039 mycobacteri	805	41	87.2	210	2	Q9A684_CAUCR	Q9A684 caulobacter
733	42	89.4	174	2	Q8XVP6_RALSO	Q8XVP6 ralestonia s	806	41	87.2	289	2	Q4IWM6_AZOVI	Q4IWM6 azotobacter
734	42	89.4	175	2	Q8LKM0_LYCFS	Q8LKM0 lycopersico	807	41	87.2	289	2	Q9HMM7_PSEAB	Q9HMM7 pseudomonas
735	42	89.4	181	2	Q6IR37_NICBE	Q6IR37 nicotiana b	808	41	87.2	290	2	Q4ZMX6_PSESY	Q4ZMX6 pseudomonas
736	42	89.4	181	2	Q6UR38_NICBE	Q6UR38 nicotiana b	809	41	87.2	290	2	Q4K589_PSEFS	Q4K589 pseudomonas
737	42	89.4	183	2	Q9LFA3_ARATH	Q9LFA3 arabidopsis	810	41	87.2	290	2	Q8BQ12_PSEPK	Q8BQ12 pseudomonas
738	42	89.4	183	2	Q9M7X9_ARATH	Q9M7X9 arabidopsis	811	41	87.2	336	2	Q8B9R3_PSESM	Q8B9R3 pseudomonas
739	42	89.4	186	2	Q6ZGX6_BURMA	Q6ZGX6 burkholderi	812	41	87.2	336	2	Q7MTCT_PORGI	Q7MTCT porphyromon
740	42	89.4	187	2	Q8DTZ1_STRMU	Q8DTZ1 streptococc	813	41	87.2	136	2	Q9B810_RHILQ	Q9B810 rhizobium
741	42	89.4	189	2	Q8H2V6_ORYSA	Q8H2V6 oryza sativ	814	40	85.1	136	2	Q7Q9B5_ANOGA	Q7Q9B5 anopheles g
742	42	89.4	197	2	Q6MJ38_BDEBA	Q6MJ38 bdellovibri	815	40	85.1	160	2	Q76877_DROME	Q76877 drosophila
743	42	89.4	207	2	Q4ILZ3_9BURK	Q4ILZ3 burkholderi	816	40	85.1	192	1	RSEA_OEBTH	RSEA oebth
744	42	89.4	209	2	Q5Z300_NOCFA	Q5Z300 nocardia fa	817	40	85.1	4810	2	Q57X24_GTYRP	Q57X24 cyranosoma
745	42	89.4	216	2	Q8M2X9_ORYSA	Q8M2X9 oryza sativ	818	39	83.0	103	2	Q71Z58_LISMF	Q71Z58 listeria mo
746	42	89.4	241	2	Q9MSD4_CHLRE	Q9MSD4 chlamydomon	819	39	83.0	103	2	Q8Y6S4_LISMF	Q8Y6S4 listeria mo
747	42	89.4	273	1	ENV_FIVT1	ENV_FIVT1	820	39	83.0	103	2	Q9ZBA0_LISIN	Q9ZBA0 listeria in
748	42	89.4	273	1	Q9U054_FIV	Q9U054 feline leuk	821	39	83.0	104	2	Q8RKA7_OBNOE	Q8RKA7 oenococcus
749	42	89.4	273	2	Q8C834_MOUSE	Q8C834 mus musculu	822	39	83.0	105	1	THIO_TREPA	THIO trepa
750	42	89.4	315	2	Q5U0E5_CRYNE	Q5U0E5 cryptococcu	823	39	83.0	105	2	Q97IU3_CIOAB	Q97IU3 clostridium
751	42	89.4	326	2	Q5K101_CRYNE	Q5K101 cryptococcu	824	39	83.0	107	2	Q5G528_WOLTR	Q5G528 wolbachia s
752	42	89.4	330	2	Q5BCU1_EMENI	Q5BCU1 aspergillus	825	39	83.0	109	2	Q87XC3_PSESM	Q87XC3 pseudomonas
753	42	89.4	336	2	Q8CA16_MOUSE	Q8CA16 mus musculu	826	39	83.0	110	2	Q97AL9_THRVO	Q97AL9 thermoplaem
754	42	89.4	370	2	Q4I218_GIBZE	Q4I218 gibberella	827	39	83.0	112	2	Q83A24_COXBU	Q83A24 coxiella bu
755	42	89.4	380	2	Q8S5U4_BRAVA	Q8S5U4 bradyrhizob	828	39	83.0	113	2	Q9HUV7_THRAC	Q9HUV7 thermoplaem
756	42	89.4	386	2	Q8JHX2_CHICK	Q8JHX2 gallus gall	829	39	83.0	114	2	Q8S3L3_PROSI	Q8S3L3 populus tre
757	42	89.4	402	2	Q7ULN6_RHOBA	Q7ULN6 rhodopirell	830	39	83.0	121	1	THIO_FUSCU	THIO fuscu
758	42	89.4	426	2	Q8JYJ3_BRARE	Q8JYJ3 brachydanio	831	39	83.0	121	2	Q4IK55_GIBZE	Q4IK55 gibberella
759	42	89.4	438	2	Q8JYJ2_BRARE	Q8JYJ2 brachydanio	832	39	83.0	123	2	Q84LP7_CIRPA	Q84LP7 citrus para
760	42	89.4	451	2	Q7UD06_RHOBA	Q7UD06 rhodopirell	833	39	83.0	131	2	Q54MX3_DICDI	Q54MX3 dicyostell
761	42	89.4	459	1	TF7L2_MOUSE	TF7L2 mus musculu	834	39	83.0	146	2	Q66542_AQUAE	Q66542 aquifex aeo

835	39	83.0	158	2	Q623U3_CAEBR	Q623U3 caenorthabdi	908	38	80.9	145	2	Q9V8Y6_DROME	Q9V8Y6 drosophila
836	39	83.0	163	2	Q6ML15_BDEBA	Q6ML15 bdeilovibri	909	38	80.9	149	2	Q5C0B0_SCHJA	Q5C0B0 schistosoma
837	39	83.0	165	1	STOA_BACSU	Q31687 bacillus su	910	38	80.9	150	2	Q4NVD1_9DEL7	Q4NVD1 anaeromyxob
838	39	83.0	165	2	Q8RF79_LBEPN	Q8RF79 leptospira	911	38	80.9	151	2	Q8YJ16_BRUME	Q8YJ16 bruceella me
839	39	83.0	165	2	Q72RV9_LBEPN	Q72RV9 leptospira	912	38	80.9	153	2	Q5YBC3_GCHLO	Q5YBC3 helicospori
840	39	83.0	168	2	Q7ZKX7_XENLA	Q7ZKX7 xenopus lae	913	38	80.9	154	2	Q91505_PSEAE	Q91505 pseudomonas
841	39	83.0	170	1	TXD12_MOUSE	Q9CQU0 mus musculu	914	38	80.9	156	2	Q41T42_AZOTI	Q41T42 azotobacter
842	39	83.0	170	1	Q5JYNI_MOUSE	Q5JYNI mus musculu	915	38	80.9	156	2	Q6GQZ1_XENLA	Q6GQZ1 xenopus lae
843	39	83.0	172	1	TXD12_MOUSE	Q9CQU0 mus musculu	916	38	80.9	171	2	Q4FNK2_9RICK	Q4FNK2 candidatus
844	39	83.0	172	1	Q5ER316_BOVIN	Q5ER316 bos tauris	917	38	80.9	172	2	Q6SXM9_CREID	Q6SXM9 ctenopharyx
845	39	83.0	172	2	Q5O3D8_BRARE	Q5O3D8 brachydantio	918	38	80.9	173	2	Q7W742_BORPA	Q7W742 bordetella
846	39	83.0	173	2	Q5KZP3_GEOXA	Q5KZP3 geobacillus	919	38	80.9	173	2	Q7W1P2_BORER	Q7W1P2 botdettella
847	39	83.0	173	2	Q5U4U7_XENLA	Q5U4U7 xenopus lae	920	38	80.9	175	2	Q51X14_PROWI	Q51X14 prototheca
848	39	83.0	177	2	Q65HX6_BACLD	Q65HX6 bacillus lae	921	38	80.9	176	1	HEIX_RHOCA	HEIX rhodococcus
849	39	83.0	178	2	Q4PEU3_USTMA	Q4PEU3 ustilago ma	922	38	80.9	179	2	Q33574_RHOSH	Q33574 rhodospacer
850	39	83.0	178	2	Q6XVR3_CAEEL	Q6XVR3 caenorthabdi	923	38	80.9	179	2	Q51R18_SILPO	Q51R18 silicibacter
851	39	83.0	178	2	Q628F4_CAEEL	Q628F4 caenorthabdi	924	38	80.9	182	2	Q4XT52_PLACH	Q4XT52 plasmodium
852	39	83.0	179	1	RESA_BACSU	P35160 bacillus su	925	38	80.9	185	2	Q96C96_HUMAN	Q96C96 homo sapien
853	39	83.0	179	2	Q95Q57_CAEEL	Q95Q57 caenorthabdi	926	38	80.9	186	2	Q6JAC4_TRITU	Q6JAC4 triticum tu
854	39	83.0	182	2	Q4NS08_9DEL7	Q4NS08 anaeromyxob	927	38	80.9	186	2	Q6NJT0_CORDI	Q6NJT0 cordi
855	39	83.0	185	2	Q7MAR8_WOLSU	Q7MAR8 wolfinella s	928	38	80.9	187	2	Q51XCI_SILPO	Q51XCI silicibacter
856	39	83.0	185	2	Q4KLDE_XENLA	Q4KLDE xenopus lae	929	38	80.9	188	2	Q6TABS_WHEAT	Q6TABS triticum ae
857	39	83.0	201	2	Q7ANQ4_BACCI	Q7ANQ4 bacillus ce	930	38	80.9	189	2	Q6JACS_TRITU	Q6JACS triticum tu
858	39	83.0	202	2	Q8CXG2_OCEIH	Q8CXG2 oceanobacill	931	38	80.9	189	2	Q6AAY6_PROAC	Q6AAY6 propionibac
859	39	83.0	222	2	Q57W40_9RTYP	Q57W40 trypanosoma	932	38	80.9	190	2	Q81QL8_DROME	Q81QL8 drosophila
860	39	83.0	222	2	Q9NS57_CAEEL	Q9NS57 caenorthabdi	933	38	80.9	192	2	Q98EAT_RHILLO	Q98EAT rhizobium l
861	39	83.0	260	2	Q619U4_CAEER	Q619U4 caenorthabdi	934	38	80.9	196	2	Q9FUL2_PRUAV	Q9FUL2 prunus avu
862	39	83.0	283	2	Q5QY72_IDILO	Q5QY72 idiomarina	935	38	80.9	198	2	Q95Z76_OSTOK	Q95Z76 oseretragia
863	39	83.0	318	2	Q9LZAS_STRCO	Q9LZAS streptomyce	936	38	80.9	203	2	Q4M0U5_9BURI	Q4M0U5 burkholderi
864	39	83.0	328	2	Q8ZJCS_STRAW	Q8ZJCS streptomyce	937	38	80.9	207	2	Q8P5D2_COREF	Q8P5D2 corynebacte
865	39	83.0	351	2	Q41046_CHVPI	Q41046 paramecium	938	38	80.9	207	2	Q8NT71_CORGL	Q8NT71 corynebacte
866	39	83.0	358	2	Q84449_CHVPI	Q84449 paramecium	939	38	80.9	208	2	Q98G37_RHILLO	Q98G37 rhizobium l
867	39	83.0	372	2	Q64A88_9ARCH	Q64A88 uncultured	940	38	80.9	210	2	Q8H703_PHYIN	Q8H703 phytophthor
868	39	83.0	392	2	Q5QMW1_ORISA	Q5QMW1 oryza sativ	941	38	80.9	211	2	Q4SYC5_TETIN	Q4SYC5 tetradon n
869	39	83.0	392	2	Q8VZQ0_ARATH	Q8VZQ0 arabidopsis	942	38	80.9	212	2	Q5YMW1_NOCFA	Q5YMW1 nocardia fa
870	39	83.0	421	2	Q6D708_ERWCT	Q6D708 erwina car	943	38	80.9	214	2	Q6XN30_RHOER	Q6XN30 rhodococcus
871	39	83.0	498	2	Q648T6_9ARCH	Q648T6 uncultured	944	38	80.9	216	2	Q9LRP6_CHLOV	Q9LRP6 chlorella v
872	39	83.0	507	2	Q64C9N_9ARCH	Q64C9N uncultured	945	38	80.9	223	2	Q5QXBI_EMIHU	Q5QXBI emiliania h
873	39	83.0	508	2	Q64AW1_9ARCH	Q64AW1 uncultured	946	38	80.9	223	2	Q8RA15_THETN	Q8RA15 thellmaniae
874	39	83.0	508	2	Q64ARA_9ARCH	Q64ARA uncultured	947	38	80.9	226	2	Q4XNK9_PLACH	Q4XNK9 plasmodium
875	39	83.0	616	2	Q51BS8_ENTHI	Q51BS8 entamoeba h	948	38	80.9	228	2	Q4V963_BRARE	Q4V963 brachydantio
876	39	83.0	622	2	Q5OXV6_ENTHI	Q5OXV6 entamoeba h	949	38	80.9	234	2	Q7R1NO_GIALA	Q7R1NO giardia lam
877	39	83.0	658	2	Q7UMQ6_RHOBA	Q7UMQ6 rhodopirell	950	38	80.9	235	2	Q97451_GIALA	Q97451 giardia lam
878	39	83.0	2567	2	Q90574_CHICK	Q90574 gallus gall	951	38	80.9	234	2	Q7XZ51_GRIJA	Q7XZ51 griffithsia
879	39	83.0	5825	2	Q82731_VICFA	Q82731 victoria faba	952	38	80.9	235	2	Q6PZEB_BRANA	Q6PZEB brassica na
880	39	80.9	26	2	Q9S880_SPTOL	Q9S880 spinacia ol	953	38	80.9	235	2	Q4J505_CORUK	Q4J505 corynebacte
881	38	80.9	63	2	Q7MIQ4_SOTBN	Q7MIQ4 glycine max	954	38	80.9	238	2	Q57AS4_BRUAB	Q57AS4 bruceella ab
882	38	80.9	76	2	Q6JAC2_WHEAT	Q6JAC2 triticum ae	955	38	80.9	238	2	Q8FYAS_BRUSU	Q8FYAS bruceella su
883	38	80.9	100	2	Q9LXZ8_ARATH	Q9LXZ8 arabidopsis	956	38	80.9	240	2	Q5YBC2_9CHLO	Q5YBC2 helicospori
884	38	80.9	106	2	Q71VT1_LISMF	Q71VT1 listeria mo	957	38	80.9	242	2	Q4PLZ2_IXOSC	Q4PLZ2 ixodes scap
885	38	80.9	106	2	Q926S8_LISIN	Q926S8 listeria in	958	38	80.9	247	2	Q5F472_CHICK	Q5F472 gallus gall
886	38	80.9	106	2	Q8Y3KS_LISMO	Q8Y3KS listeria mo	959	38	80.9	249	2	Q8X1D2_COCIM	Q8X1D2 coccidioid
887	38	80.9	107	2	Q9GTU2_HETGL	Q9GTU2 heterodera	960	38	80.9	253	2	Q5AF81_CANAL	Q5AF81 candida alb
888	38	80.9	108	2	Q7XYD7_WHEAT	Q7XYD7 triticum ae	961	38	80.9	266	2	Q5COA7_SCHJA	Q5COA7 schistosoma
889	38	80.9	110	2	Q72HU9_THET2	Q72HU9 thermus the	962	38	80.9	271	2	Q6O4D2_METCA	Q6O4D2 methylococc
890	38	80.9	110	2	Q5SH13_THET2	Q5SH13 thermus the	963	38	80.9	287	2	Q7PT26_ANOGA	Q7PT26 anopheles g
891	38	80.9	111	2	Q93CWE_LACSK	Q93CWE lactobacill	964	38	80.9	298	2	Q9MB13_ORYSA	Q9MB13 oryza sativ
892	38	80.9	112	2	Q6TAB9_WHEAT	Q6TAB9 triticum ae	965	38	80.9	318	1	MPD1_YEAST	MPD1 yeast
893	38	80.9	112	2	Q8D2Q0_WIGBR	Q8D2Q0 wigglewort	966	38	80.9	327	2	Q6PTU9_BRARE	Q6PTU9 brachytronic
894	38	80.9	116	2	Q7QX91_GIALA	Q7QX91 giardia lam	967	38	80.9	337	2	Q5XWD1_ENTHI	Q5XWD1 entamoeba h
895	38	80.9	116	2	Q9U015_GIALA	Q9U015 giardia lam	968	38	80.9	338	2	Q9PBHO_XYLFA	Q9PBHO xyella fas
896	38	80.9	116	2	Q6MRB6_BDBBA	Q6MRB6 bdellovibr	969	38	80.9	338	2	Q6DH89_BRARE	Q6DH89 brachydantio
897	38	80.9	119	2	Q5OVME_ENTHI	Q5OVME entamoeba h	970	38	80.9	341	2	Q87C67_XYLFT	Q87C67 xyella fas
898	38	80.9	121	2	Q8BTL4_CORGL	Q8BTL4 corynebacte	971	38	80.9	347	2	Q4UIS4_THEAN	Q4UIS4 theileria a
899	38	80.9	127	2	Q5OUU8_ENTHI	Q5OUU8 entamoeba h	972	38	80.9	354	2	Q9BK83_GIALA	Q9BK83 giardia lam
900	38	80.9	133	2	Q5CE99_CRYHO	Q5CE99 cryptospori	973	38	80.9	359	1	PD12_SCHPO	PD12 schistosoma
901	38	80.9	134	2	Q7XY30_GRIJA	Q7XY30 griffithsia	974	38	80.9	359	1	TTGA_ASPNG	TTGA aspergillus
902	38	80.9	134	2	Q28984_ARCFU	Q28984 archaeglob	975	38	80.9	359	2	Q4F7X2_SCHPO	Q4F7X2 schistosac
903	38	80.9	134	2	Q7OSG3_GIALA	Q7OSG3 giardia lam	976	38	80.9	359	2	P93358_TOBAC	P93358 nicotiana t
904	38	80.9	134	2	Q9NDB1_GIALA	Q9NDB1 giardia lam	977	38	80.9	360	2	Q86UYO_HUMAN	Q86UYO homo sapien
905	38	80.9	135	2	Q58ZJ4_9RTYP	Q58ZJ4 trypanosoma	978	38	80.9	361	1	PD1K6_ARATH	PD1K6 arabidopsis
906	38	80.9	138	2	Q51X15_PROWI	Q51X15 prototheca	979	38	80.9	361	2	Q546R3_ARATH	Q546R3 arabidopsis
907	38	80.9	142	2	Q7QJ17_ANOGA	Q7QJ17 anopheles g	980	38	80.9	363	2	Q6EH23_HUMAN	Q6EH23 homo sapien

```

981 38 80.9 363 2 0861A3_DICDI 0861a3 dictyostei1
982 38 80.9 363 2 015735_DICDI 015735 dictyostei1
983 38 80.9 364 1 PDIA6_MEDSA P38661 medicago sa
984 38 80.9 364 2 096600_ASPRU 096600 aspergillus
985 38 80.9 364 2 06CC54_YARLI 06CC54 yarrowia 11
986 38 80.9 364 2 095175_DROME 095175 drosophila
987 38 80.9 366 2 05C145_SCHJA 05C145 schistosoma
988 38 80.9 366 2 05EUD6_MAIZE 05EUD6 zeamays 1m
989 38 80.9 367 2 075M08_ORYSA 075M08 oryza sativ
990 38 80.9 367 2 05EUD7_MAIZE 05EUD7 zeamays 1m
991 38 80.9 368 2 05BHA5_EMBE1 05bha5 aspergillus
992 38 80.9 368 2 04WT19_ASPRU 04wt19 aspergillus
993 38 80.9 368 2 050017_ENTHI 050017 entamoeba h
994 38 80.9 369 1 ERP38_NEUCR 092249 neurospora
995 38 80.9 369 2 091815_FUGRU 091815 fugu rubrip
996 38 80.9 371 2 05EMX2_MAGGR 05emx2 magnaporthe
997 38 80.9 371 2 052C23_MAGGR 052c23 magnaporthe
998 38 80.9 371 2 0942L2_ORYSA 0942L2 oryza sativ
999 38 80.9 371 2 082WE2_NITEU 082we2 nitrosomona
1000 38 80.9 376 2 09FEG4_TRITU 09feg4 triticum tu

```

ALIGNMENTS

```

RESULT 1
04T7B7_TETNG PRELIMINARY; PRT; 80 AA.
ID 04T7B7_TETNG
AC 04T7B7_TETNG
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAP8161, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG0005813001;
OS Tetradon nigriviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
NCBI_TaxID=99883;
RX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Benoit A.,
RA Nicand S., Jaffe D., Fisher S., Lutfalla G., Dosat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castell V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cartolico L., Poulin J., De Bernardis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetradon nigriviridis reveals
RT the early vertebrate proto-karyotype."
RL Nature 431:946-957(2004).
RN
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAB01008161; CAP91215.1; -; Genomic_DNA.
FT NON TER 1 80
FT NON TER 1 80
SQ SEQUENCE 80 AA; 8611 MW; 64705ABBA4A5620E CRC64;

```

Query Match 100.0%; Score 47; DB 2; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 WCGPCK 6
Db 2 WCGPCK 7

```

```

RESULT 2
060744_HUMAN PRELIMINARY; PRT; 84 AA.
ID 060744_HUMAN
AC 060744
DT 01-ANG-1998 (TrEMBLrel. 07, Created)
DT 01-ANG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioedoxin delta 3 (Fragment).
GN Name=TXN delta 3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
NCBI_TaxID=9606;
RX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Wang Y., Wang Y.G., Zhang Y., Yuan Y., Ma D.;
RT "An alternative splice variant of human thioedoxin."
RL Chin. Sci. Bull. 43:292-295(1998).
DR EMBL; AF065241; AAC17430.1; -; mRNA.
DR HSSP; P10599; 1ERP.
DR SMR; 060744; 1-84.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR006663; Thioedox dom2.
DR InterPro; IPR012336; Thioedoxin-like.
DR InterPro; IPR012335; Thioedoxin_fold.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOEDOXIN.
DR PROSITE; PS00194; THIOEDOXIN; 1.
KW Redox-active center.
FT NON TER 1 84
FT NON TER 1 84
SQ SEQUENCE 84 AA; 9321 MW; 818FB84BA865721 CRC64;

```

Query Match 100.0%; Score 47; DB 2; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 3
05T936_HUMAN PRELIMINARY; PRT; 85 AA.
ID 05T936_HUMAN
AC 05T936
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Thioedoxin.
GN Name=TXN; ORFNames=RP11-427111.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
NCBI_TaxID=9606;
RX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Williams S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL158158; CAL14067.1; -; Genomic_DNA.
DR SMR; 05T936; 1-85.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.

```

DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox dom2.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Redox-active center.
 SQ SEQUENCE 85 AA; 9452 MW; 3CC6254BD6A1D66F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 31 WCGPCK 36

RESULT 4

OSV0J2_HALMA PRELIMINARY; PRT; 88 AA.
 ID OSV0J2_HALMA PRELIMINARY; PRT; 88 AA.
 AC OSV0J2;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE ThioRedoxin.
 GN Name=trxA3; OrderedLocuNames=trxA3; 110;
 OS Halobacterium marismortui (Halobacterium marismortui).
 OC Archaea; Euryarchaeota; Halobacteriales;
 OC Halobacteriaceae; Halobacteriales.
 OX NCBI_TaxID=2238;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 43049;
 RX PubMed=15520287; DOI=10.1101/gr.2700304;
 RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Gushman G.,
 RA Deutsch E.W., Shannon P., Chiu Y., Meng R.S., Gan R.R., Hung P.,
 RA Date S.V., Marcotte E., Hood L., Ng W.V.;
 RT "Genome sequence of Halobacterium marismortui: a halophilic archaeon from
 the Dead Sea.";
 RL Genome Res. 14:2221-2234 (2004).
 DR EMBL; AY596297; AAV46961.1; -; Genomic DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR006663; ThioRedox dom2.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 KW Complete proteome.
 SQ SEQUENCE 88 AA; 10011 MW; CFE9B8FAC1F69857 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 88;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 12 WCGPCK 17

RESULT 5

OSV0J2_HALMA PRELIMINARY; PRT; 89 AA.
 ID OSV0J2_HALMA PRELIMINARY; PRT; 89 AA.
 AC OSV0J2;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE ThioRedoxin.
 GN Name=trxA2; OrderedLocuNames=VNG2600G;
 OS Halobacterium salinarum (Halobacterium salinarum).
 OC Archaea; Euryarchaeota; Halobacteriales;

OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=2242;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
 RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogha J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
 RA Leitner S., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonksi P.E., Krebs W.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Eberhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Genome sequence of Halobacterium species NRC-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181 (2000).
 DR EMBL; AE005133; AAG20641.1; -; Genomic DNA.
 DR PIR; E84409; E84409.
 DR HSSP; P10599; IERV.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR006663; ThioRedox dom2.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 KW Complete proteome.
 SQ SEQUENCE 89 AA; 10019 MW; BDP97B3496F70BFF CRC64;

Query Match 100.0%; Score 47; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 DB 12 WCGPCK 17

RESULT 6

THIO_THIRO
 ID THIO_THIRO STANDARD; PRT; 91 AA.
 AC P96132;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE ThioRedoxin (TRX) (Fragment).
 GN Name=trxA;
 OS Thiocapsa roseopersicina.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 OC Chromatiaceae; Thiocapsa.
 OX NCBI_TaxID=1058;
 RN [1]

RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].

RC STRAIN=ML;
 RA Haverkamp T., Schwenn J.D.;
 RL Submitted (Aug-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (by
 CC similarity).
 CC -!- SIMILARITY: Belongs to the thioRedoxin family.
 CC -!- SIMILARITY: Contains 1 thioRedoxin domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; U75512; AAB36882.1; -; Genomic DNA.
 CC HSSP; P00274; ZTRX.

```
DR InterPro; IPR006662; ThioRed.  
DR InterPro; IPR006663; ThioRedox dom2.  
DR InterPro; IPR005746; ThioRedoxin.  
DR InterPro; IPR012336; ThioRedoxin-like.  
DR InterPro; IPR012335; ThioRedoxin-fold.  
DR Pfam; PF00085; ThioRedoxin_1.  
DR PRINTS; PR00421; THIOREDOXIN.  
DR TIGRPFAM; TIGR01068; ThioRedoxin; 1.  
DR PROSITE; PS00194; THIOREDOXIN; 1.  
KM Electron transport; Redox-active center; Transport.  
FT DISULFID 33 36 Redox-active (By similarity).  
FT NON_TER 91 91  
SQ SEQUENCE 91 AA; 10209 MW; 385DC641F42585D4 CRC64;  
  
Query Match 100.0%; Score 47; DB 1; Length 91;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WCGPCK 6  
Db 32 WCGPCK 37  
  
RESULT 7  
Q4XKV3 PLACH PRELIMINARY; PRT; 95 AA.  
ID Q4XKV3 PLACH PRELIMINARY;  
AC Q4XKV3;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DE ThioRedoxin, putative (Fragment).  
GN ORFNames=PC30021.00.0;  
OS Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OC NCBI_TaxID=5823;  
OX NCBI_TaxID=5823;  
RN NUCLEOTIDE SEQUENCE.  
RP Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAJ01005024; CAH82459.1; -; Genomic_DNA.  
DR InterPro; IPR006663; ThioRed.  
DR InterPro; IPR006663; ThioRedox dom2.  
DR InterPro; IPR012336; ThioRedoxin-like.  
DR InterPro; IPR012335; ThioRedoxin-fold.  
DR Pfam; PF00085; ThioRedoxin_1.  
DR PRINTS; PR00421; THIOREDOXIN.  
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.  
KM Redox-active center.  
FT NON_TER 1 1  
SQ SEQUENCE 95 AA; 10666 MW; E144E16BA1980CEC CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 95;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WCGPCK 6  
Db 20 WCGPCK 25  
  
RESULT 8  
Q4Z518 PLABE PRELIMINARY; PRT; 96 AA.  
ID Q4Z518 PLABE PRELIMINARY;
```

```
AC Q4Z518;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE ThioRedoxin, putative (Fragment).  
GN ORFNames=PB000593.00.0;  
OS Plasmodium berghei.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI_TaxID=5821;  
RN NUCLEOTIDE SEQUENCE.  
RP Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,  
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,  
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,  
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,  
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,  
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;  
RT "A comprehensive survey of the Plasmodium life cycle by genomic,  
RT transcriptomic, and proteomic analyses.";  
RL Science 307:82-86(2005).  
CC -!- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; CAJ01000448; CAH94443.1; -; Genomic_DNA.  
DR InterPro; IPR006662; ThioRed.  
DR InterPro; IPR006663; ThioRedox dom2.  
DR InterPro; IPR012336; ThioRedoxin-like.  
DR InterPro; IPR012335; ThioRedoxin-fold.  
DR Pfam; PF00085; ThioRedoxin_1.  
DR PRINTS; PR00421; THIOREDOXIN.  
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN_1.  
KM Redox-active center.  
FT NON_TER 1 1  
SQ SEQUENCE 96 AA; 10769 MW; FC08612C6FECSAAB9 CRC64;  
  
Query Match 100.0%; Score 47; DB 2; Length 96;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 WCGPCK 6  
Db 21 WCGPCK 26  
  
RESULT 9  
Q5LB12 BACEN PRELIMINARY; PRT; 98 AA.  
ID Q5LB12 BACEN PRELIMINARY;  
AC Q5LB12;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE Putative thioRedoxin.  
GN OrderelocusNames=BF3015;  
OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).  
OC Bacteriia; Bacteroidetes; Bacteroidales; Bacteroidales;  
OC Bacteroidaceae; Bacteroides.  
OX NCBI_TaxID=272559;  
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RP PubMed=15746427; DOI=10.1126/science.1107008;  
RA Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,  
RA Abratt V., Leonard N., Poxton I., Duerden B., Harris B., Quail M.A.,  
RA Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,  
RA Line A., Lord A., Nopbertczak H., Ormond D., Price C.,  
RA Rabinovitch E., Woodward J., Barrell B.G., Parkhill J.;  
RT "Extensive DNA inversions in the B. fragilis genome control variable  
RT gene expression.";  
RL Science 307:1463-1465(2005).  
DR EMBL; CR626927; CAH08710.1; -; Genomic_DNA.  
DR InterPro; IPR006662; ThioRed.  
DR InterPro; IPR006663; ThioRedox dom2.  
DR InterPro; IPR005746; ThioRedoxin.  
DR InterPro; IPR012336; ThioRedoxin-like.
```



```

DR InterPro; IPR012335; Thioresdoxin_fold.
DR Pfam; PF00085; Thioresdoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioresdoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 10
O64RG1 BACFR PRELIMINARY; PRT; 98 AA.
ID O64RG1_
AC O64RG1_
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DE Thioresdoxin.
DR OrderedLocusNames=BF3175;
OS Bacteroides fragilis;
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=817;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=YCH46;
RX PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA Kunihara S., Hattori M., Hayashi T., Ohnishi Y.;
RA "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT inversions regulating cell surface adaptation.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
DR EMBL; AP006841; BAD49920.1; -; Genomic_DNA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioresdoxin.
DR InterPro; IPR005746; Thioresdoxin_dom2.
DR InterPro; IPR005746; Thioresdoxin.
DR InterPro; IPR012336; Thioresdoxin-like.
DR InterPro; IPR012335; Thioresdoxin.
DR Pfam; PF00085; Thioresdoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioresdoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 98 AA; 11253 MW; FA22303A85FC04D7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 11
O8AB91 BACTN PRELIMINARY; PRT; 99 AA.
ID O8AB91_
AC O8AB91_
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DE Thioresdoxin C-2.
DR OrderedLocusNames=BT0219;
OS Bacteroides thetaiotaomicron.

```

```

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016926; AAO75326.1; -; Genomic_DNA.
DR HSSP; P80579; 1NM2.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR006662; Thioresdoxin.
DR InterPro; IPR005746; Thioresdoxin.
DR Pfam; PF00085; Thioresdoxin; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioresdoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
SQ SEQUENCE 99 AA; 11344 MW; 2037C6E75986C413 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 22 WCGPCK 27

RESULT 12
THIO MYCGA STANDARD; PRT; 100 AA.
ID THIO MYCGA
AC Q9REP9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioresdoxin (Trx).
GN Name=trx; Synonyms=trx; OrderedLocusNames=MYCGA6330;
GN ORFNames=MGA_0452;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A5969var.B;
RX MEDLINE=21956528; PubMed=11959450;
RA Skamrov A.V., Feoktistova E.S., Gol'dman M.A., Biblaevilli R.S.;
RT "Mycoplasma gallisepticum rpoA gene cluster.";
RL FEMS Microbiol. Lett. 208:281-285(2002).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=R(low);
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (by
CC similarity).
CC -!- SIMILARITY: Belongs to the thioresdoxin family.
CC -!- SIMILARITY: Contains 1 thioresdoxin domain.

```

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC -----
CC EMBL; J35043; AAF19044.1; -; Genomic DNA.
CC EMBL; AE016969; AAP56983.1; ALT_INIT; Genomic DNA.
CC HSSP; P80579; 1QW.
CC InterPro; IPR006662; ThioRed.
CC InterPro; IPR005746; ThioRedox dom2.
CC InterPro; IPR012336; ThioRedoxin.
CC InterPro; IPR012335; ThioRedoxin_1like.
CC InterPro; IPR011594; ThioRedoxin_fold.
CC Pfam; PF00085; ThioRedoxin_1like.
CC PRINTS; PR00421; THIOREDOXIN.
CC PRODOM; PD003679; ThioRedoxin_1like; 1.
CC TIGR; TIGR01068; ThioRedoxin; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
CC DISULFID 29 32 Redox-active (By similarity).
CC CONFLICT 15 15 S -> T (in Ref. 1).
CC CONFLICT 74 74 V -> I (in Ref. 1).
CC CONFLICT 86 86 R -> I (in Ref. 1).
CC FT SEQUENCE 100 AA; 11549 MW; B2A8ADAC82BA3968 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|
|
|
|
|
DB 28 WCGPCK 33

RESULT 13

QJUN64 MYCGA PRELIMINARY; PRT; 100 AA.

AC QJUN64;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-FAR-2004 (TREMBlrel. 26, Last annotation update)

DE ThioRedoxin.

DE Name=trx I;

OS Mycoplasma gallisepticum.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

OC NCBI_Taxid=2096;

DR GO; GO:0006118; F:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedox dom2.
DR InterPro; IPR012336; ThioRedoxin.
DR InterPro; IPR012335; ThioRedoxin_1like.
DR InterPro; IPR011594; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin_1like.
DR PRINTS; PR00421; THIOREDOXIN.
DR PRODOM; PD003679; ThioRedoxin_1like; 1.
DR TIGR; TIGR01068; ThioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR SEQUENCE 100 AA; 11577 MW; C2DFB426DBF3C8 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|
|
|
|
|
DB 28 WCGPCK 33

RESULT 14

THIO1 CHLITE STANDARD; PRT; 101 AA.

AC 08KEA4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 13-SEP-2003 (Rel. 48, Last annotation update)

DE ThioRedoxin 1 (Trx-1).

GN Name=trxl; OrderedLocustNames=CT0785;

OS Chlorobium tepidum.

OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;

OC Chlorobaculum.

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

OC NCBI_Taxid=1097;

```

DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 25 Redox-active (By similarity).
SQ SEQUENCE 101 AA; 11247 MW; BA78E511900B754 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 101;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 24 WCGPCK 29

RESULT 15
06KIE7 MYCMO
ID 06KIE7 MYCMO PRELIMINARY; PRT; 101 AA.
AC 06KIE7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Thioedoxin.
GN Name=trxA; OrderedLocustNames=MMOB1430;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=21118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Strange-Thomann N., Smith C., Decaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nussbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RT Genome Res. 14:1447-1461(2004).
DR EMBL; AE017337; AAT27629.1; -; Genomic_DNA.
DR HSSP; P10599; 1AUC.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR006663; Thioedox.
DR InterPro; IPR012336; Thioedoxin-like.
DR InterPro; IPR012335; Thioedoxin_fold.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome.
SQ SEQUENCE 101 AA; 11700 MW; 8D3C45CCB4CAGFA4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 101;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 28 WCGPCK 33

RESULT 16
THIO_CHLVCV
ID THIO_CHLVCV STANDARD; PRT; 102 AA.
AC P52327;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; Synonyms=trix; OrderedLocustNames=CCA00080;
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83357;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC STRAIN=GPIC;
RX MEDLINE=97090413; PubMed=8936321;
RA Roddy D.D., Chesebro B.B., Heinzen R.A., Hackett T.;
RT "A 28 kDa major immunogen of Chlamydia psittaci shares identity with
RT Mip proteins of Legionella spp. and Chlamydia trachomatis-cloning and
RT characterization of the C. psittaci mip-like gene.";
RL Microbiology 142:945-953(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=GPIC;
RX MEDLINE=22569155; PubMed=12682364; DOI=10.1093/nar/gkg321;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J.F., Holtzapple E.K., Khouri H.M., Fedorova N.B.,
RA White H.A., Umayam L.A., Haft D.H., Peterson J.D., Beanan M.J.,
RA Carey O., Salzberg S.L., Heia R.-C., McClarty G., Rank R.G.,
RA Bavoil P.M., Frazer C.M.;
RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiales."
RL Nucleic Acids Res. 31:2134-2147(2003).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -!- SIMILARITY: Belongs to the thioedoxin family.
CC -!- SIMILARITY: Contains 1 thioedoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; L39892; AAB41348.1; -; Genomic_DNA.
DR EMBL; AE016994; AAP04832.1; -; Genomic_DNA.
DR HSSP; P80579; 1QW.
DR TIGR; CCA00080; -.
DR InterPro; IPR006662; Thioed.
DR InterPro; IPR006663; Thioedox.
DR InterPro; IPR005746; Thioedoxin.
DR InterPro; IPR012336; Thioedoxin-like.
DR InterPro; IPR012335; Thioedoxin_fold.
DR Pfam; PF00085; Thioedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfam; TIGR01068; thioedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 28 Redox-active (By similarity).
SQ SEQUENCE 102 AA; 11159 MW; F1B57486973A6ED4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 27 WCGPCK 32

RESULT 17
THIO_CHLVCV
ID THIO_CHLVCV STANDARD; PRT; 102 AA.
AC O991K3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioedoxin (TRX).
GN Name=trxA; OrderedLocustNames=TC0826;
OS Chlamydomonas reinhardtii.
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83360;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Mopn / N199;

```

```

RX MEDLINE=20150255; PubMed=10684935; DOI=10.1093/nar/28.6.1397;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heideberg J.F.,
RA White O., Hickey E.K., Peterson J.D., Uterback T.R., Berry K.J.,
RA Bass S., Linher K.D., Weidman J.F., Knouri H.M., Craven B., Bowman C.,
RA McDouan R.J., Gwin M.L., Nelson W.C., Deboy R.T., Kolonay J.F.,
RA McClary G., Salzberg S.L., Eisen J.A., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MOpn and Chlamydia
RT pneumoniae AR39."
RU Nucleic Acids Res. 28:1397-1406(2000).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -----
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE002349; AAF39627.1; -; Genomic_DNA.
CC PIR: C81660; C81660.
CC HSSP: P80579; 1QW.
CC TIGR: TC0826; -.
CC InterPro: IPR006662; Thiored.
CC InterPro: IPR006663; Thioredox dom2.
CC InterPro: IPR005746; Thioredoxin.
CC InterPro: IPR012336; Thioredoxin-like.
CC InterPro: IPR012335; Thioredoxin_fold.
CC Pfam: PF00085; Thioredoxin_1.
CC PRINTS: PR00421; THIOREDOXIN.
CC TIGRFAMs: TIGR01068; thioredoxin; 1.
CC PROSITE: PS00194; THIOREDOXIN; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
CC DISULFID 28 31 Redox-active (By similarity).
CC FT SEQUENCE 102 AA; 1147 MW; C171B646D393428C CRC64;
SQ

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 18
THIO_CHLTR STANDARD; PRT; 102 AA.
AC 084544;
ID THIO_CHLTR
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Thioredoxin (TRX).
GN Name:trx; OrderedLocustNames=CT539;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=UW-3/Cx;
RX MEDLINE=99000809; PubMed=9784136; DOI=10.1126/science.282.5389.754;
RA Stephens R.S., Kaiman S., Lamell C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.F., Ollinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -----
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----

```

```

CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AE001324; AAC68141.1; -; Genomic_DNA.
CC PIR: B71503; B71503.
CC HSSP: P80579; 1QW.
CC PHCI-2DPAGE; 084544; -.
CC InterPro: IPR006662; Thiored.
CC InterPro: IPR006663; Thioredox dom2.
CC InterPro: IPR005746; Thioredoxin.
CC InterPro: IPR012336; Thioredoxin-like.
CC InterPro: IPR012335; Thioredoxin_fold.
CC Pfam: PF00085; Thioredoxin_1.
CC PRINTS: PR00421; THIOREDOXIN.
CC TIGRFAMs: TIGR01068; thioredoxin; 1.
CC PROSITE: PS00194; THIOREDOXIN; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
CC DISULFID 28 31 Redox-active (By similarity).
CC FT SEQUENCE 102 AA; 1197 MW; 8FAE022A5C980BE1 CRC64;
SQ

Query Match 100.0%; Score 47; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 19
THIO_MYCGE STANDARD; PRT; 102 AA.
AC P47370; Q49453;
ID THIO_MYCGE
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Thioredoxin (Trx).
GN Name:trx; Synonyms=trx; OrderedLocustNames=MG124;
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_Taxid=2097;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G.G., Kelley J.M.,
RA Eichmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.W., Phillips C.A., Merrick J.N.,
RA Tomb J.-F., Dougherty B.A., Bock K.F., Hu P.-C., Luster T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-21.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bock K.F., Hutchison C.A. III,
RA "A survey of the Mycoplasma genitalium genome by using random
RT sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----

```

```
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U39693; AAC1342.1; -; Genomic DNA.
DR EMBL; U01796; AAD12321.1; ALT_INIT; Genomic DNA.
DR PIR; G64213; G64213.
DR HSSP; P07591; 1FB6.
DR TIGR; MG124; -.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 30 33 Asp Arg; FC08F02C4170EA2D CRC64;
SQ SEQUENCE 102 AA; 11498 MW; FC08F02C4170EA2D CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 20
THIO_MYCPN STANDARD; PRT; 102 AA.
ID THIO_MYCPN
AC P75512;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trx; Synonyms=trx; OrderedLocustNames=MEN263; ORFNames=MP570;
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97346047; PubMed=9202470;
RA Ben-Menachem G., Himmelfeich R., Hermann R., Aharonowitz Y.,
RA Rotem S.;
RT "The thioRedoxin reductase system of mycoplasmae";
RN Microbiology 143:1933-1940(1997).
[2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelfeich R., Hilbert H., Plegens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae";
RN Nucleic Acids Res. 24:4420-4449(1996).
CC -!- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -!- SIMILARITY: Belongs to the thioRedoxin family.
CC -!- SIMILARITY: Contains 1 thioRedoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
```

```
CC removed.
CC -----
DR EMBL; U51987; AAC45450.1; -; Genomic DNA.
DR EMBL; AE000056; AAB96218.1; -; Genomic DNA.
DR PIR; S73896; S73896.
DR HSSP; P23400; 1DBY.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 30 33 Asp Arg; 0D17B97E976FC144 CRC64;
SQ SEQUENCE 102 AA; 11215 MW; 0D17B97E976FC144 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 21
THIO_SCHPO STANDARD; PRT; 102 AA.
ID THIO_SCHPO
AC O14463; PS8265; Q9UTS9;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TR).
GN Name=trx1; Synonyms=trx2; ORFNames=SPAC7D4_07C;
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21167391; PubMed=11267679; DOI=10.1016/S0167-4781(01)00176-2;
RA Cho Y.-W., Shin Y.H., Kim Y.-T., Kim H.-G., Lee Y.-J., Park E.-H.,
RA Fuchs J.A., Lim C.-U.;
RT "Characterization and regulation of Schizosaccharomyces pombe gene
RT encoding thioRedoxin";
RN Biochim. Biophys. Acta 1518:194-199(2001).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=972;
RA Lenaers G., Perret E., Bonin O., Picard A., Caput D.;
RT Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M.H., Lyne R., Stewart A.,
RA Sgourou J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham C.M.,
RA Gentles S., Goble A., Hamlin N., Harris D.B., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
RA James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J.R., Volkart G., Aert R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
```

RA Gabel C., Fuchs M., Duesterhoeft A., Fritz C., Holzer E., Moestl D.,
 RA Hilbert H., Borzym K., Langer I., Beck A., Lehmach H., Reinhardt R.,
 RA Pohl T.M., Egger P., Zimmermann W., Wedler H., Wambutt R., Punnett B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelure V., Mottier S.,
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
 RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Nature 415:871-880(2002).
 CC -I- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -I- SIMILARITY: Belongs to the thioredoxin family.
 CC -I- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF251279, AAF76881.1; -, Genomic_DNA.
 CC EMBL, AF192765, AAF05765.1; -, mRNA.
 CC EMBL, AJ003819, CAA06033.1; -, mRNA.
 CC EMBL, Z99532, CAB16724.1; -, Genomic_DNA.
 CC PIR, T39085, T39085.
 CC HSP, P80028, IEP7.
 CC DR GeneDB_Spmbe; SPAC7D4.07c; -.
 CC DR GO; GO:0005737; C:cyclopasm; TAS.
 CC DR GO; GO:000302; P:response to reactive oxygen species; IDA.
 CC DR InterPro: IPR006662; Thiored.
 CC DR InterPro: IPR006663; Thioredox_dom2.
 CC DR InterPro: IPR005746; Thioredoxin.
 CC DR InterPro: IPR012336; Thioredoxin-like.
 CC DR Pfam; PF00085; Thioredoxin_fold.
 CC DR PRINTS; PR00421; THIOREDOXIN.
 CC DR TIGRfams; TIGR01068; thioredoxin; 1.
 CC DR PROSITE; PS00194; THIOREDOXIN; 1.
 CC KW Complete proteome; Electron transport; Redox-active center; Transport.
 CC FT INIT MET 0 By similarity.
 CC FT ACT SITE 29 29 Nucleophile (By similarity).
 CC FT ACT SITE 32 32 Nucleophile (By similarity).
 CC FT SITE 23 23 Deprotonates C-terminal active site Cys
 CC FT SITE 30 30 (By similarity).
 CC FT SITE 31 31 Contributes to redox potential value (By
 CC FT SITE 31 31 similarity).
 CC FT DISULFID 29 32 Redox-active (By similarity).
 CC FT CONFLICT 96 101 ASIKAN -> VRUNRS (in Ref. 1; AAF05765).
 CC SQ SEQUENCE 102 AA; 11166 MW; 7069F4ACDAC34595 CRC64;
 CC
 CC Query Match 100.0%; Score 47; DB 1; Length 102;
 CC Best Local Similarity 100.0%; Pred. No. 2.4;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 WCGPCK 6
 CC DB 28 WCGPCK 33
 CC
 CC RESULT 22
 CC TRX1 YEAST STANDARD; PRT; 102 AA.
 CC AC P22217;
 CC DT 01-AUG-1991 (Rel. 19, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 10-MAY-2005 (Rel. 47, Last annotation update)
 CC DE Thioredoxin I (TR-1) (Thioredoxin 2).

GN Name=TRX1; Synonyms=TRX2; OrderedLocusNames=YLR043C;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OK NCBI_TaxId=4932;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=91107668; PubMed=1988444;
 RA Gan Z.-R.;
 RT "Yeast thioredoxin genes";
 RL J. Biol. Chem. 266:1692-1696 (1991).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RP MEDLINE=91225027; PubMed=2026619;
 RA Muller E.G.D.;
 RT "Thioredoxin deficiency in yeast prolongs S phase and shortens the G1
 RT interval of the cell cycle";
 RL J. Biol. Chem. 266:9194-9202 (1991).
 RN (3)
 RP NUCLEOTIDE SEQUENCE.
 RP PubMed=1561834;
 RA Muller E.G.D.;
 RT "Thioredoxin genes in *Saccharomyces cerevisiae*: map positions of TRX1
 RT and TRX2";
 RL Yeast 8:117-120 (1992).
 RN (4)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313267; PubMed=9169871;
 RA Johnston M., Hillier L.W., Riles L., Albermann K., Andre B.,
 RA Ansorge W., Benes V., Brueckner M., Delius H., Dubois E.,
 RA Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U.,
 RA Heumann K., Heuss-Neltzel D., Hilbert H., Hliger F., Kleine K.,
 RA Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T.,
 RA Moestl D., Mueller-Auer S., Nentwich U., Obermayer B., Piravandi E.,
 RA Pohl T.M., Portetelle D., Purnelle B., Reckmann S., Rieger M.,
 RA Rinke M., Rose M., Scharfe M., Scherens B., Scholler F., Schwager C.,
 RA Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M.,
 RA Verhaesselt P., Viereendeels F., Voet M., Volckaert G., Voss H.,
 RA Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A.,
 RA Hani U., Hobeisel J.D.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XII";
 RL Nature 387:87-90 (1997).
 RN (5)
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=S288C;
 RA Marsischky G., Rolfs A., Richardson A., Kane M., Bagui M., Taycher E.,
 RA Hu Y., Vandenberg F., Weger J., Kramer U., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzalez L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Labaer J.;
 RT "Creation of the YFLX clone resource: cloning of *Saccharomyces*
 RT cerevisiae ORFs in the Gateway recombinational cloning system";
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBS databases.
 RN (6)
 RP PROTEIN SEQUENCE OF 1-12, AND TSA1 DEPENDENCE ON THIOREDOXIN.
 RC STRAIN=ATCC 200358 / YNN 295;
 RX MEDLINE=95050519; PubMed=7961686;
 RA Chae H.Z., Chung S.J., Rhee S.G.;
 RT "Thioredoxin-dependent peroxidase reductase from yeast";
 RL J. Biol. Chem. 269:27670-27678 (1994).
 RN (7)
 RP PROTEIN SEQUENCE OF 25-33.
 RX MEDLINE=72104597; PubMed=4333602;
 RA Hall D.E., Baldesten A., Holmgren A., Reichard P.;
 RT "The covalently-bound flavin of hepatic monomeric oxidase. 2.
 RT Identification and properties of cysteinyl riboflavin";
 RL Eur. J. Biochem. 24:328-335 (1971).
 RN (8)
 RP FUNCTION, AND SULFATE ASSIMILATION AND METHIONINE METABOLISM.
 RX PubMed=3060034; DOI=10.1007/BF00408300;
 RA Schwenn J.D., Krone F.A., Hismann K.;
 RT "Yeast PAPS reductase: properties and requirements of the purified

RT enzyme.";
 RL Arch. Microbiol. 150:313-319 (1988).
 RP [19]
 RA FUNCTION, AND LMA1 COMPLEX.
 RX PubMed=9015301; DOI=10.1083/jcb.136.2.299;
 RA Xu Z., Mayer A., Muller E.G.D., Wickner W.;
 RT "A heterodimer of thioredoxin and I(B)2 cooperates with Sec18p (NSF)
 RL to promote yeast vacuole inheritance.";
 RL J. Cell Biol. 136:299-306 (1997).
 RN [10]
 RP FUNCTION, AND INTERACTION WITH SEC18.
 RX PubMed=9657146; DOI=10.1016/S0092-8674(00)81457-9;
 RA Xu Z., Sato K., Wickner W.;
 RT "LMA1 binds to vacuoles at Sec18p (NSF), transfers upon ATP hydrolysis
 RL to a t-SNARE (Vam3p) complex, and is released during fusion.";
 RL Cell 93:1125-1134 (1998).
 RN [11]
 RP FUNCTION, AND DOTS AND TSA2 DEPENDENCE ON THIOREDOXIN.
 RX PubMed=10681558; DOI=10.1074/jbc.275.8.5723;
 RA Park S.G., Cha M.K., Jeong W., Kim I.-H.;
 RT "Distinct physiological functions of thiol peroxidase isoenzymes in
 RL Saccharomyces cerevisiae.";
 RL J. Biol. Chem. 275:5723-5732 (2000).
 RN [12]
 RP FUNCTION, AND REDUCTION OF AHP1.
 RX MEDLINE=99143107; PubMed=9986867; DOI=10.1074/jbc.274.8.4537;
 RA Lee J., Spector D., Godon C., Labarre J., Toledano M.B.;
 RT "A new antioxidant with alkyl hydroperoxide defense properties in
 RL yeast.";
 RL J. Biol. Chem. 274:4537-4544 (1999).
 RN [13]
 RP FUNCTION, AND PROTECTION AGAINST REDUCING STRESS.
 RX PubMed=12410842;
 RA Trotter E.W., Grant C.M.;
 RT "Thioredoxins are required for protection against a reductive stress
 RL in the yeast Saccharomyces cerevisiae.";
 RL Mol. Microbiol. 46:869-878 (2002).
 RN [14]
 RP FUNCTION, AND REGULATION OF HVR1/GPX3.
 RX PubMed=12437921; DOI=10.1016/S0092-8674(02)01048-6;
 RA Delaney A., Pflieger D., Barriault M.-B., Vinh J., Toledano M.B.;
 RT "A thiol peroxidase is an H2O2 receptor and redox-transducer in gene
 RL activation.";
 RL Cell 111:471-481 (2002).
 RN [15]
 RP REVIEW, AND OXIDATIVE STRESS.
 RX PubMed=11018134; DOI=10.1146/annurev.micro.54.1.439;
 RA Carmel-Harel O., Storz G.;
 RT "Roles of the glutathione- and thioredoxin-dependent reduction systems
 RL in the Escherichia coli and Saccharomyces cerevisiae responses to
 RL oxidative stress.";
 RL Annu. Rev. Microbiol. 54:439-461 (2000).
 RN [16]
 RP REVIEW, AND CELLULAR REDOX FUNCTIONS.
 RX PubMed=11169096;
 RA Grant C.M.;
 RT "Role of the glutathione/glutaredoxin and thioredoxin systems in yeast
 RL growth and response to stress conditions.";
 RL Mol. Microbiol. 39:533-541 (2001).
 RN [17]
 RP REVIEW, AND VESICLE FUSION.
 RX PubMed=12914955; DOI=10.1016/S0167-4889(03)00086-7;
 RA Elazar Z., Scheetz-Shouval R., Shorer H.;
 RT "Involvement of LMA1 and GATE-16 family members in intracellular
 RL membrane dynamics.";
 RL Biochim. Biophys. Acta 1641:145-156 (2003).
 RN [18]
 RP LEVEL OF PROTEIN EXPRESSION.
 RX PubMed=14562106; DOI=10.1038/nature02046;
 RA Dehaemagham S., Huu W.-K., Bower K., Howson R.W., Belle A.,
 RA Depource N., O'Shea E.K., Weissman J.S.;
 RT "Global analysis of protein expression in yeast.";
 RT Nature 425:737-741 (2003).

RN [19]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22923954; PubMed=14562095; DOI=10.1038/nature02026;
 RA Huu W.-K., Falvo J.V., Gerke L.C., Carroll A.S., Howson R.W.,
 RA Weissman J.S., O'Shea E.K.;
 RT "Global analysis of protein localization in budding yeast.";
 RL Nature 425:686-691 (2003).
 RN [20]
 RP REDOX-ACTIVE DISULFIDE BOND.
 RX PubMed=4945270;
 RA Hall D.E., Baldesten A., Holmgren A., Reichard P.;
 RT "Yeast thioredoxin. Amino-acid sequence around the active-center
 RL disulfide of thioredoxin I and II.";
 RL Eur. J. Biochem. 23:328-335 (1971).
 CC -1- FUNCTION: Participates as a hydrogen donor in redox reactions
 CC through the reversible oxidation of its active center dithiol to a
 CC disulfide, accompanied by the transfer of 2 electrons and 2
 CC protons. It is involved in many cellular processes, including
 CC deoxyribonucleotide synthesis, repair of oxidatively damaged
 CC proteins, protein folding, sulfur metabolism, and redox
 CC homeostasis. Thioredoxin-dependent enzymes include
 CC phosphoadenosine-phosphosulfate reductase MPT16, alkyl-
 CC hydroperoxide reductase DOTS, thioredoxin peroxidases TSA1 and
 CC TSA2, alkyl hydroperoxide reductase AHP1, and peroxiredoxin HVR1.
 CC Thioredoxin is also involved in protection against reducing
 CC stress. As part of the LMA1 complex, it is involved in the
 CC facilitation of vesicle fusion such as homotypic vacuole and ER-
 CC derived COP1 vesicle fusion with the Golgi. This activity does
 CC not require the redox mechanism.
 CC SUBUNIT: Part of the heterodimeric LMA1 complex together with the
 CC proteinase inhibitor PB12. LMA1 binds to the ATPase SEC18.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic, Golgi membrane associated, and
 CC nuclear.
 CC -1- PM: Reversible disulfide bond formation between Cys-29 and Cys-
 CC 32, reverted by thioredoxin reductase TRX1 using NADPH as hydrogen
 CC donor.
 CC -1- MISCELLANEOUS: Present with 8579 molecules/cell.
 CC -1- MISCELLANEOUS: Yeast has two cytoplasmic thioredoxins, TRX1 and
 CC TRX2, and one mitochondrial, TRX3.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Query Match 100.0%; Score 47; DB 1; Length 102;
 CC Best Local Similarity 100.0%; Pred. No. 2.4;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 WGPCK 6
 CC |||||
 CC Db 28 WGPCK 33
 CC
 CC RESULT 23
 CC Q5L731 CHLAB PRELIMINARY; PRT; 102 AA.
 CC ID Q5L731
 CC AC Q5L731
 CC DT 01-FEB-2005 (TRENBLREL. 29, Created)
 CC DT 01-FEB-2005 (TRENBLREL. 29, Last sequence update)
 CC DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
 CC DE Putative thioredoxin.
 CC GN Name=trxa; OrderedLocustNames=CAB082;
 CC OS Chlamydomonas abortus.
 CC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonada.
 CC NCBI_Taxid=83555;
 CC NCBI_Taxid=83555;
 CC RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 CC STRAIN=S26/3;

```

RX PubMed=15837807; DOI=10.1101/gr.3684805;
RA Thomson N.R., Yeates C., Bell K., Holden M.T.G., Bentley S.D.,
RA Livingstone M., Cerdano-Tarraga A.-M., Harris B., Doggett J.,
RA Ormond D., Mungall K., Clarke K., Fellwell T., Hance Z., Sanders M.,
RA Quail M.A., Price C., Barrell B.G., Parkhill J., Longbottom D.,
RT "The Chlamydomonas reinhardtii genome sequence reveals an array of
RT variable proteins that contribute to interspecies variation."
RL Genome Res. 15:629-640(2005).
DR EMBL; CR48038; CAH63539.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 102 AA; 10989 MW; DA736F6B8223C35B CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 27 WCGPCK 32

RESULT 24
Q6F1T8 MESFL PRELIMINARY; PRT; 102 AA.
ID Q6F1T8 MESFL PRELIMINARY; PRT; 102 AA.
AC Q6F1T8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Thioredoxin.
GN OrderedLocNames=Mt1178;
OS Mesoplasma florum (Acholeplasma florum).
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Entomoplasmataceae; Mesoplasma.
OX NCBI_Taxid=2151;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=11 / ATCC 33453;
RA Birren B.W., Stange-Thomann N., Hafez N., Decaprio D., Fisher S.,
RA Butler J., Elkins T., Kodira C.D., Major J., Wang S., Nicol R.,
RA Nisham C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO17263; MAT75535.1; -; Genomic_DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; Thiorredoxin.
DR InterPro; IPR005746; Thiorredoxin.
DR InterPro; IPR006663; Thiorredoxin_dom2.
DR Pfam; PF00085; Thiorredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thiorredoxin; 1.
KW Complete proteome.
SQ SEQUENCE 102 AA; 11625 MW; 741401233DC8781 CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 25
Q6MUG0 MYCMS PRELIMINARY; PRT; 102 AA.
ID Q6MUG0 MYCMS PRELIMINARY; PRT; 102 AA.
AC Q6MUG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE THIOREDOXIN.
GN Name=trxA; OrderedLocNames=MSC_0072;
OS Mycoplasma mycoides (subsp. mycoides SC).

```

```

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_Taxid=44101;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RGL;
RX PubMed=14762060; DOI=10.1101/gr.1673304;
RA Westberg U., Persson A., Holmberg A., Gessmann A., Lundberg J.,
RA Johansson K.-E., Petersson B., Uhlen M.;
RT "The genome sequence of Mycoplasma mycoides subsp. mycoides SC type
RT strain PGLT, the causative agent of contagious bovine pleuropneumonia
RT (CBPP) ";
RL Genome Res. 14:221-227(2004).
DR EMBL; BX842642; CAE76724.1; -; Genomic_DNA.
DR HSSP; P10599; 1AUC.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; Thiorredoxin.
DR InterPro; IPR005746; Thiorredoxin.
DR InterPro; IPR006663; Thiorredoxin_dom2.
DR Pfam; PF00085; Thiorredoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thiorredoxin; 1.
KW Complete proteome.
SQ SEQUENCE 102 AA; 11576 MW; C6D7A9C9AAB5083D CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 102;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 26
THIO_BACSU
ID THIO_BACSU STANDARD; PRT; 103 AA.
AC P14949; O07960; Q45687;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Thioredoxin (TRX).
GN Name=trxA; Synonyms=trx; OrderedLocNames=BSU28500;
OS Bacteria; Firmicutes; Bacillales; Bacillus.
OX NCBI_Taxid=1423;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=168;
RA MEDLINE=97124191; PubMed=8969504;
RA Wipac A., Carter N., Brignell C.S., Guy J.B., Piper K., Sanders J.,
RA Emmerson P.T., Harwood C.R.;
RT "The dnaB-pheA (256 degrees-240 degrees) region of the Bacillus
RT subtilis chromosome containing genes responsible for stress responses,
RT the utilization of plant cell walls and primary metabolism."
RL Microbiology 142:3067-3078(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RX Kunet F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RX Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RX Borries R., Bourstier L., Brans A., Braun M., Brignell S.C., Bron S.,
RX Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,

```


RA Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Dentzot F., Devine K.M., Duesetoeft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Erington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Gaileron N.,
 RA Guim S.-Y., Glaser P., Goffeau A., Goldlighty E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holtsappel S., Hosono S., Hullo M.-F., Itaya M.,
 RA Jones L.-M., Joris B., Karama D., Kasahara Y., Klaett-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardin S., Lamber J.,
 RA Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Maue C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogilawa A., Oudega B.,
 RA Park S.-H., Parro V., Pohl T.M., Portetelle D., Portwollik S.,
 RA Prescott A.M., Prescan E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadate Y., Sato T., Scanlan E., Seelich S., Schroeder R.,
 RA Scotione F., Sekiguchi J., Sekowska A., Serot S.J., Serron P.,
 RA Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Takakoshi A., Tanaka T., Terpstra P.,
 RA Tomoni A., Tosato V., Uchiyama S., Vandenbol M., Vanlier F.,
 RA Vassarotti A., Viari A., Wandut R., Wedler E., Wedler H.,
 RA Welzenegger T., Winters P., Wipac A., Yamamoto H., Yamane K.,
 RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumbstein E.,
 RA Yoshikawa H., Danchin A.;
 RA "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT subtilis".
 RT Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 RN [4]
 RP PROTEIN SEQUENCE OF 1-14.
 RC STRAIN=168 / JH642;
 RX MEDLINE=96345629; PubMed=8755892;
 RT Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
 RL "Cold shock stress-induced proteins in *Bacillus subtilis*.";
 RL J. Bacteriol. 178:4611-4619(1996).
 RN [5]
 RP NUCLEOTIDE SEQUENCE OF 1-7.
 RC STRAIN=168;
 RL Riechardt S., Winkler A., Voelker U., Ernst H., Scharf C., Hecker M.;
 RL Submitted (NOV-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, J03294; AAA67315.1; -; Genomic DNA.
 DR EMBL, 275208; CAA9577.1; -; Genomic DNA.
 DR EMBL, 299118; CAA14810.1; -; Genomic DNA.
 DR EMBL, X79976; CAA56300.1; -; Genomic DNA.
 DR EMBL, X99275; CAA67667.1; -; Genomic DNA.
 DR PIR, B37192; B37192.
 DR HSP, P23400; IDB1.
 DR Subtilast; BG10348; trxa.
 DR InterPro; IPR006662; Thiored.
 DR InterPro; IPR006663; Thioredox dom2.
 DR InterPro; IPR005746; Thioredoxin.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin fold.
 DR InterPro; IPR011594; Thioredoxin-like.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR Prodom; PD003679; Thioredoxin-like; 1.
 DR TIGRfam; TIGR01068; thioredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Complete proteome; Direct protein sequencing; Electron transport;
 KW Redox-active center; Transport.

FT INIT MET 0 0
 FT DISTLFD 28 31 Redox-active.
 SQ SEQUENCE 103 AA; 11262 MW; 276B5B5D5B98F2D CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WGPCK 6
 Db 27 WGPCK 32
 RESULT 27
 TX2 YEAST
 ID TX2 YEAST STANDARD; PRT; 103 AA.
 AC P22803;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin II (TR-II) (Thioredoxin 1).
 GN Name=TX2; Synonyms=TRX1; OrderedLocNames=YGR209C; ORFNames=G7746;
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=91107668; PubMed=1988444;
 RA Gan Z.-R.;
 RT "Yeast thioredoxin genes.";
 RL J. Biol. Chem. 266:1692-1696(1991).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=91225027; PubMed=2026619;
 RA Muller E.G.D.;
 RT "Thioredoxin deficiency in yeast prolongs S phase and shortens the G1
 RT interval of the cell cycle.";
 RL J. Biol. Chem. 266:9194-9202(1991).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S288c / GRF88;
 RA Song J.M., Cheung E., Rabinowitz J.C.;
 RT "Analysis of the 15.6-kb fragment encompassing the ADE3 gene.";
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=S288c;
 RX MEDLINE=97060019; PubMed=8904340;
 RX DOI=10.1002/(SICI)1097-0061(19960315)12:3<273::AID-YEA898>3.3.CO;2-T;
 RA Guerreiro P., Barreiros T., Soares H., Cyrne L., Maia e Silva A.,
 RA Rodrigues-Pousada C.;
 RT "Sequencing of a 17.6 kb segment on the right arm of yeast chromosome
 RT VII reveals 12 ORFs, including CCT, ADE3 and TR-I genes, homologues of
 RT the yeast PMT and EFG genes, of the human and bacterial electron-
 RT transferring flavoproteins (beta-chain) and of the *Escherichia coli*
 RT phosphoserine phosphohydrolase, and five new ORFs.";
 RL Yeast 12:273-280(1996).
 RN [5]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
 RC MEDLINE=97313265; PubMed=9169869;
 RA Tetteil H., Agostoni-Carbone M.L., Albertmann K., Albers M.,
 RA Arroyo J., Backes U., Barreiros T., Berani I., Bjourson A.J.,
 RA Bruecker M., Brusch C.V., Carignani G., Castagnoli L., Cerdan E.,
 RA Clemente M.L., Coblenz A., Cogillevina M., Coissac E., Deleor E.,
 RA Del Bino S., Dellus H., Delneri D., de Wergifosse P., Dujon B.,
 RA Durand P., Entian K.-D., Eraso P., Escribano V., Fabiani L.,
 RA Fartman B., Feroli F., Feuermann M., Froncaldi L., Garcia-Gonzalez M.,
 RA Garcia-Saez M.I., Goffeau A., Guerreiro P., Hani J., Hansen M.,
 RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
 RA Indge K.J., James C.M., Kilma R., Koetter P., Kramer B., Kramer W.,
 RA Lauquin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
 RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,

RA Melchiorre P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
 RA Nawrocki A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
 RA Pauluzzi S., Plevani P., Portetelle D., Portillo P., Porter S.,
 RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
 RA Rodriguez-Ponsada C., Rodriguez-Belmonte E., Rodriguez-Torres A.M.,
 RA Rose M., Ruzi M., Saltoia M., Sanchez-Perez M., Schaefer B.,
 RA Schaefer M., Schaefer M., Schmidheini T., Schreier A., Stala J.,
 RA Souciet J.-L., Steensma H.Y., Talla E., Thierry A., Vandenhof M.,
 RA van der Aar O.J.M., Van Dyck L., Vanoni M., Verhasselt P., Voet M.,
 RA Volckaert G., Wandt R., Watson M.D., Weber N., Wedler E., Wedler H.,
 RA Wipfl F., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
 RA Zolner A., Kleine K.,
 RA "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome VII.",
 RL Nature 387:81-84(1997).
 [16]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RP STRAIN=S288c;
 RA Marischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
 RA Hu Y., Vanberg F., Weger J., Kramer J., Moreira D., Kelley F.,
 RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
 RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 RA Labaer J.,
 RT "Creation of the YLEX clone resource: cloning of *Saccharomyces*
 RT *cerevisiae* ORFs in the Gateway recombinational cloning system.",
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 [17]
 RP PROTEIN SEQUENCE OF 1-12, AND TSA1 DEPENDENCE ON THIOREDOXIN.
 RC STRAIN=ATCC 200358 / YNN 295;
 RA MEDLINE=95050519; PubMed=7961686;
 RX Chae H.Z., Chung S.J., Rhee S.G.,
 RT "Thioredoxin-dependent peroxide reductase from yeast.",
 RL J. Biol. Chem. 269:27670-27678(1994).
 [18]
 RP PROTEIN SEQUENCE OF 26-42.
 RX MEDLINE=72104597; PubMed=4333602;
 RA Hall D.E., Baldesten A., Holmgren A., Reichard P.,
 RT "The covalently-bound flavin of hepatic monooxygenase. 2.
 RT Identification and properties of cysteinyl riboflavin.",
 RL Eur. J. Biochem. 24:328-335(1971).
 [19]
 RP FUNCTION, AND SULFATE ASSIMILATION AND METHIONINE METABOLISM.
 RX PubMed=3060034; DOI=10.1007/BF00408300;
 RA Schwann J.D., Krone F.A., Huesmann K.,
 RT "Yeast PAPS reductase: properties and requirements of the purified
 RT enzyme.",
 RL Arch. Microbiol. 150:313-319(1998).
 [110]
 RP FUNCTION, AND LMA1 COMPLEX.
 RX PubMed=9015301; DOI=10.1083/jcb.136.2.299;
 RA Xu Z., Mayer A., Muller E.G.D., Wickner W.,
 RT "A heterodimer of thioredoxin and I(B)2 cooperates with Sec18p (NSF)
 RT to promote yeast vacuole inheritance.",
 RL J. Cell Biol. 136:299-306(1997).
 [111]
 RP FUNCTION, AND INTERACTION WITH SEC18.
 RX PubMed=9657146; DOI=10.1016/S0092-8674(00)81457-9;
 RA Xu Z., Sato K., Wickner W.,
 RT "LMA1 binds to vacuoles at Sec18p (NSF), transfers upon ATP hydrolysis
 RT to a c-SNARE (Vam3p) complex, and is released during fusion.",
 RL Cell 93:1123-1134(1998).
 [112]
 RP FUNCTION, AND DOTS AND TSA2 DEPENDENCE ON THIOREDOXIN.
 RX PubMed=1668158; DOI=10.1074/jbc.275.8.5723;
 RA Park S.G., Cha M.K., Jeong W., Kim I.-H.,
 RT "Distinct physiological functions of thiol peroxidase isoenzymes in
 RT *Saccharomyces cerevisiae*.",
 RL J. Biol. Chem. 275:5723-5732(2000).
 [113]
 RP FUNCTION, AND REDUCTION OF AHP1.
 RX MEDLINE=99143107; PubMed=9988687; DOI=10.1074/jbc.274.8.4537;
 RA Lee J., Spector D., Godon C., Labarre J., Tolédano M.B.,
 RT "A new antioxidant with alkyl hydroperoxide defense properties in
 RT yeast.",

RL J. Biol. Chem. 274:4537-4544(1999).
 [114]
 RP FUNCTION, AND REGULATION OF YAP1.
 RX PubMed=11013218; DOI=10.1093/emboj/19.19.5157;
 RA Delaunay A., Isnard A.D., Tolédano M.B.,
 RT "H2O2 sensing through oxidation of the Yap1 transcription factor.",
 RL EMBO J. 19:5157-5166(2000).
 [115]
 RP FUNCTION, AND REGULATION OF HYP1/GPX3.
 RX PubMed=12437921; DOI=10.1016/S0092-8674(02)01048-6;
 RA Delaunay A., Pflieger D., Barrault M.-B., Vinh J., Tolédano M.B.,
 RT "A thiol peroxidase is an H2O2 receptor and redox-transducer in gene
 RT activation.",
 RL Cell 111:471-481(2002).
 [116]
 RP FUNCTION, AND PROTECTION AGAINST REDUCING STRESS.
 RX PubMed=12410842;
 RA Trotter E.W., Grant C.M.,
 RT "Thioredoxins are required for protection against a reductive stress
 RT in the yeast *Saccharomyces cerevisiae*.",
 RL Mol. Microbiol. 46:869-878(2002).
 [117]
 RP REVIEW, AND OXIDATIVE STRESS.
 RX PubMed=11018134; DOI=10.1146/annurev.micro.54.1.439;
 RA Carmel-Harel O., Storz G.,
 RT "Roles of the glutathione- and thioredoxin-dependent reduction systems
 RT in the *Escherichia coli* and *Saccharomyces cerevisiae* responses to
 RT oxidative stress",
 RL Annu. Rev. Microbiol. 54:439-461(2000).
 [118]
 RP REVIEW, AND CELLULAR REDOX FUNCTIONS.
 RX PubMed=11169096;
 RA Grant C.M.,
 RT "Role of the glutathione/glutaredoxin and thioredoxin systems in yeast
 RT growth and response to stress conditions.",
 RL Mol. Microbiol. 39:533-541(2001).
 [119]
 RP REVIEW, AND VESICLE FUSION.
 RX PubMed=12914955; DOI=10.1016/S0167-4889(03)00086-7;
 RA Blazar Z., Schertz-Shouval R., Shore H.,
 RT "Involvement of LMA1 and GATE-16 family members in intracellular
 RT membrane dynamics.",
 RL Biochim. Biophys. Acta 1641:145-156(2003).
 [120]
 RP LEVEL OF PROTEIN EXPRESSION.
 RX PubMed=14562106; DOI=10.1038/nature02046;
 RA Ghaemmaghami S., Huh W.-K., Bower K., Howson R.W., Belle A.,
 RT Dephoure N., O'Shea E.K., Weissman J.S.,
 RT "Global analysis of protein expression in yeast.",
 RL Nature 425:737-741(2003).
 [121]
 RP SUBCELLULAR LOCATION.
 RX MEDLINE=22923954; PubMed=14562095; DOI=10.1038/nature02026;
 RA Huh W.-K., Falvo J.V., Gerke L.C., Carroll A.S., Howson R.W.,
 RA Weissman J.S., O'Shea E.K.,
 RT "Global analysis of protein localization in budding yeast.",
 RL Nature 425:686-691(2003).
 [122]
 RP REDOX-ACTIVE DISULFIDE BOND.
 RX PubMed=945270;
 RA Hall D.E., Baldesten A., Holmgren A., Reichard P.,
 RT "Yeast thioredoxin. Amino-acid sequence around the active-center
 RT disulfide of thioredoxin I and II.",
 RL Eur. J. Biochem. 23:328-335(1971).
 CC -1- FUNCTION: Participates as a hydrogen donor in redox reactions
 CC through the reversible oxidation of its active center dithiol to a
 CC disulfide, accompanied by the transfer of 2 electrons and 2
 CC protons. It is involved in many cellular processes, including
 CC deoxyribonucleotide synthesis, repair of oxidatively damaged

Query Match 100.0%; Score 47; DB 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 28
 075C00 ASHGO PRELIMINARY; PRT; 103 AA.

AC 075C00-
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE ACL131WD.
 GN Name=ACL131W;
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715; DOI=10.1126/science.1095781;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 Mohr C., Poehlmann R., Iuedi P., Choi S., Wing R.A., Flavier A.,
 Gaffney T.D., Philippsen P.;
 RA "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome";
 RL Science 304:304-307(2004).
 DR EMBL; AE016816; AAS51097.1; -; Genomic_DNA.
 DR HSSP; P10599; 1AUC.
 DR AGD; ACL131W; -.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Complete proteome.
 SQ SEQUENCE 103 AA; 11396 MW; 28B3A9A186540FE7 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 29
 06FND5 CANCA PRELIMINARY; PRT; 103 AA.

AC 06FND5;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Candida glabrata strain CBS138 chromosome K complete sequence.
 GN OrderedLocNames=CAGJ0008035;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mtosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5478;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2001 / CBS 138;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boitrame A., Boyer J., Catrolicco L., Confanioleri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
 RA Nicoud J.-M., Nikoleki M., Ozias S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).
 DR EMBL; CR380957; CAG61220.1; -; Genomic_DNA.
 DR GO; GO:0005489; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Complete proteome.
 SQ SEQUENCE 103 AA; 11171 MW; DIA6EBA8B487712 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 29 WCGPCK 34

RESULT 30
 06BUB0 DEBHA PRELIMINARY; PRT; 103 AA.

AC 06BUB0;
 DT 25-OCT-2004 (TRENBLrel. 28, Created)
 DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
 DE 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
 DE Similar to sp|P22217 Saccharomyces cerevisiae YLR043c TRX1 thioRedoxin
 DE 1.
 GN OrderedLocNames=DEBA0505126g;
 OS Debaryomyces hanseni (Yeast) (Torulaspora hanseni).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
 OX NCBI_TaxID=4959;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 36239 / CBS 767;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boitrame A., Boyer J., Catrolicco L., Confanioleri F., de Darvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
 RA Nicoud J.-M., Nikoleki M., Ozias S., Ozler-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpetti C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts";
 RL Nature 430:35-44(2004).

```

DR EMBL; CR382139; CAG90196.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF000085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome.
SQ SEQUENCE 103 AA; 11149 MW; 1F533CB671C532EC CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 31
OSACN1 CANAL PRELIMINARY; PRT; 103 AA.
ID OSACN1_
AC OSACN1_
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DE Potential thioRedoxin.
GN Name=TRX1; ORFNames=CaO19.7611;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Federspiel N.A., Chidana H., Dungan J., Kalman S.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AACQ01000032; BAL00485.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF000085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 103 AA; 11487 MW; 4B78100038A53620 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

```

```

Db 29 WCGPCK 34

RESULT 32
OSF4W8 FUSNV
ID F4W8 FUSNV PRELIMINARY; PRT; 103 AA.
AC F4W8;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE ThioRedoxin.
GN Name=FNW0931;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_Taxid=209882;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 49256;
RA Karpatal V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haseikorn R., Overbeek R., Kyrides N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABP01000093; EAA23714.1; -; Genomic_DNA.
DR HSP; P00274; IKB.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedox_dom2.
DR Pfam; PF000085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRFAMs; TIGR01068; thioRedoxin; 1.
SQ SEQUENCE 103 AA; 11369 MW; 4437B8AAD056D7C0 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 33
OSF1M1 LACAC
ID F1M1 LACAC PRELIMINARY; PRT; 103 AA.
AC F1M1;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE ThioRedoxin reductase.
GN Ordered locus Names=IBA0422;
OS Lactobacillus acidophilus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_Taxid=1579;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCFM;
RX PubMed=15671160; DOI=10.1073/pnas.0409186102;
RA Alterman E., Russell W.M., Azcarate-Peril M.A., Barrangou R.,
RA Buck B.L., McAnuliffe O., Souther N., Dobson A., Duong T., Callanan M.,
RA Lick S., Hamrick A., Cano R., Klaenhammer T.R.;
RT "Complete genome sequence of the probiotic lactic acid bacterium
RT Lactobacillus acidophilus NCFM";
RL Proc. Natl. Acad. Sci. U.S.A. 102:3906-3912(2005).
DR EMBL; CP000033; AAV42313.1; -; Genomic_DNA.

```

DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 KW SEQUENCE 103 AA; 11754 MW; F888C9923C13B9BE CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 34
 Q8RH23 FUSNN PRELIMINARY; PRT; 103 AA.

AC Q8RH23_01-UN-2002 (TREMBLrel. 21, Created)
 DT 01-UN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE ThioRedoxin.
 GN Ordered locus names=FNO093;
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
 CC Fusobacterium.
 NCBI_Taxid=76856;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=2186394; PubMed=11889109;
 RX DOI=10.1128/JB.184.7.2005-2018.2002;
 RA Kapteinaal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Gotsman E., Bernal A.,
 RA Larsen N., D'Souza M., Malunas T., Puech G., Haselkorn R.,
 RA Fomselein M., Kyzpides N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586."
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE009951; AML94306.1; -; Genomic_DNA.
 DR HSSP; P00274; 1T7P.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 DR Complete proteome.
 KW SEQUENCE 103 AA; 11342 MW; 27E003A221A4C780 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 35
 Q7AKU7 LACJO PRELIMINARY; PRT; 103 AA.

AC Q7AKU7_05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE ThioRedoxin.
 GN Ordered locus names=LJ0480;
 OS Lactobacillus johnsonii.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 CC Lactobacillus.
 NCBI_Taxid=33959;
 [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=NC 533;
 RX PubMed=14963040; DOI=10.1073/pnas.0307327101;
 RA Pidmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
 RA Pitter A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
 RA Mollet B., Mercier A., Klaenhammer T., Arigoni F., Scheil M.A.;
 RT "The genome sequence of the probiotic intestinal bacterium
 Lactobacillus johnsoni NC 533."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
 DR EMBL; AE017201; AAS08472.1; -; Genomic_DNA.
 DR HSSP; P10599; 1AUC.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; ThioRed.
 DR InterPro; IPR006663; ThioRedox_dom2.
 DR InterPro; IPR005746; ThioRedoxin.
 DR InterPro; IPR012336; ThioRedoxin-like.
 DR InterPro; IPR012335; ThioRedoxin_fold.
 DR Pfam; PF00085; ThioRedoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfams; TIGR01068; thioRedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome.
 KW SEQUENCE 103 AA; 11762 MW; B1FC16C916B944C3 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 Db 27 WCGPCK 32

RESULT 36
 THIO_BOVIN STANDARD; PRT; 104 AA.
 ID THIO_BOVIN_16-OCT-2001 (Rel. 40, Created)
 AC 097680;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE ThioRedoxin.
 GN Name=TXN;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 NCBI_Taxid=9913;
 [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC MEDLINE=20189621; PubMed=10727087;
 RX Terashima H., Gotoh S., Yagi K., Mizoguchi T.;
 RT "cDNA sequence of bovine thioRedoxin."
 RL DNA Seq. 10:331-333(1999).

-!- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC

```
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF104105; AAC83380.1; -, mRNA.
CC HSSP: P10599; 1ERT.
CC SMR: O97680; 1-104.
CC InterPro: IPR006662; Thiored.
CC InterPro: IPR006663; Thioredox dom2.
CC InterPro: IPR005746; Thioredoxin.
CC InterPro: IPR012336; Thioredoxin-like.
CC InterPro: IPR012335; Thioredoxin_fold.
CC Pfam: PF00085; Thioredoxin_1.
CC PRINTS: PR00421; THIOREDOXIN.
CC TIGRPFAM: TIGR01068; thioredoxin; 1.
CC PROSITE: PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INIT MET 0 By similarity.
CC ACT SITE 31 31 Nucleophile (By similarity).
CC ACT SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11681 MW; 506CFP696A208D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 37
THIO_CALJA STANDARD; PRT; 104 AA.
ID THIO_CALJA
AC O9BDJ3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin.
GN Name=TXN; Synonyms=TRX;
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;
OC Callitrichidae; Callitrichi.
OX NCBI_TaxID=9483;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=21576430; PubMed=11719593; DOI=10.1093/molenv/7.12.1159;
RA Lopata A., Sibson M.C., Sanders A.C., Bloomfield K.L., Gregory M.S.,
RA Trapani G.D., Perkins A.V., Tonnissen K.F., Clarke F.M.;
RA "Expression and localization of thioredoxin during early implantation
RT in the marmoset monkey.";
RT Mol. Hum. Reprod. 7:1159-1165(2001).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
```

```
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AF353204; AK30295.1; -, mRNA.
CC HSSP: P10599; 1ERT.
CC SMR: O9BDJ3; 1-104.
CC InterPro: IPR006662; Thiored.
CC InterPro: IPR006663; Thioredox dom2.
CC InterPro: IPR005746; Thioredoxin.
CC InterPro: IPR012336; Thioredoxin-like.
CC InterPro: IPR012335; Thioredoxin_fold.
CC Pfam: PF00085; Thioredoxin_1.
CC PRINTS: PR00421; THIOREDOXIN.
CC TIGRPFAM: TIGR01068; thioredoxin; 1.
CC PROSITE: PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC INIT MET 0 By similarity.
CC ACT SITE 31 31 Nucleophile (By similarity).
CC ACT SITE 34 34 Nucleophile (By similarity).
CC SITE 25 25 Deprotonates C-terminal active site Cys
CC (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11626 MW; 3E0F5243A04BB581 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 38
THIO_CHICK STANDARD; PRT; 104 AA.
ID THIO_CHICK
AC P08629;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin.
GN Name=TXN;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=88257080; PubMed=2838473;
RA Jones S.W., Lusk K.-C.;
RA "Isolation of a chicken thioredoxin cDNA clone. Thioredoxin mRNA is
RT differentially expressed in normal and Rous sarcoma virus-transformed
RT chicken embryo fibroblasts.";
RT J. Biol. Chem. 263:9607-9611(1988).
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
```

```

CC removed.
CC -----
CC EMBL: J03882; AAA49092.1; -, mRNA.
CC PIR: A30006; A30006.
CC HSSP: P10599; 1ERT.
CC SMR: P08629; 1-104.
CC DR Ensembl: ENSGALG00000015704; Gallus gallus.
CC DR InterPro: IPR006662; Thiorod.
CC DR InterPro: IPR006663; Thiorodox_dom2.
CC DR InterPro: IPR012336; Thiorodoxin-like.
CC DR InterPro: IPR012335; Thiorodoxin_fold.
CC DR Pfam: PF00085; Thiorodoxin_1.
CC DR PRINTS: PR00421; THIOREDOXIN.
CC DR PROSITE: PS00194; THIOREDOXIN; 1.
CC DR Electron transport; Redox-active center; Transport.
CC FT INT_MET 0 0 By similarity.
CC FT ACT_SITE 31 31 Nucleophile (By similarity).
CC FT ACT_SITE 34 34 Nucleophile (By similarity).
CC FT SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 32 32 (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11569 MW; 60B6B759010B12 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 39
THIO HORSE STANDARD; PRT; 104 AA.
AC 097508;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thiorodoxin.
GN Name=TXN;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC STRAIN=Thoroughbred;
RA Tajima Y., Ishida N.;
RT "Molecular cloning of equine thiorodoxin."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes disulfide exchange reactions.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the thiorodoxin family.
CC -1- SIMILARITY: Contains 1 thiorodoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: AB022431; BAA37154.1; -, mRNA.
CC HSSP: P10599; 3TRX.
CC SMR: O97508; 1-104.
CC DR InterPro: IPR006662; Thiorod.
CC DR InterPro: IPR006663; Thiorodox_dom2.

```

```

DR InterPro: IPR005746; Thiorodoxin.
DR InterPro: IPR012336; Thiorodoxin-like.
DR InterPro: IPR012335; Thiorodoxin_fold.
DR Pfam: PF00085; Thiorodoxin_1.
DR PRINTS: PR00421; THIOREDOXIN.
DR TIGRFAMs: TIGR01068; thiorodoxin_1.
CC DR PROSITE: PS00194; THIOREDOXIN; 1.
CC DR Electron transport; Redox-active center; Transport.
CC FT INT_MET 0 0 By similarity.
CC FT ACT_SITE 31 31 Nucleophile (By similarity).
CC FT ACT_SITE 34 34 Nucleophile (By similarity).
CC FT SITE 25 25 Deprotonates C-terminal active site Cys
CC SITE 32 32 (By similarity).
CC SITE 32 32 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC SITE 33 33 Contributes to redox potential value (By
CC SITE 33 33 similarity).
CC DISULFID 31 34 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11605 MW; 5B6C1092964C206D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 30 WCGPCK 35

RESULT 40
THIO HUMAN STANDARD; PRT; 104 AA.
AC P10599; Q96KT3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thiorodoxin (ATL-derived factor) (ADF) (Surface associated sulphhydryl
DE protein) (SASP).
GN Name=TXN; Synonyms=PRDX, TRX, TRX1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89008454; PubMed=1874447; DOI=10.1016/0378-1119(91)90081-L;
RA Tomassen K.F., Wells J.R.E.;
RT "Isolation and characterization of human thiorodoxin-encoding genes."
RL Gene 102:221-226(1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89008454; PubMed=3170595;
RA Wollman E.E., D'Aurilio L., Rinsky L., Shaw A., Jacquot J.-P.,
RA Wingfield P., Graber P., Dessars F.;
RT "Cloning and expression of a cDNA for human thiorodoxin."
RL J. Biol. Chem. 263:15506-15512(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89251607; PubMed=2785919;
RA Tagaya Y., Meda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
RA Brown N., Arai K.-I., Yokota T., Makasugi H., Yodoi J.;
RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
RT thiorodoxin; possible involvement of dithiol-reduction in the IL-2
RT receptor induction."
RL EMBO J. 8:757-764(1989).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Reddy P.G., Bhuyan D.K., Bhuyan K.C.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.

```

RC TISSUE=Iens;
RA Liu A., Lou M.F.;
RT "Cloning, purification and characterization of human lens
thioredoxin.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE [MRNA].
RC TISSUE=Brain;
RA Xu J.Y., Xu L., Li K.S., Dai R.;
RT "Cloning and sequencing of thioredoxin cDNA from human brain.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNPE, environmental genome project. NIHES E815478, Department
of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Cervix;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Shat N.K.,
Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gunaratne P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
Schmacher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP PROTEIN SEQUENCE OF 1-14.
RA MEDLINE=91151337; PubMed=1998498;
RA Martin H., Dean M.;
RT "Identification of a thioredoxin-related protein associated with
plasma membranes.";
RL Biochem. Biophys. Res. Commun. 175:123-128(1991).
RN [10]
RP STRUCTURE BY NMR.
RA MEDLINE=90057393; PubMed=2684271;
RA Forman-Kay J.D., Clore G.M., Driscoll P.C., Wingfield P.,
Richards P.M., Gronenborn A.M.;
RT "A proton nuclear magnetic resonance assignment and secondary
structure determination of recombinant human thioredoxin.";
RL Biochemistry 28:7088-7097(1989).
RN [11]
RP STRUCTURE BY NMR.
RA MEDLINE=91159399; PubMed=2001356;
RA Forman-Kay J.D., Clore G.M., Wingfield P., Gronenborn A.M.;
RT "High-resolution three-dimensional structure of reduced recombinant
human thioredoxin in solution.";
RL Biochemistry 30:2685-2698(1991).
RN [12]
RP STRUCTURE BY NMR.
RA MEDLINE=95006318; PubMed=7922028;
RA Qin J., Clore G.M., Gronenborn A.M.;
RT "The high-resolution three-dimensional solution structures of the
oxidized and reduced states of human thioredoxin.";
RL Structure 2:503-522(1994).
RN [13]

RP STRUCTURE BY NMR.
RX MEDLINE=96347359; PubMed=8736558; DOI=10.1016/S0969-2126(96)00065-2;
RA Qin J., Clore G.M., Kennedy W.P., Kuszewski J., Gronenborn A.M.;
RT "The solution structure of human thioredoxin complexed with its target
from Ref-1 reveals peptide chain reversal.";
RL Structure 4:613-620(1996).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=96939719; PubMed=8805557; DOI=10.1016/S0969-2126(96)00079-2;
RA Weltsch A., Gasdaske J.R., Powis G., Montfort W.R.;
RT "Crystal structures of reduced, oxidized, and mutated human
thioredoxins: evidence for a regulatory homodimer.";
RL Structure 4:735-751(1996).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF MUTANT ASN-60.
RX MEDLINE=98039128; PubMed=9369469; DOI=10.1021/1971004s;
RA Andersen J.F., Sanders D.A., Gasdaske J.R., Powis G.,
Montfort W.R.;
RT "Human thioredoxin homodimers: regulation by pH, role of aspartate 60,
and crystal structure of the aspartate 60 --> asparagine mutant.";
RL Biochemistry 36:13979-13988(1997).
RN [16]
RP ACTIVITY.
RX MEDLINE=91097576; PubMed=2176490;
RA Jacquot J.-P., de Lamotte F., Fontecay M., Schnermann P.,
Decottignies P., Migniac-Maslow M., Wollman E.;
RT "Human thioredoxin reactivity-structure/function relationship.";
RL Biochem. Biophys. Res. Commun. 173:1375-1381(1990).
CC -1- FUNCTION: Participates in various redox reactions through the
reversible oxidation of its active center dithiol to a disulfide
and catalyzes dithiol-disulfide exchange reactions.
CC -1- FUNCTION: ADP augments the expression of the interleukin-2
receptor TAC (IL2R/P55).
CC -1- SUBUNIT: Homodimer.
CC -1- INTERACTION:
CC -1- Q92805:CORP5; Nbrxp-5; Inlact-EBI-594644, EBI-594661;
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC
CC EMBL: X7584; CAA54687.1; -; mRNA.
CC EMBL: X54539; CAA38410.1; -; Genomic_DNA.
CC EMBL: X54540; CAA38410.1; JOINED; Genomic_DNA.
CC EMBL: X54541; CAA38410.1; JOINED; Genomic_DNA.
CC EMBL: J04026; AAA74596.1; -; mRNA.
CC EMBL: AF276919; AAF86466.1; -; mRNA.
CC EMBL: AY004872; AAF87085.1; -; mRNA.
CC EMBL: AF313911; AAG34699.1; -; mRNA.
CC EMBL: AF548001; AAN03187.1; -; Genomic_DNA.
CC EMBL: BC000377; AAN03377.1; -; mRNA.
CC EMBL: BC054866; AAH54866.1; -; mRNA.
CC PIR: JH0568; JH0568.
CC PDB: 1ATU; X-ray; @=1-104.
CC PDB: 1AUC; X-ray; @=1-104.
CC PDB: 1COG; NMR; A=1-104.
CC PDB: 1COH; NMR; A=1-104.
CC PDB: 1ERT; X-ray; @=1-104.
CC PDB: 1ERU; X-ray; @=1-104.
CC PDB: 1ERV; X-ray; @=1-104.
CC PDB: 1ERW; X-ray; @=1-104.
CC PDB: 1W7T; NMR; A=-.
CC PDB: 1MDI; NMR; A=1-104.
CC PDB: 1MDJ; NMR; A=1-104.
CC PDB: 1MDK; NMR; A=1-104.
CC PDB: 1TPS; NMR; @=1-104.
CC PDB: 1TRU; NMR; @=1-104.
CC PDB: 1TRV; NMR; @=1-104.

DR PDB; 1TRW; NMR; @=1-104.
 DR PDB; 3TRX; NMR; @=1-104.
 DR PDB; 4TRX; NMR; @=1-104.
 DR IntAct; P10599; -.
 DR SWISS-2DPAGE; P10599; HUMAN.
 DR Aaihus/Ghent-2DPAGE; 8006; IEF.
 DR PHCI-2DPAGE; P10599; -.
 DR Siema-2DPAGE; P10599; -.
 DR Ensembl; ENSG00000136810; Homo sapiens.
 DR HGNC; HGNC:12435; TXN.
 DR H-InvDB; HIX0008275; -.
 DR Reactome; P10599; -.
 DR

Query Match
 Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 41
 THIO_MACMU STANDARD; PRT; 104 AA.
 AC P29451;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin.
 GN Name=TXN;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Macaca.
 NCBI_Taxid=9544;
 [1]
 RX NUCLEOTIDE SEQUENCE [MRNA].
 RA MEDLINE=92181438; PubMed=1543487;
 RA An G., Wu R.;
 RT "Thioedoxin gene expression is transcriptionally up-regulated by
 retinol in monkey conducting airway epithelial cells."
 RL Biochem. Biophys. Res. Commun. 183:170-175(1992).
 CC -1- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioedoxin family.
 CC -1- SIMILARITY: Contains 1 thioedoxin domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; M84643; AAA36921.1; -. mRNA.
 DR PIR; J50667; J50667.
 DR HSSP; P10599; IERT.
 DR SMR; P29451; 1-104.
 DR InterPro; IPR006662; Thioedox.
 DR InterPro; IPR006663; Thioedox domz.
 DR InterPro; IPR005746; Thioedoxin.
 DR InterPro; IPR012336; Thioedoxin-like.
 DR InterPro; IPR012335; Thioedoxin_fold.
 DR Pfam; PF00805; Thioedoxin_1.
 DR PRINTS; PR00421; THIOEDOXIN.
 DR TIGRFAWS; TIGR01068; thioedoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KM Electron transport; Redox-active center; Transport.
 FT INIT_MET 0
 FT ACT_SITE 31 By similarity.
 FT ACT_SITE 34 Nucleophile (By similarity).
 FT ACT_SITE 34 Nucleophile (By similarity).

FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT SITE 32 32 (By similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT SITE 33 33 similarity).
 FT DISULFID 31 34 Contributes to redox potential value (By
 FT DISULFID 31 34 similarity).
 SQ SEQUENCE 104 AA; 11606 MW; C804D5152F8870EB CRC64;

Query Match
 Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 Db 30 WCGPCK 35

RESULT 42
 THIO_MOUSE STANDARD; PRT; 104 AA.
 AC P10639; Q9P8R0;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioedoxin (ATL-derived factor) (ADF).
 GN Name=Txn; Synonyms=Txnl;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 RX NUCLEOTIDE SEQUENCE [MRNA].
 RA MEDLINE=89251607; PubMed=2785919;
 RA Tagaya Y., Maeda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
 RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
 RT "ATL-derived factor (ADF), an IL-2 receptor/Tac inducer homologous to
 thioedoxin; possible involvement of dithiol-reduction in the IL-2
 receptor induction."
 RT receptor induction."
 RL EMBO J. 8:757-764(1989).
 [2]
 RP ERRATUM, AND SEQUENCE REVISION.
 RX MEDLINE=94244626; PubMed=8187776;
 RA Tagaya Y., Maeda Y., Mitsui A., Kudo N., Matsui H., Hamuro J.,
 RA Brown N., Arai K.-I., Yokota T., Wakasugi H., Yodoi J.;
 RL EMBO J. 13:2244-2244(1994).
 [3]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RC STRAIN=129/Sv; TISSUE=Liver;
 RX MEDLINE=95137382; PubMed=7835695; DOI=10.1016/0378-1119(94)00707-Y;
 RA Matsui M., Taniguchi Y., Hirota K., Taketo M., Yodoi J.;
 RT "Structure of the mouse thioedoxin-encoding gene and its processed
 RT pseudogene."
 RL Gene 152:165-171(1995).
 [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=C57BL/6J; TISSUE=Pancreas;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oeato N., Saito R., Suzuki H., Yamataka H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Balardini R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schiml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbett L.E., Cousins S.,
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Gilmard S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

KM	Electron transport; Redox-active center; Transport.
FT	INT_MET 0 0
FT	ACT_SITE 31 31 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Nucleophile (By similarity).
FT	ACT_SITE 25 25 Deprotonates C-terminal active site Cys (By similarity).
FT	SITE 32 32 Contributes to redox potential value (By similarity).
FT	SITE 33 33 Contributes to redox potential value (By similarity).
FT	DISULFID 31 34 Redox-active (By similarity).
FT	CONFLICT 99 99 S -> C (in Ref. 4; BAB25256).
SO	SEQUENCE 104 AA; 11544 MW; 60BE6196090ACT73 CRC64;
Qy	Query Match 100.0%; Score 47; DB 1; Length 104;
	Best Local Similarity 100.0%; Pred. No. 2.5;
	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	1 WCGPCK 6
	30 WCGPCK 35
RESULT 43	
ID	THIO_OPHHA STANDARD; PRT; 104 AA.
AC	Q96TX1;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	13-SEP-2005 (Rel. 48, Last annotation update)
DE	Thioredoxin.
GN	Name:TXN;
OS	Ophiophagus hannah (King cobra) (Naja hannah).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC	Elapidae; Elapinae; Ophiophagus.
OX	NCBI_TaxID=8665;
RN	[1]
RP	NUCLEOTIDE SEQUENCE [mRNA].
RC	TISSUE=Venom gland;
RA	Lee W., Liu H., Zhang Y.;
RT	"cDNA sequence of Ophiophagus hannah venom gland thioredoxin protein".
RL	Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC	- FUNCTION: Participates in various redox reactions through the reversible oxidation of its active center dithiol to a disulfide and catalyzes dithiol-disulfide exchange reactions (By similarity).
CC	- SIMILARITY: Belongs to the thioredoxin family.
CC	- SIMILARITY: Contains 1 thioredoxin domain.
CC	-----
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC	-----
DR	EMBL; AF321769; AAK09384.1; -; mRNA.
DR	HSSP; P10599; TRX.
DR	InterPro; IPR006662; ThioRed.
DR	InterPro; IPR006663; Thioredox dom2.
DR	InterPro; IPR012336; Thioredoxin-like.
DR	InterPro; IPR012335; Thioredoxin_1f.
DR	Pfam; PF00085; Thioredoxin; 1.
DR	PRINTS; PR00421; THIOREDOXIN.
DR	PROSITE; PS00194; THIOREDOXIN; 1.
KM	Electron transport; Redox-active center; Transport.
FT	INT_MET 0 0
FT	ACT_SITE 31 31 Nucleophile (By similarity).
FT	ACT_SITE 34 34 Nucleophile (By similarity).
FT	SITE 25 25 Deprotonates C-terminal active site Cys (By similarity).
FT	SITE 32 32 Contributes to redox potential value (By similarity).

FT SITE 33 33 similarity).
 FT SITE 33 33 contributes to redox potential value (By
 FT DISULFID 31 34 similarity). (By similarity).
 FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11872 MW; 852896C8BF850AFB CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 30 WCGPCK 35
 RESULT 44
 THIO_PIG STANDARD; PRT; 104 AA.
 AC P82460; Q95JF9; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin.
 GN Name=TXN;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 NCBI_TaxID=9823;
 RN NCB1_TaxID=9823;
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Liver;
 RA "Yu G.W., Xu J.Y., Xu L., Cheung P.Y., Lee K.S.,
 RT Submitted (May-2001) to the EMBL/GenBank/DBD databases.
 [2]
 RP PROTEIN SEQUENCE OF 1-33.
 RC TISSUE=Erythrocyte;
 RA Lee K.S., Tang W.K., Cheung P.Y., Siu Y.L., Wong N.S.;
 RL Submitted (May-2000) to Swiss-Prot.
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- TISSUE SPECIFICITY: Erythrocytes.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL, AF382821; AAK60272.1; -, mRNA.
 DR HSSP; P10599; 1ERY.
 DR SMR; P82460; 1-104.
 DR InterPro; IPR006662; Thiored.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR005746; Thioredoxin.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR Pfam; PF00085; Thioredoxin_fold.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PR00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thioredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Direct protein sequencing; Electron transport; Redox-active center;
 KW Transport.
 FT INIT MET 0 0
 FT ACT SITE 31 31 Nucleophile (By similarity).
 FT ACT SITE 34 34 Nucleophile (By similarity).
 FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT (By similarity).

FT SITE 32 32 similarity).
 FT SITE 32 33 contributes to redox potential value (By
 FT DISULFID 31 34 similarity). (By similarity).
 FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11697 MW; 9B16FP9696A2396A CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 47; DB 1; Length 104;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 DB 30 WCGPCK 35
 RESULT 45
 THIO_RABIT STANDARD; PRT; 104 AA.
 AC P08628; 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-MAY-2005 (Rel. 47, Last annotation update)
 DE Thioredoxin.
 GN Name=TXN;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
 OC Oryctolagus.
 NCBI_TaxID=9986;
 RN NCB1_TaxID=9986;
 RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Bone marrow;
 RA MEDLINE=88257078; PubMed=3164311;
 RX Johnson R.S., Mathews W.R., Blewett K., Hopper S.;
 RT "Amino acid sequence of thioredoxin isolated from rabbit bone marrow
 RT determined by tandem mass spectrometry.";
 RL J. Biol. Chem. 263:9589-9597(1988).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; A28086; A28086.
 DR HSSP; P10599; 1ERY.
 DR SMR; P08628; 1-104.
 DR InterPro; IPR006662; Thiored.
 DR InterPro; IPR006663; Thioredox_dom2.
 DR InterPro; IPR005746; Thioredoxin.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin; 1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRfam; TIGR01068; thioredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Direct protein sequencing; Electron transport; Redox-active center;
 KW Transport.
 FT ACT SITE 31 31 Nucleophile (By similarity).
 FT ACT SITE 34 34 Nucleophile (By similarity).
 FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT (By similarity).
 FT SITE 32 32 contributes to redox potential value (By
 FT (By similarity).
 FT SITE 33 33 contributes to redox potential value (By
 FT (By similarity).

FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11629 MW; CAB66E5EBEC231F CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 46
 THIO_RAT STANDARD; PRT; 104 AA.
 AC P11332;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin.
 OS Name=Txn;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Liver;
 RX MEDLINE=89282399; PubMed=2734107;
 RA Tonissen K.F., Robins A.J., Wells J.R.E.;
 RT "Nucleotide sequence of a cDNA encoding rat thioredoxin.";
 RL Nucleic Acids Res. 17:3973-3973(1989).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RA Xie Z.H., Liu C.Z., He Y.H., Wang A.M., Ma C.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Plutitary;
 RN NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X14878; CA43019.1; -; mRNA.
 DR EMBL; AF11055; AAG49923.1; -; mRNA.
 DR EMBL; BC058454; AA58454.1; -; mRNA.
 DR PIR; S04352; S04352.
 DR HSSP; P10599; IERT.
 DR SMR; P11332; 1-103.
 DR Ensemble; ENSRNOG0000012081; Rattus norvegicus.
 DR RGD; 621157; Txn.
 DR GO; GO:0004791; F:thioredoxin-disulfide reductase activity; TAS.
 DR GO; GO:0006118; P:electron transport; TAS.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR012336; Thioredoxin_dom2.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.

KW Electron transport; Redox-active center; Transport.
 FT INIT MET 0 0 By similarity.
 FT ACT SITE 31 31 Nucleophile (By similarity).
 FT ACT_SITE 34 34 Nucleophile (By similarity).
 FT SITE 25 25 Deprotonates C-terminal active site Cys
 FT (By similarity).
 FT SITE 32 32 Contributes to redox potential value (By
 FT similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT similarity).
 FT SITE 33 33 Contributes to redox potential value (By
 FT similarity).
 FT DISULFID 31 34 Redox-active (By similarity).
 SQ SEQUENCE 104 AA; 11542 MW; 60ACF19609ED773 CRC64;
 Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 47
 THIO_SHEEP STANDARD; PRT; 104 AA.
 ID THIO_SHEEP
 AC P50413;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Thioredoxin.
 OS Name=Txn;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Caprinae; Ovis.
 OX NCBI_TaxId=9940;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=95078463; PubMed=7987015;
 RA Droegmans L., Cleuter Y., Molman B.E., Kettmann R., Burny A.;
 RT "Nucleotide sequence of ovine thioredoxin cDNA.";
 RL DNA Seq. 4:277-279(1994).
 CC -1- FUNCTION: Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the thioredoxin family.
 CC -1- SIMILARITY: Contains 1 thioredoxin domain.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; Z25864; CA481083.1; -; mRNA.
 DR HSSP; P10599; IERT.
 DR SMR; P50413; 1-104.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR012336; Thioredoxin_dom2.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR012336; Thioredoxin_dom2.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR006663; Thiored.
 DR InterPro; IPR012336; Thioredoxin_dom2.
 DR InterPro; IPR012336; Thioredoxin-like.
 DR InterPro; IPR012335; Thioredoxin_fold.
 DR Pfam; PF00085; Thioredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR PROSITE; PS00194; THIOREDOXIN; 1.

FT SITE 33 33 similarity).
 FT DISUPLD 31 34 contributes to redox potential value (By
 FT SEQUENCE 104 AA; 11711 MM; 506CE54C5642208D CRC64; similarity).
 SO Redox-active (By similarity).

Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 30 WCGPCK 35

RESULT 48
 THIO_STAAH STANDARD; PRT; 104 AA.

AC POAOK4; Q9ZEH4;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE ThioRedoxin (TRX).
 GN Name=trxA; OrderedLocustNames=SAV1145;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=158878;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).

CC -!- FUNCTION: Component of the thioredoxin-thioredoxin reductase
 CC system. Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).

CC -!- SIMILARITY: Belongs to the thioredoxin family.
 CC -!- SIMILARITY: Contains 1 thioredoxin domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; BA000017; BAB57307.1; -; Genomic_DNA.

DR HSSP; P00274; 1T7P.
 DR InterPro; IPR006662; Thired.
 DR InterPro; IPR006663; Thiredox_dom2.
 DR InterPro; IPR005746; Thiredoxin.
 DR InterPro; IPR012336; Thiredoxin-like.
 DR InterPro; IPR012335; Thiredoxin_fold.
 DR Pfam; PF00085; Thiredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thiredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome; Electron transport; Redox-active center; Transport.
 FT DISUPLD 29 32 Redox-active (By similarity).
 FT SEQUENCE 104 AA; 11440 MM; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 28 WCGPCK 33

RESULT 49
 THIO_STAAH STANDARD; PRT; 104 AA.
 ID THIO_STAAH
 AC P99132; Q9ZEH4;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE ThioRedoxin (TRX).
 GN Name=trxA; OrderedLocustNames=SA00992;
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OK NCBI_TaxID=158879;
 RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX MEDLINE=2111952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani U. Y., Takahashi N. K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus";
 RL Lancet 357:1225-1240(2001).

CC -!- FUNCTION: Component of the thioredoxin-thioredoxin reductase
 CC system. Participates in various redox reactions through the
 CC reversible oxidation of its active center dithiol to a disulfide
 CC and catalyzes dithiol-disulfide exchange reactions (By
 CC similarity).

CC -!- SIMILARITY: Belongs to the thioredoxin family.
 CC -!- SIMILARITY: Contains 1 thioredoxin domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC EMBL; BA000018; BAB4241.1; -; Genomic_DNA.
 CC PIR; E89885; E89885.

DR HSSP; P00274; 1T7P.
 DR SWISS-2DPAGE; P99122; STAAH.
 DR InterPro; IPR006662; Thired.
 DR InterPro; IPR006663; Thiredox_dom2.
 DR InterPro; IPR005746; Thiredoxin.
 DR InterPro; IPR012336; Thiredoxin-like.
 DR InterPro; IPR012335; Thiredoxin_fold.
 DR Pfam; PF00085; Thiredoxin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRFAMs; TIGR01068; thiredoxin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 DR Complete proteome; Electron transport; Redox-active center; Transport.
 FT DISUPLD 29 32 Redox-active (By similarity).
 FT SEQUENCE 104 AA; 11440 MM; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
 Db 28 WCGPCK 33

RESULT 50
 THIO_STAAH STANDARD; PRT; 104 AA.
 ID THIO_STAAH

```

AC O6GHU0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trxA; OrderedLocNames=SAR1118;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282458;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioRedoxin family.
CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BX571856; CAG40121.1; -; Genomic_DNA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

```

```

RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Errington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jørgels K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioRedoxin family.
CC -1- SIMILARITY: Contains 1 thioRedoxin domain.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; BX571857; CAG42854.1; -; Genomic_DNA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfams; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KM Complete proteome; Electron transport; Redox-active center; Transport.
FT DISULFID 29 32 Redox-active (By similarity).
SQ SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

```

```

RESULT 52
THIO_STNAU
ID THIO_STNAU STANDARD; PRT; 104 AA.
AC POA0K6; Q9ZEH4;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE ThioRedoxin (TRX).
GN Name=trxA;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Oxiford;
RA Uziel O., Borovok I., Schreiber R., Cohen G., Aharonowitz Y.;
RT "Transcriptional analysis of the thioRedoxin (trxA) and thioRedoxin
RT reductase (trxB) genes in Staphylococcus aureus.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Component of the thioRedoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the

```

```
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AJ223480; CA11404.1; -; Genomic_DNA.
CC HSSP; P00274; 177P.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thiored_dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin_fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRfam; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Electron transport; Redox-active center; Transport.
CC FT DISULFID 29 32 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 53
THIO_STAAP STANDARD; PRT; 104 AA.
AC POA0F5; Q9ZE94;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DR Thioredoxin (TRX).
DE Name:trxA; OrderedLocustNames=MM1028;
OS Staphylococcus aureus (strain MM02).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=196620;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Yamaguchi Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratake K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
CC -1- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BA000033; BAB94893.1; -; Genomic_DNA.
CC HSSP; P00274; 177P.
```

```
DR InterPro; IPR006662; Thiored.
DR InterPro; IPR006663; Thiored_dom2.
DR InterPro; IPR005746; Thioredoxin.
DR InterPro; IPR012336; Thioredoxin-like.
DR InterPro; IPR012335; Thioredoxin_fold.
DR Pfam; PF00085; Thioredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRfam; TIGR01068; thioredoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
DR Complete proteome; Electron transport; Redox-active center; Transport.
DR FT DISULFID 29 32 Redox-active (By similarity).
DR SEQUENCE 104 AA; 11440 MW; FE61559DB27B3920 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 28 WCGPCK 33

RESULT 54
THIO_STAAP STANDARD; PRT; 104 AA.
AC O8CPF5;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thioredoxin (TRX).
DE Name:trxA; OrderedLocustNames=SE0838;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
ON NCBI_TaxID=1282;
RX MEDLINE=22832016; PubMed=12950922;
DOI=10.1046/j.1365-2958.2003.03671.x;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA Qian Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT "Genome-based analysis of virulence genes in a non-biofilm-forming
RT Staphylococcus epidermidis strain (ATCC 12228).";
RL Mol. Microbiol. 49:1577-1593(2003).
CC -1- FUNCTION: Component of the thioredoxin-thioredoxin reductase
CC system. Participates in various redox reactions through the
CC reversible oxidation of its active center dithiol to a disulfide
CC and catalyzes dithiol-disulfide exchange reactions (By
CC similarity).
CC -1- SIMILARITY: Belongs to the thioredoxin family.
CC -1- SIMILARITY: Contains 1 thioredoxin domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE016746; AA004435.1; -; Genomic_DNA.
CC HSSP; P00274; 177P.
CC InterPro; IPR006662; Thiored.
CC InterPro; IPR006663; Thiored_dom2.
CC InterPro; IPR005746; Thioredoxin.
CC InterPro; IPR012336; Thioredoxin-like.
CC InterPro; IPR012335; Thioredoxin_fold.
CC Pfam; PF00085; Thioredoxin_1.
CC PRINTS; PR00421; THIOREDOXIN.
CC TIGRfam; TIGR01068; thioredoxin; 1.
CC PROSITE; PS00194; THIOREDOXIN; 1.
CC Complete proteome; Electron transport; Redox-active center; Transport.
CC FT DISULFID 29 32 Redox-active (By similarity).
CC SEQUENCE 104 AA; 11443 MW; DBBC61D2DA7E770 CRC64;
```

```

Query Match          100.0%; Score 47; DB 1; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
   |||||
Db 29 WCGPCK 34

RESULT 55
Q6CN03_KLULA PRELIMINARY; PRT; 104 AA.
ID Q6CN03_KLULA PRELIMINARY; PRT; 104 AA.
AC Q6CN03;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P22217|Saccharomyces cerevisiae YLR043c TRX1 thioredoxin
DE 1.
GN OrderedLocustNames=KLULA0B16401g;
OS Kluyveromyces lactic (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 / IFO 1140 / NRRL Y-1140 / WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul S., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boistrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Portier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
EMBL: CB82125; CAG9773.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiredox.
DR InterPro; IPR006663; Thiredox_dom2.
DR InterPro; IPR005746; Thiredoxin.
DR InterPro; IPR012336; Thiredoxin-like.
DR InterPro; IPR012335; Thiredoxin_fold.
DR Pfam; PF00085; Thiredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; thiredoxin_1.
DR PROSITE; PS00194; THIOREDOXIN_1.
KW Complete proteome.
SQ
SEQUENCE 104 AA; 11332 MW; D2EAE1F82EDFE5 CRC64;

Query Match          100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
   |||||
Db 29 WCGPCK 34

RESULT 56
Q6C399_YARLI PRELIMINARY; PRT; 104 AA.
ID Q6C399_YARLI PRELIMINARY; PRT; 104 AA.
AC Q6C399;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

```

```

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P22803|Saccharomyces cerevisiae YER209c TRX2 thioredoxin
DE 1.
GN OrderedLocustNames=YAL10F01496g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CLIB 122 / E 150;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangoul S., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Goffard N., Frangoul S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boistrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreay F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicand J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Portier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof B., Wirth B.,
RA Zenlou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Galliard C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
EMBL: CB82132; CAG77665.1; -; Genomic DNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; Thiredox.
DR InterPro; IPR006663; Thiredox_dom2.
DR InterPro; IPR005746; Thiredoxin.
DR InterPro; IPR012336; Thiredoxin-like.
DR InterPro; IPR012335; Thiredoxin_fold.
DR Pfam; PF00085; Thiredoxin_1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; thiredoxin_1.
DR PROSITE; PS00194; THIOREDOXIN_1.
KW Complete proteome.
SQ
SEQUENCE 104 AA; 11336 MW; 9A92D40C2B494CFB CRC64;

Query Match          100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
   |||||
Db 30 WCGPCK 35

RESULT 57
Q5KKS5_CRYNE PRELIMINARY; PRT; 104 AA.
ID Q5KKS5_CRYNE PRELIMINARY; PRT; 104 AA.
AC Q5KKS5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Thioredoxin (Allergen cop c 2), putative.
GN ORFNames=CNC04200;
OS Crypococcus neoformans var. neoformans JEC21.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=214684;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=JEC21;
RA Loftus B., Amedeo P., Roncaglia P., Vamathavan J., Utterback T.,
RA Van Aken S., Fraser C.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [2]

```


RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=JEC21;
 RX PubMed=15653466; DOI=10.1126/science.1103773;
 RA Loftus B.J., Fung B., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
 RA Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
 RA Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
 RA D'Souza C.A., Fox D.S., Grubler V., Fu J., Fukushima M., Haas B.J.,
 RA Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
 RA Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
 RA Mathewson C.A., Mitchell T.G., Perlea M., Riggs F.R., Salzberg S.L.,
 RA Schein J.E., Schwartzbeyn A., Shin H., Shumway M., Specht C.A.,
 RA Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
 RA Wye N.H., Kronstad J.W., Lodge J.K., Heltman J., Davis R.W.,
 RA Fraser C.M., Hyman R.W.;
 RT "The genome of the basidiomycetous yeast and human pathogen
 RT *Cryptococcus neoformans*."
 RL Science 307:1321-1324(2005).
 DR EMBL; AB017343; AA42360.1; -, Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiorod.
 DR InterPro; IPR006663; Thiorodex_dom2.
 DR InterPro; IPR005746; Thiorodexin.
 DR InterPro; IPR012336; Thiorodexin-like.
 DR InterPro; IPR012335; Thiorodexin_fold.
 DR Pfam; PF00085; Thiorodexin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPM; TIGR01068; thiorodexin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 104 AA; 11451 MW; 1594CF5F30868BA CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 58
 OS5W38 CRYNE PRELIMINARY; PRT; 104 AA.
 ID 05W38_CRYNE PRELIMINARY; PRT; 104 AA.
 AC 05W38;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=CNBC2990;
 OS *Cryptococcus neoformans* var. *neoformans* B-3501A.
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellales; Tremellaceae; Tremellales; Filobasidiella.
 OC NCBI_TaxID=283643;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B-3501A;
 RA Fung B., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
 RA Wickes B.L., Fu J., Davis R.W.;
 RT "Cryptococcus neoformans serotype D sequencing."
 RT Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AA01000013; EU22161.1; -, Genomic DNA.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiorod.
 DR InterPro; IPR006663; Thiorodex_dom2.
 DR InterPro; IPR005746; Thiorodexin.
 DR InterPro; IPR012336; Thiorodexin-like.
 DR InterPro; IPR012335; Thiorodexin_fold.
 DR Pfam; PF00085; Thiorodexin_1.

DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPM; TIGR01068; thiorodexin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 104 AA; 11451 MW; 1594CF5F30868BA CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 59
 OS9NIR2 PLAFa PRELIMINARY; PRT; 104 AA.
 ID 09NIR2_PLAFa PRELIMINARY; PRT; 104 AA.
 AC 09NIR2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thiorodexin_1.
 GN Name=TXR1;
 OS *Plasmodium falciparum*.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20568274; PubMed=11013257; DOI=10.1074/jbc.M007633200;
 RA Kanak S.M., Schimer R.H., Turbachova I., Iozef R., Becker K.;
 RT "The thiorodexin system of the malaria parasite *Plasmodium falciparum*.
 RT Glutathione reduction revisited".
 RL J. Biol. Chem. 275:40180-40186(2000).
 DR EMBL; AF202664; AA34541.1; -, mRNA.
 DR HSSP; P80028; 1EP7.
 DR SMR; 09NIR2; 1-103.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR006662; Thiorod.
 DR InterPro; IPR006663; Thiorodex_dom2.
 DR InterPro; IPR005746; Thiorodexin.
 DR InterPro; IPR012336; Thiorodexin-like.
 DR InterPro; IPR012335; Thiorodexin_fold.
 DR Pfam; PF00085; Thiorodexin_1.
 DR PRINTS; PR00421; THIOREDOXIN.
 DR TIGRPM; TIGR01068; thiorodexin; 1.
 DR PROSITE; PS00194; THIOREDOXIN; 1.
 SQ SEQUENCE 104 AA; 11717 MW; 2F507E17F276171F CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WCGPCK 6
 Db 29 WCGPCK 34

RESULT 60
 OS9NFK9 PLAFa PRELIMINARY; PRT; 104 AA.
 ID 09NFK9_PLAFa PRELIMINARY; PRT; 104 AA.
 AC 09NFK9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Thiorodexin.
 GN Name=txr;
 OS *Plasmodium falciparum*.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

```

RC STRAIN=3D7;
RL Krnajtski Z., Gilberger T.W., Walter R.D., Mueller S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; A2277839; CAB90828.1; -; mRNA.
DR GO; GO:0005489; F:electron transport activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR012336; ThioRedoxin.
DR InterPro; IPR012335; ThioRedoxin-like.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 61
ID Q7RH10_PLAYO PRELIMINARY; PRT; 104 AA.
AC Q7RH10;
DT 01-MAR-2004 (TEMBLrel. 26, Created)
DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE ThioRedoxin.
GN Name=pf04185;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1YXN;
RC MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlson J.M., Angluoli S.V., Suh B.B., Kooij T.W., Perrea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., Van Aken S.E., Riedmiller S.B., Feldlynn T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01001248; EAA16007.1; -; Genomic_DNA.
DR HSSP; P80028; 18P7.
DR SKR; Q7RH10; 1-103.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; UNKNOWN 1.
SQ SEQUENCE 104 AA; 11622 MW; A29D2915116F2B83 CRC64;

```

```

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 62
ID Q7KOL8_PLAF7 PRELIMINARY; PRT; 104 AA.
AC Q7KOL8;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE ThioRedoxin.
DE ORFNames=PF14_0545;
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=36329;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Bisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallom S.J., Suh B., Peterson J., Angluoli S.,
RA Perrea M., Allen J., Selengut J., Hatt D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.G.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RL Nature 419:498-511(2002).
DR EMBL; AE014825; AAN37158.1; -; Genomic DNA.
DR PDB; 1SYR; X-ray; A/B/C/D/E/F/G/H/I/J/K/L=1-104.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAM; TIGR01068; thioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 104 AA; 11716 MW; 0129998AEB88770C CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGSPCK 6
DB 29 WCGSPCK 34

RESULT 63
ID O6B963_SCHMA PRELIMINARY; PRT; 104 AA.
AC O6B963;
DT 25-OCT-2004 (TEMBLrel. 28, Created)
DT 25-OCT-2004 (TEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TEMBLrel. 28, Last annotation update)
DE ThioRedoxin 2.
DE Name=Trx-2;
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.

```

OX NCBI_TaxID=6183;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Puerto Rican.
RA Beers L.F., Williams D.L.;
RT "Thioredoxin-2 in Schistosoma mansoni";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY673828; AAT76629.1; -; mRNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
SQ SEQUENCE 104 AA; 11995 MW; 8D36E829BF6A44A2 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
|||||
DB 30 WCGPCK 35

RESULT 64
OSDAX8 SCHUA PRELIMINARY; PRT; 104 AA.
ID OSDAX8_SCHUA PRELIMINARY;
AC OSDAX8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Han Z.;
RT "The full-length cDNA sequences of Schistosoma japonicum genes";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY815296; AAW27028.1; -; mRNA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR006663; ThioRedox_dom2.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR012336; ThioRedoxin-like.
DR InterPro; IPR012335; ThioRedoxin_fold.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
DR PROSITE; PS00194; THIOREDOXIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 104 AA; 11921 MW; 8D36E83058742262 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
|||||
DB 30 WCGPCK 35

RESULT 65
Q48985_MYCCA

ID Q48985_MYCCA PRELIMINARY; PRT; 104 AA.

AC Q48985;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Thioredoxin (Fragment).
OS Mycoplasma capricolum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2095;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 27343;
RX MEDLINE=96059641; PubMed=7476192;
RA Bork P., Ouzounis C., Casari G., Schneider R., Sander C., Dolan M.,
RA Gilbert W., Gillevert P.M.;
RT "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
its physiology";
RL Mol. Microbiol. 16:955-967(1995).
DR EMBL; Z33053; CAA83726.1; -; Genomic_DNA.
DR PIR; S77780; S77780.
DR HSSP; P80028; 1BP7.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006662; ThioRed.
DR InterPro; IPR005746; ThioRedoxin.
DR InterPro; IPR006663; ThioRedox_dom2.
DR Pfam; PF00085; ThioRedoxin; 1.
DR PRINTS; PR00421; THIOREDOXIN.
DR TIGRPFAMs; TIGR01068; ThioRedoxin; 1.
FT NON TER 1
SQ SEQUENCE 104 AA; 11825 MW; C133AFBFB027A001 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 66
Q4HNMS_CAMUP PRELIMINARY; PRT; 104 AA.
ID Q4HNMS_CAMUP PRELIMINARY;
AC Q4HNMS;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Thioredoxin.

GN Name:trx; ORFNames=CUP1008;
OS Campylobacter upsaliensis RM3195.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Birkack L.M., Deboy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
genomes of multiple Campylobacter species";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA01000012; EAL52411.1; -; Genomic_DNA.
SQ SEQUENCE 104 AA; 11271 MW; 3056CAA6930B8F74 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 28 WCGPCK 33

RESULT 67

07M09_CLOPA

ID 07M09_CLOPA PRELIMINARY; PRT; 104 AA.

AC 07M09; 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)

DE Thioresdoxin.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1501;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=21685756; PubMed=11827546; DOI=10.1021/bi011802p;

RA Reynolds C.M., Meyer J., Poole L.B.;

RT "NADH-dependent bacterial thioresdoxin reductase-like protein, in
conjunction with a glutaredoxin homologue, form a unique peroxithioresdoxin
(Abpc) reducing system in Clostridium pasteurianum.";

RT Biochemistry 41:1390-2001(2002).

RN [2]

RP PROTEIN SEQUENCE.

RA Reynolds C.M., Poole L.B., Hammel K.E., Wada K., Buchanan B.B.;

RL Submitted (SEP-2001) to the PIR data bank.

DR PIR; B59394; B59394.

DR HSSP; P00274; 1FGW.

DR GO; GO:0005489; P:electron transporter activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR006662; Thioresdoxin.

DR InterPro; IPR005746; Thioresdoxin dom2.

DR InterPro; IPR012336; Thioresdoxin-like.

DR InterPro; IPR012335; Thioresdoxin-fold.

DR Pfam; PF00085; Thioresdoxin_1.

DR PRINTS; PR00421; THIOREDOXIN.

DR TIGRFAWS; TIGR01068; thioresdoxin; 1.

DR PROSITE; PS00194; THIOREDOXIN; 1.

SQ SEQUENCE 104 AA; 11413 MW; 6A60C767560B7ED2 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 27 WCGPCK 32

RESULT 68

OSLHJ1_BACFN

ID 05LHJ1_BACFN PRELIMINARY; PRT; 104 AA.

AC 05LHJ1; 01-FEB-2005 (TrEMBLrel. 29, Created)

DT 01-FEB-2005 (TrEMBLrel. 29, last sequence update)

DT 01-FEB-2005 (TrEMBLrel. 29, last annotation update)

DE Putative thioresdoxin.

GN Name=trixA; OrderedLocNames=BPO642;

OS Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).

OC Bacteria; Bacteroidetes; Bacteroidales; Bacteroidaceae;

OC Bacteroidaceae; Bacteroides.

OX NCBI_TaxID=272559;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=15746427; DOI=10.1126/science.1107008;

Cerdano-Tarraga A.-M., Patrick S., Crossman L.C., Blakey G.,

RA Abrecht V., Lennard N., Foxton I., Duerden B., Harris B., Quail M.A.,
RA Barron A., Clark L., Cotton C., Doggett J., Holden M.T.G., Larke N.,
RA Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA Rabinowitch E., Woodward J., Barrell B.G., Parkhill J.;

RT "Extensive DNA inversions in the B. fragilis genome control variable
gene expression.";

RL Science 307:1463-1465(2005).

DR EMBL; CR626927; CAH06389.1; -; Genomic_DNA.

DR InterPro; IPR006662; Thioresdoxin.

DR InterPro; IPR006663; Thioresdoxin dom2.

DR InterPro; IPR005746; Thioresdoxin.

DR InterPro; IPR012336; Thioresdoxin-like.

DR InterPro; IPR012335; Thioresdoxin-fold.

DR Pfam; PF00085; Thioresdoxin_1.

DR PRINTS; PR00421; THIOREDOXIN.

DR TIGRFAWS; TIGR01068; thioresdoxin; 1.

DR PROSITE; PS00194; THIOREDOXIN; 1.

KW Complete proteome.

SQ SEQUENCE 104 AA; 11470 MW; 5B9541D3930F918 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 28 WCGPCK 33

RESULT 69

Q4L5FO_STAHJ

ID Q4L5FO_STAHJ PRELIMINARY; PRT; 104 AA.

AC Q4L5FO; 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, last sequence update)

DT 13-SEP-2005 (TrEMBLrel. 31, last annotation update)

DE Thioresdoxin.

GN Name=trixA; ORFNames=SH1816;

OS Staphylococcus haemolyticus (strain JCS41435).

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=279808;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=JCS41435;

RA Takeuchi F., Matsumoto S., Baba T., Yuzawa H., Ito T., Cui L.,

RA Morimoto Y., Kuroda M., Takahashi M., Anai A., Baba S., Fukui S.,

RA Lee J.C., Hiramatsu K.;

RT "Whole genome sequencing of Staphylococcus haemolyticus uncovers
extreme plasticity of its genome and dynamism in the evolution of
human-colonizing staphylococcal species.";

RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP006716; BAE05125.1; -; Genomic DNA.

SQ SEQUENCE 104 AA; 11453 MW; 6CC2B6F00A063592 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 28 WCGPCK 33

RESULT 70

Q817I8_BACRC

ID Q817I8_BACRC PRELIMINARY; PRT; 104 AA.

AC Q817I8; 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)

DE Thioresdoxin.

OS OrderedListNames=BC4521;

GN Bacillus cereus (strain ATCC 14579 / DSM 31).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NCLECTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Gotsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pasch G., Haaseltorn R., Fomstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL: AE017012; AAP11431.1; -; Genomic_DNA.
DR HSSP: P80579; INSW.
DR GO: GO:0005489; F:electron transporter activity; IEA.
DR GO: GO:0006118; P:electron transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR006662; ThioRed.
DR InterPro: IPR005746; ThioRedoxin.
DR InterPro: IPR006663; ThioRedoxin.
DR Pfam: PF00085; ThioRedoxin; 1.
DR PRINTS: PR00421; THIOREDOXIN.
DR TIGRFAMs: TIGR01068; thioRedoxin; 1.
DR PROSITE: PS00134; THIOREDOXIN; 1.
KM Complete proteome.
SQ SEQUENCE 104 AA; 11478 MW; B3689CCCC245EB87 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 28 WCGPCK 33

Search completed: February 23, 2006, 00:42:00
Job time : 161.5 secs

This Page Blank (uspofo)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:19 ; Search time 34.5 Seconds
(without alignments)
14.378 Million cell updates/sec

Title: US-10-660-118A-3
Perfect score: 47
Sequence: 1 MCGPCK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/H COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/ECTUS COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	6	1 US-08-883-804-5	Sequence 5, Appl1
2	47	100.0	6	2 US-08-627-907A-6	Sequence 6, Appl1
3	47	100.0	6	2 US-07-901-713A-3	Sequence 3, Appl1
4	47	100.0	12	2 US-08-750-142B-54	Sequence 54, Appl1
5	47	100.0	104	6 5210073-1	Patent No. 5210073
6	47	100.0	105	1 US-08-826-910-3	Sequence 3, Appl1
7	47	100.0	105	1 US-08-826-910-4	Sequence 4, Appl1
8	47	100.0	105	2 US-09-601-144-68	Sequence 68, Appl1
9	47	100.0	105	2 US-09-513-999C-8037	Sequence 8037, Ap
10	47	100.0	106	1 US-08-386-729A-10	Sequence 10, Appl
11	47	100.0	109	1 US-07-745-382-22	Sequence 22, Appl
12	47	100.0	109	1 US-07-921-848-22	Sequence 22, Appl
13	47	100.0	109	1 US-08-165-301A-22	Sequence 22, Appl
14	47	100.0	109	1 US-08-165-301A-26	Sequence 26, Appl
15	47	100.0	109	1 US-08-165-301A-28	Sequence 28, Appl
16	47	100.0	109	2 US-08-810-436-22	Sequence 22, Appl
17	47	100.0	109	2 US-08-810-436-26	Sequence 26, Appl
18	47	100.0	109	2 US-08-810-436-28	Sequence 28, Appl
19	47	100.0	109	2 US-09-485-885-17	Sequence 17, Appl
20	47	100.0	109	2 US-09-166-966E-10	Sequence 10, Appl
21	47	100.0	109	2 US-09-248-796A-19911	Sequence 19911, A
22	47	100.0	109	4 PCT-US94-14179-22	Sequence 22, Appl
23	47	100.0	109	4 PCT-US94-14179-26	Sequence 26, Appl
24	47	100.0	109	4 PCT-US94-14179-28	Sequence 28, Appl
25	47	100.0	111	2 US-09-264-419C-6	Sequence 6, Appl1
26	47	100.0	111	2 US-09-134-001C-3859	Sequence 3859, Ap
27	47	100.0	116	2 US-09-882-835-5	Sequence 5, Appl1

28	47	100.0	122	2 US-09-543-681A-4397	Sequence 4397, Ap
29	47	100.0	124	2 US-09-489-039A-8017	Sequence 8017, Ap
30	47	100.0	125	2 US-09-949-016-9663	Sequence 9663, Ap
31	47	100.0	134	2 US-09-272-342B-5	Sequence 5, Appl1
32	47	100.0	137	2 US-08-961-083-40	Sequence 40, Appl
33	47	100.0	137	2 US-09-536-784-40	Sequence 40, Appl
34	47	100.0	137	2 US-09-765-271-40	Sequence 40, Appl
35	47	100.0	137	2 US-09-765-272A-40	Sequence 40, Appl
36	47	100.0	145	2 US-09-328-352-5360	Sequence 5360, Ap
37	47	100.0	159	2 US-09-166-966E-8	Sequence 8, Appl1
38	47	100.0	166	1 US-08-775-978-1	Sequence 1, Appl1
39	47	100.0	166	1 US-08-775-978-3	Sequence 3, Appl1
40	47	100.0	167	2 US-09-741-243C-4	Sequence 4, Appl1
41	47	100.0	170	2 US-09-270-767-32473	Sequence 32473, A
42	47	100.0	170	2 US-09-270-767-47690	Sequence 47690, A
43	47	100.0	177	2 US-09-272-342B-6	Sequence 6, Appl1
44	47	100.0	185	2 US-09-583-110-5222	Sequence 5222, Ap
45	47	100.0	194	2 US-09-107-433-5104	Sequence 5104, Ap
46	47	100.0	209	2 US-09-166-966E-11	Sequence 11, Appl
47	47	100.0	210	2 US-08-180-371-6	Sequence 6, Appl1
48	47	100.0	210	4 PCT-US92-05707-6	Sequence 6, Appl1
49	47	100.0	265	2 US-08-778-717-17	Sequence 17, Appl
50	47	100.0	296	1 US-07-745-382-14	Sequence 14, Appl
51	47	100.0	296	1 US-07-921-848-14	Sequence 14, Appl
52	47	100.0	296	1 US-08-115-680-4	Sequence 4, Appl1
53	47	100.0	296	1 US-07-941-372-4	Sequence 4, Appl1
54	47	100.0	296	1 US-08-165-301A-14	Sequence 14, Appl
55	47	100.0	296	2 US-08-810-436-14	Sequence 14, Appl
56	47	100.0	296	4 PCT-US93-08247-4	Sequence 4, Appl1
57	47	100.0	296	4 PCT-US94-14179-14	Sequence 14, Appl
58	47	100.0	355	2 US-10-012-896-1011	Sequence 1011, Ap
59	47	100.0	408	1 US-08-683-007A-2	Sequence 2, Appl1
60	47	100.0	467	2 US-09-513-442-2	Sequence 2, Appl1
61	47	100.0	500	1 US-08-260-589-77	Sequence 77, Appl
62	47	100.0	500	4 PCT-US95-05471-77	Sequence 77, Appl
63	47	100.0	546	2 US-10-057-531A-2	Sequence 1, Appl1
64	47	100.0	551	2 US-09-741-243C-2	Sequence 2, Appl1
65	47	100.0	580	2 US-09-252-991A-22943	Sequence 22943, A
66	47	100.0	824	2 US-09-626-589-3	Sequence 3, Appl1
67	47	100.0	858	2 US-10-237-551-92	Sequence 92, Appl
68	47	100.0	1285	2 US-08-974-549A-600	Sequence 600, App
69	47	100.0	1285	2 US-08-912-951-314	Sequence 314, App
70	47	100.0	1285	2 US-09-402-181B-600	Sequence 600, App
71	47	100.0	1285	2 US-09-721-456-600	Sequence 600, App
72	47	100.0	102	2 US-09-198-452A-697	Sequence 697, App
73	47	100.0	112	2 US-09-583-110-3078	Sequence 3078, Ap
74	47	100.0	112	2 US-09-107-532A-6739	Sequence 6739, Ap
75	47	100.0	114	2 US-09-897-425-41	Sequence 41, Appl
76	47	100.0	114	2 US-09-107-433-2930	Sequence 2930, Ap
77	47	100.0	114	2 US-09-786-715-11	Sequence 11, Appl
78	47	100.0	118	2 US-09-786-715-10	Sequence 10, Appl
79	47	100.0	118	2 US-09-786-715-13	Sequence 13, Appl
80	47	100.0	118	2 US-09-786-715-15	Sequence 15, Appl
81	47	100.0	120	2 US-09-438-185A-661	Sequence 661, App
82	47	100.0	120	2 US-09-786-715-6	Sequence 6, Appl1
83	47	100.0	122	2 US-09-540-014-2	Sequence 2, Appl1
84	47	100.0	122	2 US-09-538-864-25	Sequence 25, Appl
85	47	100.0	122	2 US-10-091-841A-2	Sequence 2, Appl1
86	47	100.0	122	2 US-09-786-715-2	Sequence 2, Appl1
87	47	100.0	123	2 US-09-786-715-8	Sequence 8, Appl1
88	47	100.0	124	2 US-09-603-208A-70	Sequence 70, Appl
89	47	100.0	125	2 US-09-902-039A-11628	Sequence 11628, A
90	47	100.0	125	2 US-09-902-540-151247	Sequence 1247, A
91	47	100.0	127	2 US-09-786-715-12	Sequence 12, Appl
92	47	100.0	127	2 US-09-540-014-4	Sequence 4, Appl1
93	47	100.0	130	2 US-10-091-841A-4	Sequence 4, Appl1
94	47	100.0	130	2 US-09-540-014-6	Sequence 6, Appl1
95	47	100.0	160	2 US-09-489-039A-11628	Sequence 11628, A
96	47	100.0	169	2 US-09-897-425-44	Sequence 44, Appl
97	47	100.0	183	2 US-09-902-540-19882	Sequence 14982, A
98	47	100.0	232	2 US-09-897-425-46	Sequence 46, Appl
99	47	100.0	291	2 US-09-949-016-11416	Sequence 11416, A
100	47	100.0	468	2 US-09-949-016-10793	Sequence 10793, A

101	44	93.6	511	1	US-08-821-355A-9	Sequence 9, Appl1	174	38	80.9	304	2	US-09-949-016-10270	Sequence 10270, A
102	44	93.6	511	1	US-09-003-687A-9	Sequence 9, Appl1	175	38	80.9	324	2	US-09-489-847-203	Sequence 203, App
103	44	93.6	511	2	US-09-136-605-9	Sequence 9, Appl1	176	38	80.9	343	2	US-09-807-258-24	Sequence 24, Appl
104	44	93.6	536	1	US-08-821-355A-6	Sequence 6, Appl1	177	38	80.9	363	2	US-09-489-847-361	Sequence 361, App
105	44	93.6	536	1	US-09-003-687A-6	Sequence 6, Appl1	178	38	80.9	364	1	US-08-650-275-4	Sequence 4, Appl1
106	44	93.6	536	2	US-09-136-605-6	Sequence 6, Appl1	179	38	80.9	364	2	US-09-181-318-4	Sequence 4, Appl1
107	43	91.5	329	2	US-09-248-796A-19909	Sequence 19909, A	180	38	80.9	364	2	US-09-807-258-31	Sequence 31, Appl
108	43	91.5	747	2	US-09-999-833A-459	Sequence 459, App	181	38	80.9	366	2	US-08-984-919A-11	Sequence 11, Appl
109	43	91.5	747	2	US-10-020-445A-459	Sequence 459, App	182	38	80.9	368	2	US-08-781-420-11	Sequence 11, Appl
110	42	89.4	89	2	US-09-621-976-6168	Sequence 6168, Ap	183	38	80.9	368	2	US-08-874-102-11	Sequence 11, Appl
111	42	89.4	169	2	US-09-902-540-10496	Sequence 10496, A	184	38	80.9	368	2	US-09-066-595A-11	Sequence 11, Appl
112	42	89.4	174	2	US-08-311-731A-261	Sequence 261, App	185	38	80.9	390	2	US-09-949-016-11598	Sequence 11598, A
113	42	89.4	525	2	US-10-101-464A-613	Sequence 613, App	186	38	80.9	396	2	US-09-854-133-436	Sequence 436, App
114	42	89.4	553	2	US-09-447-497-14	Sequence 14, Appl	187	38	80.9	418	2	US-09-417-251A-6	Sequence 6, Appl1
115	41	87.2	126	2	US-09-328-352-7886	Sequence 7886, Ap	188	38	80.9	418	2	US-09-417-251A-6	Sequence 6, Appl1
116	41	87.2	353	2	US-09-252-991A-26394	Sequence 26394, A	189	38	80.9	426	2	US-09-807-258-26	Sequence 26, Appl
117	39	83.0	122	2	US-09-621-976-3959	Sequence 3959, Ap	190	38	80.9	432	2	US-09-999-833A-90	Sequence 90, Appl
118	39	83.0	172	2	US-09-902-540-11920	Sequence 11920, A	191	38	80.9	432	2	US-10-020-445A-90	Sequence 90, Appl
119	39	83.0	172	2	US-08-916-576B-4	Sequence 4, Appl1	192	38	80.9	433	2	US-09-807-258-32	Sequence 32, Appl
120	39	83.0	172	2	US-10-078-337-4	Sequence 4, Appl1	193	38	80.9	433	2	US-09-807-258-32	Sequence 32, Appl
121	38	80.9	6	1	US-08-068-395A-4	Sequence 4, Appl1	194	38	80.9	466	2	US-08-984-919A-33	Sequence 33, Appl
122	38	80.9	6	1	US-08-464-365-4	Sequence 4, Appl1	195	38	80.9	468	2	US-08-874-102-33	Sequence 33, Appl
123	38	80.9	6	2	US-08-627-307A-5	Sequence 5, Appl1	196	38	80.9	470	2	US-08-984-919A-55	Sequence 55, Appl
124	38	80.9	6	2	US-07-901-713A-1	Sequence 1, Appl1	197	38	80.9	472	2	US-08-874-102-55	Sequence 55, Appl
125	38	80.9	7	1	US-08-923-536A-5	Sequence 5, Appl1	198	38	80.9	485	1	US-08-068-395A-1	Sequence 1, Appl1
126	38	80.9	8	2	US-08-557-122A-24	Sequence 24, Appl	199	38	80.9	488	2	US-08-464-365-1	Sequence 1, Appl1
127	38	80.9	8	2	US-09-262-666-24	Sequence 24, Appl	200	38	80.9	488	2	US-09-807-258-14	Sequence 14, Appl
128	38	80.9	10	2	US-07-901-713A-4	Sequence 4, Appl1	201	38	80.9	489	2	US-09-807-258-12	Sequence 12, Appl
129	38	80.9	19	2	US-09-469-847-359	Sequence 359, App	202	38	80.9	489	2	US-09-807-258-29	Sequence 29, Appl
130	38	80.9	19	2	US-09-489-847-360	Sequence 360, App	203	38	80.9	491	1	US-07-872-672B-3	Sequence 3, Appl1
131	38	80.9	80	2	US-09-902-540-15658	Sequence 15658, A	204	38	80.9	491	2	US-09-807-258-16	Sequence 16, Appl
132	38	80.9	110	2	US-09-417-251A-2	Sequence 2, Appl1	205	38	80.9	491	2	US-09-807-258-16	Sequence 16, Appl
133	38	80.9	110	2	US-09-902-540-11228	Sequence 11228, A	206	38	80.9	493	2	US-08-557-122A-31	Sequence 31, Appl
134	38	80.9	110	2	US-09-417-251A-2	Sequence 2, Appl1	207	38	80.9	493	2	US-09-262-666-31	Sequence 31, Appl
135	38	80.9	113	2	US-08-874-102-58	Sequence 58, Appl	208	38	80.9	495	2	US-08-984-919A-47	Sequence 47, Appl
136	38	80.9	113	2	US-08-984-919A-58	Sequence 58, Appl	209	38	80.9	496	2	US-09-807-258-4	Sequence 4, Appl1
137	38	80.9	129	1	US-08-557-122A-11	Sequence 11, Appl	210	38	80.9	496	2	US-09-807-258-4	Sequence 4, Appl1
138	38	80.9	129	1	US-09-262-666-11	Sequence 11, Appl	211	38	80.9	497	2	US-09-807-258-27	Sequence 27, Appl
139	38	80.9	131	1	US-08-557-122A-10	Sequence 10, Appl	212	38	80.9	497	2	US-08-874-102-47	Sequence 47, Appl
140	38	80.9	131	2	US-09-262-666-10	Sequence 10, Appl	213	38	80.9	499	2	US-09-807-258-8	Sequence 8, Appl1
141	38	80.9	133	2	US-09-807-258-6	Sequence 6, Appl1	214	38	80.9	503	2	US-09-270-767-45560	Sequence 45560, A
142	38	80.9	134	2	US-09-598-747-4	Sequence 4, Appl1	215	38	80.9	504	1	US-08-441-139-18	Sequence 18, Appl
143	38	80.9	139	2	US-08-874-102-36	Sequence 36, Appl	216	38	80.9	505	1	US-08-068-395A-3	Sequence 3, Appl1
144	38	80.9	141	1	US-08-984-919A-36	Sequence 9, Appl1	218	38	80.9	505	2	US-08-464-365-3	Sequence 2, Appl
145	38	80.9	141	1	US-08-557-122A-9	Sequence 9, Appl1	219	38	80.9	505	2	US-08-627-907A-2	Sequence 2, Appl1
146	38	80.9	141	1	US-09-262-666-9	Sequence 9, Appl1	220	38	80.9	508	1	US-08-557-122A-37	Sequence 37, Appl
147	38	80.9	143	1	US-08-557-122A-8	Sequence 8, Appl1	221	38	80.9	508	2	US-09-198-603C-4	Sequence 4, Appl1
148	38	80.9	143	2	US-09-262-666-8	Sequence 8, Appl1	222	38	80.9	508	2	US-09-262-666-37	Sequence 37, Appl
149	38	80.9	158	2	US-09-417-251A-4	Sequence 4, Appl1	223	38	80.9	508	2	US-09-807-258-30	Sequence 30, Appl
150	38	80.9	158	2	US-09-417-251A-4	Sequence 4, Appl1	223	38	80.9	509	1	US-08-557-122A-27	Sequence 27, Appl
151	38	80.9	163	1	US-08-557-122A-7	Sequence 7, Appl1	224	38	80.9	509	1	US-08-557-122A-29	Sequence 29, Appl
152	38	80.9	163	2	US-09-262-666-7	Sequence 7, Appl1	225	38	80.9	509	2	US-08-557-122A-29	Sequence 29, Appl
153	38	80.9	174	1	US-08-557-122A-6	Sequence 6, Appl1	226	38	80.9	509	2	US-09-262-666-27	Sequence 27, Appl
154	38	80.9	174	2	US-09-262-666-6	Sequence 6, Appl1	227	38	80.9	509	2	US-09-262-666-29	Sequence 29, Appl
155	38	80.9	179	2	US-08-874-102-41	Sequence 41, Appl	228	38	80.9	510	1	US-08-441-139-20	Sequence 20, Appl
156	38	80.9	179	2	US-08-874-102-44	Sequence 44, Appl	229	38	80.9	510	1	US-08-557-122A-28	Sequence 28, Appl
157	38	80.9	179	2	US-08-984-919A-41	Sequence 41, Appl	230	38	80.9	510	1	US-08-557-122A-30	Sequence 30, Appl
158	38	80.9	179	2	US-08-984-919A-44	Sequence 44, Appl	231	38	80.9	510	1	US-08-557-122A-36	Sequence 36, Appl
159	38	80.9	179	2	US-09-248-796A-18386	Sequence 18386, A	232	38	80.9	510	2	US-09-262-666-28	Sequence 28, Appl
160	38	80.9	200	1	US-08-557-122A-12	Sequence 12, Appl	233	38	80.9	510	2	US-09-262-666-30	Sequence 30, Appl
161	38	80.9	200	2	US-09-262-666-12	Sequence 12, Appl	234	38	80.9	510	2	US-09-262-666-36	Sequence 36, Appl
162	38	80.9	201	2	US-09-252-991A-29895	Sequence 29895, A	235	38	80.9	511	1	US-08-557-122A-4	Sequence 4, Appl1
163	38	80.9	207	2	US-09-603-208A-68	Sequence 68, Appl	236	38	80.9	511	2	US-09-262-666-4	Sequence 4, Appl1
164	38	80.9	207	2	US-09-605-703B-1726	Sequence 1726, Ap	237	38	80.9	512	1	US-08-557-122A-33	Sequence 33, Appl
165	38	80.9	235	2	US-08-781-420-6	Sequence 6, Appl1	238	38	80.9	512	2	US-09-262-666-33	Sequence 33, Appl
166	38	80.9	235	2	US-08-874-102-6	Sequence 6, Appl1	239	38	80.9	515	1	US-08-557-122A-3	Sequence 3, Appl1
167	38	80.9	235	2	US-08-984-919A-6	Sequence 6, Appl1	240	38	80.9	515	1	US-08-557-122A-34	Sequence 34, Appl
168	38	80.9	235	2	US-09-006-595A-6	Sequence 6, Appl1	241	38	80.9	515	2	US-09-262-666-3	Sequence 3, Appl1
169	38	80.9	244	2	US-09-807-258-20	Sequence 20, Appl	242	38	80.9	515	2	US-09-262-666-34	Sequence 34, Appl
170	38	80.9	266	2	US-09-248-796A-19900	Sequence 19900, A	243	38	80.9	515	2	US-09-807-258-38	Sequence 38, Appl
171	38	80.9	281	1	US-08-557-122A-5	Sequence 5, Appl1	244	38	80.9	521	1	US-08-557-122A-32	Sequence 32, Appl
172	38	80.9	281	2	US-09-262-666-5	Sequence 5, Appl1	245	38	80.9	521	2	US-09-262-666-32	Sequence 32, Appl
173	38	80.9	289	2	US-09-807-258-22	Sequence 22, Appl	246	38	80.9	522	2	US-09-368-588-2	Sequence 2, Appl1

247	38	80.9	530	1	US-08-557-122A-35	Sequence 35, Appl	320	34	72.3	362	2	US-09-296-840A-2	Sequence 2, Appl1
248	38	80.9	531	2	US-09-262-666-35	Sequence 35, Appl	321	34	72.3	367	2	US-09-296-840A-3	Sequence 3, Appl1
249	38	80.9	530	1	US-08-923-536A-12	Sequence 12, Appl	322	34	72.3	415	2	US-10-315-432-6	Sequence 6, Appl1
250	38	80.9	566	1	US-08-419-078-2	Sequence 2, Appl1	323	34	72.3	494	2	US-09-949-016-7790	Sequence 7790, Ap
251	38	80.9	566	1	US-08-726-883-2	Sequence 2, Appl1	324	34	72.3	541	2	US-09-417-251A-8	Sequence 8, Appl1
252	38	80.9	638	1	US-08-557-122A-38	Sequence 38, Appl1	325	34	72.3	541	2	US-09-417-251A-8	Sequence 8, Appl1
253	38	80.9	638	2	US-09-262-666-38	Sequence 38, Appl	326	34	72.3	541	2	US-09-902-540-11972	Sequence 11972, A
254	38	80.9	645	2	US-09-538-092-920	Sequence 920, App	327	34	72.3	551	2	US-09-417-251A-16	Sequence 16, Appl
255	38	80.9	3052	1	US-08-557-122A-26	Sequence 26, Appl	328	34	72.3	551	2	US-09-417-251A-16	Sequence 16, Appl
256	38	80.9	3052	2	US-09-262-666-26	Sequence 26, Appl	329	34	72.3	570	2	US-09-417-251A-10	Sequence 10, Appl
257	37	78.7	183	2	US-09-543-681A-5268	Sequence 5268, Ap	330	34	72.3	570	2	US-09-417-251A-10	Sequence 10, Appl
258	37	78.7	252	2	US-09-248-796A-18387	Sequence 18387, A	331	34	72.3	591	2	US-09-252-991A-31286	Sequence 3186, A
259	37	78.7	312	2	US-09-270-767-46652	Sequence 46652, A	332	34	72.3	675	2	US-10-104-047-3810	Sequence 3810, A
260	37	78.7	581	2	US-09-649-747A-13	Sequence 13, Appl	333	33	70.2	8	2	US-08-882-046-105	Sequence 105, App
261	37	78.7	581	2	US-09-649-747A-21	Sequence 21, Appl	334	33	70.2	8	2	US-09-566-047-105	Sequence 105, App
262	36	76.6	37	2	US-09-330-914A-10	Sequence 10, Appl	335	33	70.2	38	2	US-08-504-538A-17	Sequence 17, Appl
263	36	76.6	40	2	US-09-270-767-61997	Sequence 61997, A	336	33	70.2	38	2	US-08-630-032-17	Sequence 17, Appl
264	36	76.6	63	2	US-09-252-991A-22358	Sequence 22358, A	337	33	70.2	38	4	US-09-513-999C-5904	Sequence 5904, Ap
265	36	76.6	80	2	US-09-330-914A-4	Sequence 4, Appl1	338	33	70.2	53	2	US-09-248-796A-22500	Sequence 22500, A
266	36	76.6	104	2	US-09-583-110-3678	Sequence 5853, Ap	339	33	70.2	65	2	US-09-513-999C-5905	Sequence 5905, Ap
267	36	76.6	105	2	US-09-107-532A-6799	Sequence 6799, Ap	340	33	70.2	67	2	US-09-513-999C-5905	Sequence 5905, Ap
268	36	76.6	109	2	US-09-107-433-3306	Sequence 3306, Ap	341	33	70.2	78	2	US-09-513-999C-5905	Sequence 5905, Ap
269	36	76.6	109	2	US-09-107-433-3306	Sequence 3306, Ap	342	33	70.2	91	2	US-09-621-976-6450	Sequence 4906, Ap
270	36	76.6	109	2	US-09-902-540-13327	Sequence 13327, A	343	33	70.2	97	2	US-09-621-976-6450	Sequence 6454, Ap
271	36	76.6	126	2	US-09-902-540-15842	Sequence 15842, A	344	33	70.2	109	2	US-09-252-991A-28451	Sequence 28451, A
272	36	76.6	127	2	US-09-489-039A-13310	Sequence 13310, A	345	33	70.2	114	2	US-08-918-288-71	Sequence 71, Appl
273	36	76.6	127	2	US-09-621-976-6292	Sequence 6292, Ap	346	33	70.2	114	2	US-09-282-357-71	Sequence 71, Appl
274	36	76.6	129	2	US-10-104-047-2145	Sequence 2145, Ap	347	33	70.2	121	2	US-10-360-101-251	Sequence 251, App
275	36	76.6	140	2	US-09-330-914A-9	Sequence 9, Appl1	348	33	70.2	122	2	US-09-630-273-1	Sequence 11, Appl1
276	36	76.6	150	2	US-09-330-914A-6	Sequence 6, Appl1	349	33	70.2	125	2	US-09-199-637A-317	Sequence 317, App
277	36	76.6	168	2	US-09-252-991A-30752	Sequence 30752, A	350	33	70.2	130	2	US-09-621-976-6905	Sequence 4905, Ap
278	36	76.6	173	2	US-09-270-767-32359	Sequence 32359, A	351	33	70.2	134	2	US-08-543-246B-20	Sequence 20, Appl
279	36	76.6	173	2	US-09-270-767-47576	Sequence 47576, A	352	33	70.2	145	2	US-09-252-991A-13200	Sequence 13200, A
280	36	76.6	225	2	US-09-252-991A-29348	Sequence 29348, A	353	33	70.2	145	2	US-09-489-039A-13200	Sequence 13200, A
281	36	76.6	368	2	US-09-252-991A-32498	Sequence 32498, A	354	33	70.2	151	2	US-09-252-991A-17203	Sequence 17203, A
282	36	76.6	380	2	US-08-468-846-2	Sequence 2, Appl1	355	33	70.2	163	2	US-09-252-991A-22083	Sequence 22083, A
283	36	76.6	380	2	US-08-915-096A-2	Sequence 2, Appl1	356	33	70.2	171	2	US-09-902-540-13819	Sequence 13819, A
284	36	76.6	384	2	US-09-949-016-9661	Sequence 9661, Ap	357	33	70.2	178	2	US-08-748-506-17	Sequence 17, Appl
285	36	76.6	404	2	US-09-248-796A-15586	Sequence 15586, A	358	33	70.2	182	2	US-09-252-991A-17152	Sequence 17152, A
286	36	76.6	445	2	US-09-252-991A-20277	Sequence 20277, A	359	33	70.2	196	2	US-09-252-991A-26388	Sequence 26388, A
287	36	76.6	451	2	US-09-489-039A-12526	Sequence 12526, A	360	33	70.2	199	2	US-08-543-246B-9	Sequence 27691, A
288	36	76.6	461	2	US-09-543-681A-4286	Sequence 4286, Ap	361	33	70.2	216	2	US-08-543-246B-9	Sequence 9, Appl1
289	36	76.6	462	2	US-09-328-352-4742	Sequence 4742, Ap	362	33	70.2	216	2	US-08-543-246B-24	Sequence 24, Appl
290	36	76.6	491	2	US-09-540-236-2383	Sequence 2383, Ap	363	33	70.2	223	2	US-09-543-681A-8063	Sequence 8063, Ap
291	36	76.6	537	2	US-09-252-991A-31581	Sequence 31581, A	364	33	70.2	223	2	US-09-949-002-508	Sequence 508, App
292	36	76.6	572	2	US-09-949-016-11207	Sequence 11207, A	365	33	70.2	228	2	US-09-252-991A-32898	Sequence 32898, A
293	36	76.6	609	2	US-09-270-767-46418	Sequence 46418, A	366	33	70.2	234	2	US-08-918-288-9	Sequence 9, Appl1
294	36	76.6	627	2	US-09-902-540-15743	Sequence 15743, A	367	33	70.2	234	2	US-09-282-357-9	Sequence 5, Appl1
295	36	76.6	671	2	US-09-248-796A-15763	Sequence 15763, A	368	33	70.2	256	2	US-09-270-767-45809	Sequence 45809, A
296	36	76.6	671	2	US-09-657-472-4	Sequence 4, Appl1	369	33	70.2	258	2	US-08-303-861-18	Sequence 18, Appl
297	36	76.6	671	2	US-09-657-472-4	Sequence 4, Appl1	370	33	70.2	258	2	US-08-303-861-19	Sequence 19, Appl
298	36	76.6	961	4	PCT-US83-11725-4	Sequence 10131, A	371	33	70.2	258	2	US-09-213-343-2	Sequence 2, Appl1
299	35	74.5	105	2	US-09-949-016-10131	Sequence 10131, A	372	33	70.2	287	1	US-08-424-641B-10	Sequence 10, Appl
300	35	74.5	174	2	US-09-598-747-5	Sequence 5, Appl1	373	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
301	35	74.5	261	1	US-07-971-096-2	Sequence 11944, A	374	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
302	35	74.5	261	1	US-08-175-096-2	Sequence 2, Appl1	375	33	70.2	287	1	US-08-820-980-10	Sequence 10, Appl
303	35	74.5	663	2	US-09-270-767-45897	Sequence 45897, A	376	33	70.2	291	2	US-09-438-165A-359	Sequence 359, App
304	34	72.3	111	2	US-10-315-432-2	Sequence 30, Appl1	377	33	70.2	302	2	US-08-303-861-20	Sequence 20, Appl
305	34	72.3	138	2	US-09-898-659-30	Sequence 30, Appl1	378	33	70.2	302	2	US-09-248-796A-19800	Sequence 19800, A
306	34	72.3	148	2	US-09-270-767-46808	Sequence 46808, A	379	33	70.2	311	2	US-09-248-796A-20384	Sequence 20384, A
307	34	72.3	150	2	US-09-252-991A-29049	Sequence 29049, A	380	33	70.2	321	2	US-08-748-506-10	Sequence 10, Appl
308	34	72.3	163	2	US-09-252-991A-25077	Sequence 25077, A	381	33	70.2	321	2	US-08-748-506-11	Sequence 11, Appl
309	34	72.3	193	2	US-09-270-767-61072	Sequence 61072, A	382	33	70.2	321	2	US-08-748-506-12	Sequence 12, Appl
310	34	72.3	220	2	US-09-417-251A-12	Sequence 12, Appl	383	33	70.2	321	2	US-08-748-506-13	Sequence 13, Appl
311	34	72.3	220	2	US-09-417-251A-12	Sequence 12, Appl	384	33	70.2	321	2	US-08-748-506-18	Sequence 18, Appl
312	34	72.3	251	2	US-08-811-682-17	Sequence 17, Appl	385	33	70.2	321	2	US-08-748-506-19	Sequence 19, Appl
313	34	72.3	284	2	US-09-489-039A-7596	Sequence 7596, Ap	386	33	70.2	321	2	US-08-748-506-19	Sequence 19, Appl
314	34	72.3	294	2	US-09-417-251A-20	Sequence 20, Appl	387	33	70.2	358	2	US-10-104-047-3307	Sequence 3307, Ap
315	34	72.3	294	2	US-09-417-251A-20	Sequence 20, Appl	388	33	70.2	394	2	US-09-252-991A-28045	Sequence 28045, A
316	34	72.3	302	2	US-09-270-767-32413	Sequence 32413, A	389	33	70.2	433	2	US-09-252-991A-20376	Sequence 20376, A
317	34	72.3	302	2	US-09-270-767-47630	Sequence 47630, A	390	33	70.2	472	2	US-09-902-540-15926	Sequence 15926, A
318	34	72.3	330	2	US-09-252-991A-27803	Sequence 27803, A	391	33	70.2	477	2	US-09-876-221-2	Sequence 2, Appl1
319	34	72.3	331	2	US-09-252-991A-21022	Sequence 21022, A	392	33	70.2	482	2	US-09-902-540-14708	Sequence 14708, A

393	33	70.2	524	2	US-09-252-991A-19294	Sequence 19294, A	466	32	68.1	149	1	US-08-425-673-5	Sequence 5, Appl1
394	33	70.2	559	2	US-09-512-260A-3	Sequence 3, Appl1	467	32	68.1	152	2	US-09-270-767-62449	Sequence 62449, A
395	33	70.2	566	2	US-09-252-991A-18531	Sequence 18531, A	468	32	68.1	163	1	US-08-463-262A-10	Sequence 10, Appl1
396	33	70.2	580	2	US-09-252-991A-29484	Sequence 29484, A	469	32	68.1	163	1	US-08-463-989-10	Sequence 10, Appl1
397	33	70.2	585	2	US-09-248-796A-20439	Sequence 20439, A	470	32	68.1	163	2	US-09-003-577-10	Sequence 10, Appl1
398	33	70.2	604	1	US-08-735-041A-4	Sequence 4, Appl1	471	32	68.1	163	2	US-09-003-577-10	Sequence 10, Appl1
399	33	70.2	604	2	US-09-190-476B-4	Sequence 4, Appl1	472	32	68.1	163	2	US-08-864-541A-10	Sequence 10, Appl1
400	33	70.2	604	2	US-09-190-889A-4	Sequence 4, Appl1	473	32	68.1	207	2	US-08-811-519-16	Sequence 16, Appl1
401	33	70.2	604	2	US-09-190-889A-4	Sequence 4, Appl1	474	32	68.1	207	2	US-08-811-519-16	Sequence 16, Appl1
402	33	70.2	610	2	US-09-902-540-13312	Sequence 13312, A	475	32	68.1	259	2	US-09-270-767-48758	Sequence 48758, A
403	33	70.2	615	2	US-09-345-473E-49	Sequence 49, Appl1	476	32	68.1	282	2	US-09-461-912A-38	Sequence 38, Appl1
404	33	70.2	615	2	US-09-862-027-49	Sequence 49, Appl1	477	32	68.1	304	2	US-09-397-550-16	Sequence 16, Appl1
405	33	70.2	659	2	US-09-270-767-44991	Sequence 44991, A	478	32	68.1	305	2	US-09-327-767-41419	Sequence 41419, A
406	33	70.2	701	1	US-08-735-041A-6	Sequence 6, Appl1	479	32	68.1	323	2	US-09-397-550-17	Sequence 17, Appl1
407	33	70.2	701	2	US-09-190-476B-6	Sequence 6, Appl1	480	32	68.1	326	2	US-09-252-991A-10870	Sequence 10870, A
408	33	70.2	701	2	US-09-190-889A-6	Sequence 6, Appl1	481	32	68.1	333	2	US-09-252-991A-13345	Sequence 13345, A
409	33	70.2	701	2	US-09-190-889A-6	Sequence 6, Appl1	482	32	68.1	335	2	US-09-252-991A-24494	Sequence 24494, A
410	33	70.2	717	2	US-09-949-016-6273	Sequence 6273, Ap	483	32	68.1	350	2	US-09-397-550-18	Sequence 18, Appl1
411	33	70.2	772	2	US-09-949-016-7655	Sequence 7655, Ap	484	32	68.1	370	2	US-09-902-540-10486	Sequence 10486, A
412	33	70.2	850	2	US-10-029-180-96	Sequence 96, Appl1	485	32	68.1	373	2	US-09-149-476-374	Sequence 374, Ap
413	33	70.2	859	2	US-10-029-180-108	Sequence 108, App	486	32	68.1	382	2	US-09-328-352-7738	Sequence 7738, Ap
414	33	70.2	956	2	US-09-949-016-11332	Sequence 11332, A	487	32	68.1	388	2	US-09-605-703B-2250	Sequence 2250, Ap
415	33	70.2	1010	2	US-08-882-046-7	Sequence 7, Appl1	488	32	68.1	405	2	US-09-799-978-38	Sequence 38, Appl1
416	33	70.2	1010	2	US-09-566-047-7	Sequence 7, Appl1	489	32	68.1	411	1	US-08-381-432A-4	Sequence 4, Appl1
417	33	70.2	1036	2	US-09-068-740A-6	Sequence 6, Appl1	490	32	68.1	411	2	US-08-981-189B-12	Sequence 12, Appl1
418	33	70.2	1067	2	US-09-579-536C-18	Sequence 18, Appl1	491	32	68.1	411	2	US-09-799-978-18	Sequence 18, Appl1
419	33	70.2	1187	2	US-09-068-740A-7	Sequence 7, Appl1	492	32	68.1	411	2	US-09-881-401-4	Sequence 4, Appl1
420	33	70.2	1193	1	US-08-400-159-10	Sequence 10, Appl1	493	32	68.1	430	1	US-09-799-978-26	Sequence 26, Appl1
421	33	70.2	1193	2	US-08-611-729A-10	Sequence 10, Appl1	494	32	68.1	431	2	US-08-381-432A-2	Sequence 2, Appl1
422	33	70.2	1193	2	US-09-195-524-10	Sequence 10, Appl1	495	32	68.1	431	2	US-08-981-189B-11	Sequence 11, Appl1
423	33	70.2	1193	2	US-09-310-685-8	Sequence 8, Appl1	496	32	68.1	431	2	US-08-981-189B-13	Sequence 13, Appl1
424	33	70.2	1208	2	US-09-199-865-1	Sequence 1, Appl1	497	32	68.1	431	2	US-08-482-746-10	Sequence 10, Appl1
425	33	70.2	1208	2	US-10-213-329-1	Sequence 1, Appl1	498	32	68.1	431	2	US-09-580-734-10	Sequence 10, Appl1
426	33	70.2	1218	1	US-08-400-159-6	Sequence 6, Appl1	499	32	68.1	431	2	US-08-374-009-10	Sequence 10, Appl1
427	33	70.2	1218	2	US-08-611-729A-6	Sequence 6, Appl1	500	32	68.1	431	2	US-09-191-724-10	Sequence 10, Appl1
428	33	70.2	1218	2	US-08-862-046-2	Sequence 2, Appl1	501	32	68.1	431	2	US-09-799-978-20	Sequence 20, Appl1
429	33	70.2	1218	2	US-09-214-278-7	Sequence 7, Appl1	502	32	68.1	431	2	US-09-799-978-24	Sequence 24, Appl1
430	33	70.2	1218	2	US-09-068-740A-11	Sequence 11, Appl1	503	32	68.1	431	2	US-09-881-401-2	Sequence 2, Appl1
431	33	70.2	1218	2	US-09-855-740A-7	Sequence 7, Appl1	504	32	68.1	461	2	US-09-252-991A-19438	Sequence 19438, A
432	33	70.2	1218	2	US-09-566-047-2	Sequence 2, Appl1	505	32	68.1	483	2	US-09-252-991A-32383	Sequence 32383, A
433	33	70.2	1218	2	US-09-917-254-85	Sequence 85, Appl1	506	32	68.1	484	2	US-09-554-726A-12	Sequence 12, Appl1
434	33	70.2	1218	2	US-09-195-524-6	Sequence 6, Appl1	507	32	68.1	484	2	US-09-554-726A-12	Sequence 12, Appl1
435	33	70.2	1218	2	US-09-579-536C-1	Sequence 1, Appl1	508	32	68.1	522	2	US-10-070-634-11	Sequence 11, Appl1
436	33	70.2	1218	2	US-09-949-016-5902	Sequence 5902, Ap	509	32	68.1	625	2	US-09-252-991A-19871	Sequence 19871, A
437	33	70.2	1218	2	US-09-310-685-4	Sequence 4, Appl1	510	32	68.1	638	1	US-08-463-262A-11	Sequence 11, Appl1
438	33	70.2	1219	2	US-08-882-046-5	Sequence 5, Appl1	511	32	68.1	638	1	US-08-463-989-11	Sequence 11, Appl1
439	33	70.2	1219	2	US-09-566-047-5	Sequence 5, Appl1	512	32	68.1	638	2	US-09-003-574-11	Sequence 11, Appl1
440	33	70.2	1254	2	US-09-949-016-10297	Sequence 10297, A	513	32	68.1	638	2	US-09-003-574-11	Sequence 11, Appl1
441	33	70.2	1551	2	US-09-231-899-73	Sequence 73, Appl1	514	32	68.1	638	2	US-09-864-541A-11	Sequence 11, Appl1
442	33	70.2	1622	2	US-09-231-899-72	Sequence 72, Appl1	515	32	68.1	676	2	US-09-003-574-34	Sequence 34, Appl1
443	33	70.2	2146	2	US-09-949-016-6947	Sequence 6947, Ap	516	32	68.1	676	2	US-09-003-574-34	Sequence 34, Appl1
444	33	70.2	29	2	US-09-149-476-627	Sequence 627, App	517	32	68.1	676	2	US-09-864-541A-34	Sequence 34, Appl1
445	32	68.1	50	2	US-10-178-449A-26	Sequence 26, Appl1	518	32	68.1	692	2	US-09-003-574-31	Sequence 31, Appl1
446	32	68.1	64	2	US-09-149-476-504	Sequence 504, App	519	32	68.1	692	2	US-09-003-570-31	Sequence 31, Appl1
447	32	68.1	68	2	US-09-248-796A-24682	Sequence 24682, A	520	32	68.1	692	2	US-09-864-541A-31	Sequence 31, Appl1
448	32	68.1	70	2	US-08-482-746-8	Sequence 8, Appl1	521	32	68.1	765	2	US-09-949-016-10117	Sequence 10117, A
449	32	68.1	70	2	US-09-580-734-8	Sequence 8, Appl1	522	32	68.1	976	1	US-08-449-645A-18	Sequence 18, Appl1
450	32	68.1	70	2	US-08-374-009-8	Sequence 8, Appl1	523	32	68.1	976	1	US-08-702-367A-18	Sequence 18, Appl1
451	32	68.1	70	2	US-09-191-724-8	Sequence 8, Appl1	524	32	68.1	976	2	US-09-949-016-6499	Sequence 6499, Ap
452	32	68.1	76	2	US-10-178-449A-28	Sequence 28, Appl1	525	32	68.1	976	4	PCR-US95-04681-18	Sequence 18, Appl1
453	32	68.1	82	2	US-09-902-540-15132	Sequence 15132, A	526	32	68.1	977	1	US-08-673-789-8	Sequence 8, Appl1
454	32	68.1	103	1	US-08-241-853-27	Sequence 27, Appl1	527	32	68.1	1013	2	US-09-949-016-7991	Sequence 7991, Ap
455	32	68.1	103	1	US-08-850-917-27	Sequence 27, Appl1	528	32	68.1	1214	2	US-10-164-595-24	Sequence 24, Appl1
456	32	68.1	110	2	US-09-621-976-4028	Sequence 4028, Ap	529	32	68.1	1214	2	US-08-185-432-19	Sequence 19, Appl1
457	32	68.1	110	2	US-09-513-899C-7856	Sequence 7856, Ap	530	32	68.1	2703	2	US-08-899-232-4	Sequence 4, Appl1
458	32	68.1	143	2	US-10-012-231A-302	Sequence 302, App	531	32	68.1	2703	2	US-09-121-457-4	Sequence 4, Appl1
459	32	68.1	143	2	US-10-015-389A-302	Sequence 302, App	532	32	68.1	2813	2	US-08-896-449A-2	Sequence 2, Appl1
460	32	68.1	143	2	US-10-006-768A-302	Sequence 302, App	533	32	68.1	2813	2	US-09-132-652-2	Sequence 2, Appl1
461	32	68.1	143	2	US-10-015-671A-302	Sequence 302, App	534	32	68.1	2813	2	US-09-886-900A-2	Sequence 2, Appl1
462	32	68.1	143	2	US-10-015-393A-302	Sequence 302, App	535	32	68.1	2813	2	US-09-662-478C-2	Sequence 2, Appl1
463	32	68.1	143	2	US-10-011-833A-302	Sequence 302, App	536	32	68.1	4302	2	US-08-658-136-5	Sequence 5, Appl1
464	32	68.1	143	2	US-10-006-041A-302	Sequence 302, App	537	32	68.1	4302	2	US-09-052-462-8	Sequence 8, Appl1
465	32	68.1	143	2	US-10-012-064A-302	Sequence 302, App	538	32	68.1	4302	2	US-08-422-585-8	Sequence 8, Appl1

539	32	68.1	4302	2	US-09-052-262-8	Sequence 8, Appli	612	31	66.0	191	2	US-09-355-700-56	Sequence 56, Appli
540	32	68.1	4303	1	US-08-460-751-2	Sequence 2, Appli	613	31	66.0	191	2	US-08-882-816-2	Sequence 2, Appli
541	32	68.1	4303	2	US-09-479-478A-2	Sequence 2, Appli	614	31	66.0	191	2	US-09-574-708A-6	Sequence 6, Appli
542	32	68.1	4303	2	US-09-655-160-2	Sequence 2, Appli	615	31	66.0	191	2	US-08-802-052B-2	Sequence 2, Appli
543	31	66.0	4	1	US-07-820-688A-5	Sequence 5, Appli	616	31	66.0	191	2	US-09-431-888-4	Sequence 4, Appli
544	31	66.0	4	1	US-08-274-043B-5	Sequence 5, Appli	617	31	66.0	191	2	US-09-532-310B-2	Sequence 2, Appli
545	31	66.0	4	1	US-08-586-729A-5	Sequence 5, Appli	618	31	66.0	191	2	US-08-671-573B-5	Sequence 5, Appli
546	31	66.0	4	1	US-08-687-276-3	Sequence 5, Appli	619	31	66.0	191	2	US-09-392-931-6	Sequence 6, Appli
547	31	66.0	4	1	US-08-883-804-2	Sequence 2, Appli	620	31	66.0	191	2	US-09-631-092B-5	Sequence 15, Appli
548	31	66.0	4	2	US-08-504-538A-21	Sequence 21, Appli	621	31	66.0	191	2	US-08-734-443-14	Sequence 44, Appli
549	31	66.0	4	2	US-09-579-883A-1	Sequence 1, Appli	622	31	66.0	191	2	US-09-534-376A-56	Sequence 56, Appli
550	31	66.0	4	2	US-09-679-705-2	Sequence 1, Appli	623	31	66.0	191	2	US-10-268-447-6	Sequence 6, Appli
551	31	66.0	6	1	US-08-883-804-4	Sequence 4, Appli	624	31	66.0	191	6	5332671-4	Patent No. 5332671
552	31	66.0	8	1	US-08-571-985-27	Sequence 27, Appli	625	31	66.0	192	2	US-09-438-046-10	Sequence 10, Appli
553	31	66.0	8	1	US-09-116-766-27	Sequence 27, Appli	626	31	66.0	192	2	US-09-902-540-1548	Sequence 15448, A
554	31	66.0	8	2	US-08-836-480-34	Sequence 34, Appli	627	31	66.0	196	2	US-09-944-016-7039	Sequence 7039, Ap
555	31	66.0	8	2	US-09-562-897-34	Sequence 34, Appli	628	31	66.0	208	2	US-09-244-583-26	Sequence 26, Appli
556	31	66.0	16	2	US-09-160-513-217	Sequence 17, App	629	31	66.0	211	2	US-09-286-529-20	Sequence 20, Appli
557	31	66.0	28	2	US-09-330-041-31	Sequence 31, Appli	630	31	66.0	214	2	US-09-963-156A-1	Sequence 1, Appli
558	31	66.0	29	2	US-09-881-572A-25	Sequence 25, Appli	631	31	66.0	214	6	5240848-11	Patent No. 5240848
559	31	66.0	30	2	US-09-881-572A-5	Sequence 5, Appli	632	31	66.0	215	2	US-08-807-992B-3	Sequence 3, Appli
560	31	66.0	35	2	US-10-044-359-26	Sequence 26, Appli	633	31	66.0	215	2	US-08-586-039B-49	Sequence 49, Appli
561	31	66.0	38	1	US-08-339-256-16	Sequence 16, Appli	634	31	66.0	215	2	US-09-699-769-49	Sequence 49, Appli
562	31	66.0	43	2	US-09-244-583-20	Sequence 20, Appli	635	31	66.0	215	2	US-09-532-310B-3	Sequence 3, Appli
563	31	66.0	44	2	US-09-583-638-11	Sequence 11, Appli	636	31	66.0	215	2	US-09-392-931-8	Sequence 8, Appli
564	31	66.0	45	2	US-09-579-420B-19	Sequence 1, Appli	637	31	66.0	215	6	5219739-32	Patent No. 5219739
565	31	66.0	50	2	US-09-579-420B-19	Sequence 19, Appli	638	31	66.0	215	6	5219739-32	Patent No. 5219739
566	31	66.0	51	2	US-09-513-999C-7852	Sequence 7252, Ap	639	31	66.0	215	6	5240848-7	Patent No. 5240848
567	31	66.0	58	1	US-08-676-125A-36	Sequence 36, Appli	640	31	66.0	217	2	US-09-252-991A-24627	Sequence 24627, A
568	31	66.0	58	1	US-09-136-012A-36	Sequence 36, Appli	641	31	66.0	224	2	US-10-104-047-3343	Sequence 3343, Ap
569	31	66.0	58	2	US-08-676-124-67	Sequence 67, Appli	642	31	66.0	231	4	PCR-US96-09001-10	Sequence 10, Appli
570	31	66.0	58	2	US-09-414-878-67	Sequence 67, Appli	643	31	66.0	232	1	US-08-999-811-7	Sequence 7, Appli
571	31	66.0	58	2	US-09-240-136-67	Sequence 67, Appli	644	31	66.0	232	1	US-08-824-996-9	Sequence 9, Appli
572	31	66.0	58	2	US-09-638-770A-67	Sequence 67, Appli	645	31	66.0	232	2	US-08-807-992B-4	Sequence 4, Appli
573	31	66.0	58	2	US-10-167-351-67	Sequence 67, Appli	646	31	66.0	232	2	US-09-042-105-7	Sequence 7, Appli
574	31	66.0	77	2	US-09-502-540-11828	Sequence 11828, A	647	31	66.0	232	2	US-09-574-708A-10	Sequence 10, Appli
575	31	66.0	82	2	US-09-630-273-2	Sequence 2, Appli	648	31	66.0	232	2	US-09-532-310B-4	Sequence 4, Appli
576	31	66.0	88	2	US-09-902-540-10178	Sequence 10178, A	649	31	66.0	232	2	US-08-465-968-5	Sequence 5, Appli
577	31	66.0	102	2	US-09-621-976-5629	Sequence 5629, Ap	650	31	66.0	232	2	US-10-084-488-7	Sequence 7, Appli
578	31	66.0	106	2	US-09-383-586-13	Sequence 13, Appli	651	31	66.0	232	2	US-09-214-982-33	Sequence 33, Appli
579	31	66.0	106	2	US-09-823-038A-13	Sequence 13, Appli	652	31	66.0	232	2	US-10-268-447-10	Sequence 10, Appli
580	31	66.0	109	2	US-09-134-001C-5529	Sequence 5529, Ap	653	31	66.0	244	2	US-09-538-092-259	Sequence 259, Appli
581	31	66.0	113	2	US-10-104-047-3199	Sequence 3199, Ap	654	31	66.0	261	2	US-09-461-322-413	Sequence 413, App
582	31	66.0	126	2	US-09-107-532A-5571	Sequence 5571, Ap	655	31	66.0	261	2	US-10-012-542-413	Sequence 413, App
583	31	66.0	130	1	US-08-826-910-1	Sequence 1, Appli	656	31	66.0	261	2	US-10-115-123-413	Sequence 413, App
584	31	66.0	136	2	US-09-134-001C-5147	Sequence 5147, Ap	657	31	66.0	264	2	US-09-949-016-11555	Sequence 11555, A
585	31	66.0	136	2	US-09-252-991A-17421	Sequence 17421, A	658	31	66.0	268	2	US-09-270-767-42351	Sequence 42351, A
586	31	66.0	139	2	US-09-248-796A-28003	Sequence 28003, A	659	31	66.0	271	2	US-09-936-019-1	Sequence 1, Appli
587	31	66.0	146	2	US-09-690-454-47	Sequence 47, Appli	660	31	66.0	299	2	US-09-286-529-17	Sequence 17, Appli
588	31	66.0	146	2	US-09-523-323-59	Sequence 59, Appli	661	31	66.0	300	1	US-08-794-796-2	Sequence 2, Appli
589	31	66.0	147	2	US-08-469-260A-520	Sequence 520, Appli	662	31	66.0	300	2	US-09-632-277A-2	Sequence 2, Appli
590	31	66.0	147	2	US-08-488-446-520	Sequence 520, App	663	31	66.0	300	2	US-09-523-323-52	Sequence 52, Appli
591	31	66.0	147	2	US-08-467-344A-520	Sequence 520, App	664	31	66.0	300	2	US-09-896-096A-1	Sequence 1, Appli
592	31	66.0	147	2	US-08-424-550B-520	Sequence 520, App	665	31	66.0	300	2	US-09-936-019-3	Sequence 3, Appli
593	31	66.0	163	2	US-09-949-016-10680	Sequence 10680, A	666	31	66.0	301	2	US-09-252-991A-36483	Sequence 26483, A
594	31	66.0	163	6	5194596-17	Patent No. 5194596	667	31	66.0	308	2	US-09-252-991A-31991	Sequence 31991, A
595	31	66.0	164	6	5219739-17	Patent No. 5219739	668	31	66.0	310	2	US-09-949-016-7763	Sequence 7763, Ap
596	31	66.0	164	6	5219739-18	Patent No. 5219739	669	31	66.0	325	2	US-09-599-360B-74	Sequence 74, Appli
597	31	66.0	165	2	US-08-882-816-3	Sequence 3, Appli	670	31	66.0	329	2	US-09-252-991A-25774	Sequence 25774, A
598	31	66.0	165	2	US-08-802-052B-3	Sequence 3, Appli	671	31	66.0	330	2	US-09-252-991A-24637	Sequence 24637, A
599	31	66.0	165	2	US-09-706-722A-3	Sequence 3, Appli	672	31	66.0	333	2	US-09-949-016-7678	Sequence 7678, Ap
600	31	66.0	165	6	5194596-18	Patent No. 5194596	673	31	66.0	374	2	US-09-732-615-10	Sequence 10, Appli
601	31	66.0	165	6	5219739-19	Patent No. 5219739	674	31	66.0	374	2	US-10-273-051-10	Sequence 10, Appli
602	31	66.0	180	2	US-09-270-767-35692	Sequence 35692, A	675	31	66.0	383	2	US-09-489-039A-11768	Sequence 11768, A
603	31	66.0	180	2	US-09-270-767-50509	Sequence 50909, A	676	31	66.0	388	2	US-09-248-796A-17265	Sequence 17265, A
604	31	66.0	188	2	US-09-252-991A-32934	Sequence 32934, A	677	31	66.0	392	2	US-09-764-325A-23	Sequence 23, Appli
605	31	66.0	188	2	US-09-893-737-16	Sequence 16, Appli	678	31	66.0	392	2	US-09-912-935-23	Sequence 23, Appli
606	31	66.0	188	6	5332671-3	Patent No. 5332671	679	31	66.0	392	2	US-09-912-935-23	Sequence 23, Appli
607	31	66.0	191	2	US-08-567-200A-2	Sequence 2, Appli	680	31	66.0	392	2	US-09-943-016-6202	Sequence 6202, Ap
608	31	66.0	191	2	US-08-807-992B-2	Sequence 2, Appli	681	31	66.0	406	2	US-09-543-681A-5458	Sequence 5458, Ap
609	31	66.0	191	2	US-08-691-794-2	Sequence 2, Appli	682	31	66.0	406	2	US-09-543-681A-5458	Sequence 5458, Ap
610	31	66.0	191	2	US-08-795-430-56	Sequence 56, Appli	683	31	66.0	416	2	US-09-949-016-6201	Sequence 6201, Ap
611	31	66.0	191	2	US-09-392-932-3	Sequence 3, Appli	684	31	66.0	425	2	US-09-252-991A-29556	Sequence 29556, A

685	31	66.0	425	2	US-09-912-935-35	Sequence 35, App1	758	31	66.0	1003	2	US-09-430-323-217	Sequence 217, App
686	31	66.0	426	2	US-08-675-499A-6	Sequence 6, App1	759	31	66.0	1003	2	US-09-402-181B-336	Sequence 336, App
687	31	66.0	426	2	US-08-812-008-6	Sequence 6, App1	760	31	66.0	1003	2	US-09-721-456-336	Sequence 336, App
688	31	66.0	428	2	US-09-423-340-2	Sequence 2, App1	761	31	66.0	1003	2	US-10-054-295-217	Sequence 217, App
689	31	66.0	428	2	US-09-423-340-4	Sequence 4, App1	762	31	66.0	1003	2	US-09-438-486A-217	Sequence 217, App
690	31	66.0	428	2	US-09-820-155-2	Sequence 4, App1	763	31	66.0	1004	2	US-09-949-016-9925	Sequence 9925, App
691	31	66.0	428	2	US-09-820-155-4	Sequence 4, App1	764	31	66.0	1055	2	US-09-214-278-2	Sequence 2, App1
692	31	66.0	430	2	US-10-104-047-2204	Sequence 2204, App	765	31	66.0	1055	2	US-09-855-722-3	Sequence 3, App1
693	31	66.0	433	2	US-09-949-016-10900	Sequence 10900, App	766	31	66.0	1060	2	US-09-248-796A-18062	Sequence 18062, A
694	31	66.0	436	2	US-09-949-016-6983	Sequence 6983, App	767	31	66.0	1065	1	US-08-400-159-8	Sequence 8, App1
695	31	66.0	448	2	US-09-342-681C-17	Sequence 17, App1	768	31	66.0	1073	2	US-09-949-016-9771	Sequence 9771, App
696	31	66.0	448	2	US-09-342-681C-19	Sequence 19, App1	769	31	66.0	1148	2	US-08-882-046-4	Sequence 4, App1
697	31	66.0	449	2	US-09-912-935-34	Sequence 34, App1	770	31	66.0	1148	2	US-09-566-047-4	Sequence 4, App1
698	31	66.0	454	1	US-08-166-316-2	Sequence 2, App1	771	31	66.0	1196	2	US-10-237-551-200	Sequence 200, App
699	31	66.0	457	2	US-09-949-016-7165	Sequence 7165, App	772	31	66.0	1196	2	US-10-237-551-232	Sequence 232, App
700	31	66.0	473	2	US-09-902-540-13895	Sequence 13895, A	773	31	66.0	1208	2	US-09-463-702A-2	Sequence 2, App1
701	31	66.0	476	2	US-09-949-016-11726	Sequence 11726, A	774	31	66.0	1208	2	US-09-699-138-2	Sequence 2, App1
702	31	66.0	479	2	US-09-248-796A-15907	Sequence 15907, A	775	31	66.0	1212	2	US-09-214-278-3	Sequence 3, App1
703	31	66.0	484	2	US-09-248-796A-18223	Sequence 18223, A	776	31	66.0	1212	2	US-09-855-722-3	Sequence 3, App1
704	31	66.0	484	2	US-09-949-016-9440	Sequence 9440, App	777	31	66.0	1238	2	US-09-214-278-5	Sequence 5, App1
705	31	66.0	499	2	US-09-912-935-31	Sequence 31, App1	778	31	66.0	1238	2	US-09-855-722-5	Sequence 5, App1
706	31	66.0	529	2	US-09-912-935-28	Sequence 28, App1	779	31	66.0	1248	2	US-08-882-046-6	Sequence 6, App1
707	31	66.0	529	2	US-09-912-935-40	Sequence 40, App1	780	31	66.0	1248	2	US-09-566-047-6	Sequence 6, App1
708	31	66.0	530	2	US-09-912-935-38	Sequence 38, App1	781	31	66.0	1257	2	US-08-611-729A-8	Sequence 8, App1
709	31	66.0	584	1	US-08-313-888B-17	Sequence 17, App1	782	31	66.0	1257	2	US-09-195-524-8	Sequence 8, App1
710	31	66.0	585	2	US-09-370-807-4	Sequence 4, App1	783	31	66.0	1441	2	US-09-310-685-6	Sequence 6, App1
711	31	66.0	585	2	US-09-921-259-4	Sequence 4, App1	784	31	66.0	1452	2	US-09-949-016-10397	Sequence 2, App1
712	31	66.0	585	2	US-09-370-767-59685	Sequence 59685, A	785	31	66.0	1452	2	US-09-127-127-2	Sequence 2, App1
713	31	66.0	622	2	US-09-352-991A-30739	Sequence 30739, A	786	31	66.0	1564	2	US-09-976-594-309	Sequence 309, App
714	31	66.0	622	2	US-09-352-991A-23842	Sequence 23842, A	787	31	66.0	1125	2	US-09-562-702A-20	Sequence 20, App1
715	31	66.0	645	2	US-09-315-127-8	Sequence 8, App1	788	31	66.0	1125	2	US-09-561-818A-20	Sequence 20, App1
716	31	66.0	645	2	US-09-315-127-9	Sequence 9, App1	789	31	66.0	1257	2	US-10-037-182-12	Sequence 12, App1
717	31	66.0	654	2	US-09-315-127-11	Sequence 11, App1	790	31	66.0	1186	2	US-09-562-702A-18	Sequence 18, App1
718	31	66.0	654	2	US-09-315-127-12	Sequence 12, App1	791	31	66.0	1186	2	US-09-561-818A-18	Sequence 18, App1
719	31	66.0	657	2	US-09-348-796A-17674	Sequence 17674, A	792	31	66.0	1186	2	US-10-037-182-10	Sequence 10, App1
720	31	66.0	657	2	US-09-315-127-5	Sequence 5, App1	793	30.5	64.9	44	2	US-09-443-780C-30	Sequence 30, App1
721	31	66.0	657	2	US-09-315-127-6	Sequence 6, App1	794	30.5	64.9	44	2	US-09-079-723-14	Sequence 14, App1
722	31	66.0	657	2	US-09-070-630-13	Sequence 13, App1	795	30.5	64.9	145	2	US-09-471-276-1156	Sequence 1156, App
723	31	66.0	687	1	US-08-164-839-31	Sequence 31, App1	796	30	63.8	10	1	US-08-335-832-35	Sequence 35, App1
724	31	66.0	687	1	US-08-164-839-33	Sequence 33, App1	797	30	63.8	13	1	US-08-335-832-39	Sequence 39, App1
725	31	66.0	687	1	US-08-583-799-31	Sequence 31, App1	798	30	63.8	14	2	US-10-158-847-110	Sequence 130, App
726	31	66.0	687	1	US-08-583-799-33	Sequence 33, App1	799	30	63.8	14	2	US-10-158-847-130	Sequence 130, App
727	31	66.0	688	1	US-08-164-839-70	Sequence 70, App1	800	30	63.8	15	2	US-09-142-524D-104	Sequence 104, App
728	31	66.0	688	1	US-08-164-839-72	Sequence 72, App1	801	30	63.8	15	2	US-09-142-524D-105	Sequence 105, App
729	31	66.0	688	1	US-08-583-799-70	Sequence 70, App1	802	30	63.8	22	2	US-10-158-847-34	Sequence 34, App1
730	31	66.0	688	1	US-08-583-799-72	Sequence 72, App1	803	30	63.8	22	2	US-10-158-847-34	Sequence 34, App1
731	31	66.0	694	1	US-08-164-839-4	Sequence 4, App1	804	30	63.8	24	2	US-08-467-023-191	Sequence 191, App
732	31	66.0	694	1	US-08-583-799-4	Sequence 4, App1	805	30	63.8	32	2	US-08-632-511A-6	Sequence 6, App1
733	31	66.0	695	1	US-08-164-839-6	Sequence 6, App1	806	30	63.8	32	2	US-09-091-590A-12	Sequence 12, App1
734	31	66.0	695	1	US-08-164-839-8	Sequence 8, App1	807	30	63.8	32	2	US-09-488-200-6	Sequence 6, App1
735	31	66.0	695	1	US-08-583-799-6	Sequence 6, App1	808	30	63.8	37	2	US-09-205-258-447	Sequence 447, App
736	31	66.0	695	1	US-08-583-799-8	Sequence 8, App1	809	30	63.8	37	2	US-10-004-860-447	Sequence 447, App
737	31	66.0	696	1	US-08-164-839-10	Sequence 10, App1	810	30	63.8	58	2	US-10-178-213-228	Sequence 228, App
738	31	66.0	696	1	US-08-583-799-10	Sequence 10, App1	811	30	63.8	58	2	US-10-178-213-231	Sequence 231, App
739	31	66.0	780	1	US-08-887-798-2	Sequence 2, App1	812	30	63.8	58	2	US-10-178-213-234	Sequence 234, App
740	31	66.0	786	2	US-09-949-016-10898	Sequence 10898, A	813	30	63.8	86	2	US-10-178-213-227	Sequence 227, App
741	31	66.0	801	2	US-09-270-767-44264	Sequence 44264, A	814	30	63.8	86	2	US-10-178-213-233	Sequence 230, App
742	31	66.0	816	2	US-09-949-016-10664	Sequence 10664, A	815	30	63.8	86	2	US-10-178-213-230	Sequence 233, App
743	31	66.0	832	1	US-08-677-734A-12	Sequence 12, App1	816	30	63.8	87	2	US-09-252-998A-20264	Sequence 20264, A
744	31	66.0	832	2	US-09-097-053-12	Sequence 12, App1	817	30	63.8	111	1	US-08-543-328-8	Sequence 8, App1
745	31	66.0	881	2	US-09-489-039A-10137	Sequence 10137, A	818	30	63.8	111	1	US-08-420-526-8	Sequence 8, App1
746	31	66.0	886	4	US-09-543-681A-5627	Sequence 5627, App	819	30	63.8	118	2	US-09-198-452A-1234	Sequence 1234, App
747	31	66.0	889	4	PCT-US93-11725-2	Sequence 2, App1	820	30	63.8	127	2	US-08-467-023-188	Sequence 188, App
748	31	66.0	893	2	US-09-328-352-6626	Sequence 6626, App	821	30	63.8	127	2	US-08-467-023-190	Sequence 190, App
749	31	66.0	898	2	US-09-902-540-11561	Sequence 11561, A	822	30	63.8	144	2	US-10-101-464A-789	Sequence 789, App
750	31	66.0	905	2	US-10-104-047-2728	Sequence 2728, App	823	30	63.8	165	2	US-09-148-545-149	Sequence 149, App
751	31	66.0	915	2	US-09-540-236-3026	Sequence 3026, App	824	30	63.8	165	2	US-09-621-011-149	Sequence 149, App
752	31	66.0	958	1	US-08-426-236-4	Sequence 4, App1	825	30	63.8	175	2	US-09-552-991A-25708	Sequence 25708, A
753	31	66.0	965	2	US-09-538-092-650	Sequence 650, App	826	30	63.8	187	2	US-09-252-991A-29971	Sequence 29971, A
754	31	66.0	968	2	US-08-426-236-2	Sequence 2, App1	827	30	63.8	217	2	US-09-902-540-15578	Sequence 15578, A
755	31	66.0	1003	2	US-08-851-833A-217	Sequence 217, App	828	30	63.8	223	2	US-09-541-759-1	Sequence 1, App1
756	31	66.0	1003	2	US-08-974-549A-336	Sequence 336, App	829	30	63.8	227	2	US-09-823-038A-50	Sequence 50, App1
757	31	66.0	1003	2	US-08-854-050-217	Sequence 217, App	830	30	63.8	230	2	US-09-148-545-214	Sequence 214, App

831	30	63.8	230	2	US-09-621-011-214	Sequence 214, App	904	29	61.7	389	2	US-09-949-002-501	Sequence 501, App
832	30	63.8	231	2	US-09-252-991A-22801	Sequence 22801, A	905	29	61.7	391	2	US-09-270-767-59093	Sequence 59093, A
833	30	63.8	231	2	US-09-148-545-215	Sequence 215, App	906	29	61.7	427	2	US-09-902-540-10191	Sequence 10191, A
834	30	63.8	231	2	US-09-621-011-215	Sequence 215, App	907	29	61.7	430	2	US-09-902-540-10816	Sequence 10816, A
835	30	63.8	269	2	US-09-134-000C-5214	Sequence 5214, App	908	29	61.7	449	1	US-08-819-458A-16	Sequence 16, App
836	30	63.8	273	2	US-09-270-767-37504	Sequence 37504, A	909	29	61.7	523	2	US-10-104-047-2046	Sequence 2046, App
837	30	63.8	273	2	US-09-270-767-52721	Sequence 52721, A	910	29	61.7	570	2	US-09-252-991A-16680	Sequence 16680, A
838	30	63.8	277	2	US-09-538-092-710	Sequence 710, App	911	29	61.7	662	2	US-09-061-768A-25	Sequence 25, App
839	30	63.8	285	2	US-09-538-092-148	Sequence 148, App	912	29	61.7	662	2	US-09-949-002-315	Sequence 315, App
840	30	63.8	326	1	US-08-292-549-4	Sequence 4, App1	913	29	61.7	662	2	US-09-949-002-315	Sequence 315, App
841	30	63.8	326	4	PCT-US91-02207-4	Sequence 4, App1	914	29	61.7	674	2	US-09-270-767-43706	Sequence 43706, A
842	30	63.8	349	2	US-09-438-185A-935	Sequence 935, App	915	29	61.7	838	2	US-10-104-047-2819	Sequence 2819, App
843	30	63.8	391	2	US-09-252-991A-28342	Sequence 28342, A	916	29	61.7	934	2	US-09-949-016-7286	Sequence 7286, App
844	30	63.8	484	2	US-09-252-991A-19511	Sequence 19511, A	917	29	61.7	1026	2	US-10-104-047-2509	Sequence 2509, App
845	30	63.8	489	2	US-09-393-171-7	Sequence 7, App1	918	29	61.7	2052	2	US-09-045-201A-2	Sequence 2, App1
846	30	63.8	514	2	US-08-467-023-134	Sequence 134, App	919	29	61.7	2052	2	US-09-619-062-2	Sequence 2, App1
847	30	63.8	582	1	US-08-431-080-16	Sequence 16, App	920	29	61.7	2296	1	US-08-288-819A-27	Sequence 27, App1
848	30	63.8	582	1	US-08-938-534-16	Sequence 16, App1	921	29	61.7	2296	1	US-08-980-337-27	Sequence 27, App1
849	30	63.8	582	2	US-09-145-294-16	Sequence 16, App1	922	29	61.7	2296	2	US-09-357-375-27	Sequence 27, App1
850	30	63.8	596	2	US-09-171-337A-6	Sequence 6, App1	923	29	61.7	4019	2	US-09-854-133-425	Sequence 425, App
851	30	63.8	634	2	US-09-631-022-6	Sequence 6, App1	924	28.5	60.6	54	2	US-08-469-260A-177	Sequence 177, App
852	30	63.8	634	2	US-09-489-039A-8399	Sequence 8399, App	925	28.5	60.6	54	2	US-08-469-260A-177	Sequence 177, App
853	30	63.8	681	2	US-09-943-681A-5453	Sequence 5453, App	926	28.5	60.6	54	2	US-08-467-344A-177	Sequence 177, App
854	30	63.8	681	2	US-09-489-039A-11863	Sequence 11863, A	927	28.5	60.6	54	2	US-08-424-550B-177	Sequence 177, App
855	30	63.8	691	2	US-09-889-746-8	Sequence 8, App1	928	28.5	60.6	877	1	US-08-072-574-12	Sequence 12, App1
856	30	63.8	742	2	US-09-252-991A-24489	Sequence 24489, A	929	28.5	60.6	877	1	US-08-468-270-12	Sequence 12, App1
857	30	63.8	930	2	US-09-177-650-96	Sequence 96, App1	930	28.5	60.6	877	2	US-08-367-264-12	Sequence 12, App1
858	30	63.8	989	2	US-09-954-987B-171	Sequence 171, App	931	28.5	60.6	877	2	US-09-153-757-12	Sequence 12, App1
859	30	63.8	1049	2	US-09-999-833A-496	Sequence 496, App	932	28.5	60.6	877	2	US-09-459-715-12	Sequence 12, App1
860	30	63.8	1049	2	US-09-954-987B-170	Sequence 170, App	933	28.5	60.6	942	2	US-09-695-481-2	Sequence 2, App1
861	30	63.8	1049	2	US-09-954-987B-172	Sequence 172, App	934	28.5	60.6	1043	2	US-09-695-481-6	Sequence 6, App1
862	30	63.8	1049	2	US-10-020-445A-496	Sequence 496, App	935	28.5	60.6	1180	1	US-08-072-574-8	Sequence 8, App1
863	30	63.8	2523	1	US-08-185-432-18	Sequence 18, App1	936	28.5	60.6	1180	1	US-08-468-270-8	Sequence 8, App1
864	30	63.8	2523	2	US-08-899-232-3	Sequence 3, App1	937	28.5	60.6	1180	2	US-08-367-264-8	Sequence 8, App1
865	30	63.8	2523	2	US-09-121-457-3	Sequence 3, App1	938	28.5	60.6	1180	2	US-08-660-148-2	Sequence 2, App1
866	30	63.8	2556	1	US-08-185-432-17	Sequence 17, App1	939	28.5	60.6	1180	2	US-09-153-757-8	Sequence 8, App1
867	30	63.8	2556	1	US-08-083-590A-20	Sequence 20, App1	940	28.5	60.6	1180	2	US-09-459-715-8	Sequence 8, App1
868	30	63.8	2556	2	US-08-532-384-20	Sequence 20, App1	941	28.5	60.6	1212	1	US-08-072-574-10	Sequence 10, App1
869	30	63.8	2556	2	US-08-899-232-2	Sequence 2, App1	942	28.5	60.6	1212	1	US-08-468-270-10	Sequence 10, App1
870	30	63.8	2556	2	US-09-121-457-2	Sequence 2, App1	943	28.5	60.6	1212	2	US-08-367-264-10	Sequence 10, App1
871	29	61.7	14	2	US-09-646-691B-86	Sequence 86, App1	944	28.5	60.6	1212	2	US-08-660-148-5	Sequence 5, App1
872	29	61.7	16	2	US-09-646-691B-85	Sequence 85, App1	945	28.5	60.6	1212	2	US-08-153-757-10	Sequence 10, App1
873	29	61.7	16	2	US-09-646-691B-84	Sequence 84, App1	946	28.5	60.6	1212	2	US-09-459-715-10	Sequence 10, App1
874	29	61.7	17	2	US-09-646-691B-83	Sequence 83, App1	947	28.5	60.6	1212	2	US-09-695-481-7	Sequence 7, App1
875	29	61.7	18	2	US-09-806-781-57	Sequence 57, App1	948	28	59.6	6	1	US-08-079-812-32	Sequence 32, App1
876	29	61.7	18	2	US-09-880-132-57	Sequence 57, App1	949	28	59.6	7	2	US-08-891-271-20	Sequence 20, App1
877	29	61.7	18	2	US-09-646-691B-81	Sequence 81, App1	950	28	59.6	11	2	US-10-004-381-33	Sequence 33, App1
878	29	61.7	38	2	US-09-646-691B-50	Sequence 50, App1	951	28	59.6	15	1	US-08-377-432-21	Sequence 21, App1
879	29	61.7	38	2	US-09-646-691B-53	Sequence 53, App1	952	28	59.6	15	1	US-08-377-432-22	Sequence 22, App1
880	29	61.7	38	2	US-09-646-691B-57	Sequence 57, App1	953	28	59.6	15	1	US-08-377-432-23	Sequence 23, App1
881	29	61.7	44	2	US-09-270-767-34152	Sequence 34152, A	954	28	59.6	15	2	US-08-900-241-21	Sequence 21, App1
882	29	61.7	44	2	US-09-270-767-49369	Sequence 49369, A	955	28	59.6	15	2	US-08-900-241-22	Sequence 22, App1
883	29	61.7	58	1	US-08-358-160-90	Sequence 90, App1	956	28	59.6	15	2	US-08-900-241-23	Sequence 23, App1
884	29	61.7	63	2	US-09-008-271A-1	Sequence 1, App1	957	28	59.6	15	2	US-09-807-148-24	Sequence 24, App1
885	29	61.7	92	1	US-09-368-415-1	Sequence 1, App1	958	28	59.6	15	2	US-09-807-148-25	Sequence 25, App1
886	29	61.7	93	1	US-08-737-825-7	Sequence 7, App1	959	28	59.6	15	2	US-09-807-148-26	Sequence 26, App1
887	29	61.7	100	2	US-09-248-796A-21060	Sequence 21060, A	960	28	59.6	16	2	US-08-433-441A-17	Sequence 17, App1
888	29	61.7	109	2	US-09-252-991A-27445	Sequence 27445, A	961	28	59.6	16	2	US-09-620-091-108	Sequence 108, App
889	29	61.7	122	2	US-09-270-767-40970	Sequence 40970, A	962	28	59.6	18	1	US-08-084-718-30	Sequence 30, App1
890	29	61.7	122	2	US-09-270-767-56186	Sequence 56186, A	963	28	59.6	18	1	US-08-443-976-30	Sequence 30, App1
891	29	61.7	155	2	US-09-857-896A-24	Sequence 24, App1	964	28	59.6	18	1	US-08-443-976-30	Sequence 30, App1
892	29	61.7	159	2	US-09-252-991A-29329	Sequence 29329, A	965	28	59.6	20	1	US-08-084-718-35	Sequence 35, App1
893	29	61.7	253	2	US-09-355-166-13	Sequence 13, App1	966	28	59.6	20	1	US-08-443-976-35	Sequence 35, App1
894	29	61.7	262	2	US-10-104-047-2276	Sequence 2276, App	967	28	59.6	20	1	US-08-443-977-35	Sequence 35, App1
895	29	61.7	269	2	US-09-538-092-396	Sequence 396, App	968	28	59.6	28	2	US-09-713-950-1	Sequence 1, App1
896	29	61.7	290	2	US-09-252-991A-19463	Sequence 19463, A	969	28	59.6	38	2	US-09-646-691B-9	Sequence 9, App1
897	29	61.7	319	2	US-09-489-039A-7864	Sequence 7864, App	970	28	59.6	38	2	US-09-646-691B-17	Sequence 17, App1
898	29	61.7	325	2	US-09-270-767-38483	Sequence 38483, A	971	28	59.6	38	2	US-09-646-691B-48	Sequence 48, App1
899	29	61.7	325	2	US-09-270-767-53700	Sequence 53700, A	972	28	59.6	38	2	US-09-646-691B-56	Sequence 56, App1
900	29	61.7	326	2	US-09-252-991A-29943	Sequence 29943, A	973	28	59.6	38	2	US-09-646-691B-59	Sequence 59, App1
901	29	61.7	357	2	US-09-552-991A-26979	Sequence 26979, A	974	28	59.6	38	2	US-09-646-691B-60	Sequence 60, App1
902	29	61.7	365	2	US-09-503-219B-8	Sequence 8, App1	975	28	59.6	38	2	US-09-646-691B-74	Sequence 74, App1
903	29	61.7	365	2	US-10-039-659A-10	Sequence 10, App1	976	28	59.6	41	2	US-09-270-767-38184	Sequence 38184, A

977	28	59.6	41	2	US-09-270-767-53401	Sequence 53401, A
978	28	59.6	45	2	US-08-286-747C-65	Sequence 65, Appl
979	28	59.6	45	2	US-08-965-903B-17	Sequence 17, Appl
980	28	59.6	45	2	US-08-965-903B-18	Sequence 18, Appl
981	28	59.6	45	2	US-08-834-130A-65	Sequence 65, Appl
982	28	59.6	46	2	US-09-423-418D-4	Sequence 4, Appl
983	28	59.6	49	2	US-08-905-223-463	Sequence 463, App
984	28	59.6	52	2	US-09-621-976-7037	Sequence 7037, App
985	28	59.6	56	1	US-07-598-737C-23	Sequence 23, Appl
986	28	59.6	56	1	US-07-598-737C-25	Sequence 25, Appl
987	28	59.6	56	1	US-07-598-737C-27	Sequence 27, Appl
988	28	59.6	56	1	US-07-598-737C-28	Sequence 28, Appl
989	28	59.6	56	1	US-07-598-737C-33	Sequence 33, Appl
990	28	59.6	56	1	US-08-084-718-5	Sequence 5, Appl
991	28	59.6	56	1	US-08-084-718-6	Sequence 6, Appl
992	28	59.6	56	1	US-08-084-718-8	Sequence 8, Appl
993	28	59.6	56	1	US-08-084-718-9	Sequence 9, Appl
994	28	59.6	56	1	US-08-084-718-29	Sequence 29, Appl
995	28	59.6	56	1	US-08-084-718-34	Sequence 34, Appl
996	28	59.6	56	1	US-08-443-976-5	Sequence 5, Appl
997	28	59.6	56	1	US-08-443-976-6	Sequence 6, Appl
998	28	59.6	56	1	US-08-443-976-8	Sequence 8, Appl
999	28	59.6	56	1	US-08-443-976-9	Sequence 9, Appl
1000	28	59.6	56	1	US-08-443-976-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-883-804-5
; Sequence 5, Application US/08883804
; Patent No. 5985261
; GENERAL INFORMATION:
; APPLICANT: white, Carl W.
; APPLICANT: Dae, Kumda C.
; TITLE OF INVENTION: USE OF THIOREDOXIN-LIKE MOLECULES FOR
; TITLE OF INVENTION: INDUCTION OF MMSD TO TREAT OXIDATIVE DAMAGE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross P.C.
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,804
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-40
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-883-804-5

Query Match 100.0%; Score 47; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 1 WCGPCK 6

RESULT 2
US-08-627-907A-6
; Sequence 6, Application US/08627907A
; Patent No. 6060302
; GENERAL INFORMATION:
; APPLICANT: HIRANO, Naoto
; APPLICANT: HIRAI, Hisamaru
; TITLE OF INVENTION: HUMAN PHOSPHOLIPASE C-ALPHA AND DNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,907A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-238402
; FILING DATE: 24-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01572
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-627-907A-6

Query Match 100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 1 WCGPCK 6

RESULT 3
US-07-901-713A-3
; Sequence 3, Application US/07901713A
; Patent No. 6291205
; GENERAL INFORMATION:
; APPLICANT: Tuille, Michael F.
; APPLICANT: Freedman, Robert B.
; APPLICANT: Markus, Henry Z.
; APPLICANT: Schultz, Loren D.
; APPLICANT: Montgomery, Donna L.

APPLICANT: Ellis, Ronald W.
TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF
TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES
TITLE OF INVENTION: CEREVISIAE
FILE REFERENCE: 18469
CURRENT APPLICATION NUMBER: US/07/901,713A
CURRENT FILING DATE: 1992-06-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S. cerevisiae PDI thioredoxin active site
US-07-901-713A-3

Query Match 100.0%; Score 47; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
DB 1 WCGPCK 6

RESULT 4
US-08-750-142B-54
Sequence 54, Application US/08750142B
Patent No. 6228373
GENERAL INFORMATION:
APPLICANT: Bergerstrand, Hakan
APPLICANT: Eriksson, Tomas
APPLICANT: Lindvall, Magnus
APPLICANT: Samstrand, Bengt
TITLE OF INVENTION: NEW PEPTIDES WITH
TITLE OF INVENTION: IMMUNOMODULATORY EFFECTS
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,142B
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/SE96/00365
FILING DATE: 23-MAR-1996
APPLICATION NUMBER: SE9501067-4
FILING DATE: 24-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06225/062001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-750-142B-54

Query Match 100.0%; Score 47; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
DB 1 WCGPCK 6

RESULT 5
5210073-1
Patent No. 5210073
APPLICANT: YODOI, JUNJI,UCHIDA, ATSUSHI,TAGAWA, YUTAKA
MITSUI, AKIRA,HIRAKAWA, TADASHI
TITLE OF INVENTION: METHOD FOR TREATING CANCER THERAPY
RADIATION DAMAGE OR ARTERIOSCLEROSIS USING HUMAN ADP
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/589,616
FILING DATE: 28-SEP-1990
SEQ ID NO:1
LENGTH: 104
5210073-1

Query Match 100.0%; Score 47; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
 |||||
DB 30 WCGPCK 35

RESULT 6
US-08-826-910-3
Sequence 3, Application US/08826910
Patent No. 5919657
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Putvi
TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,910
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0268 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 339649
US-08-826-910-3

Query Match 100.0%; Score 47; DB 1; length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 7
US-08-826-910-4
Sequence 4, Application US/08826910
Patent No. 5919657
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: THIOREDOXIN-LIKE PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,910
FILING DATE: Herewith
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0268 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 453972
US-08-826-910-4

Query Match 100.0%; Score 47; DB 1; length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 8

US-09-601-144-68
Sequence 68, Application US/09601144
Patent No. 6566514
GENERAL INFORMATION:
APPLICANT: Wright, Jim A.
APPLICANT: Young, Aiping H.
APPLICANT: Lee, Yoon S.
TITLE OF INVENTION: OLIGONUCLEOTIDE SEQUENCES COMPLEMENTARY TO THIOREDOXIN
TITLE OF INVENTION: AND THIOREDOXIN REDUCTASE GENES AND METHODS OF USING
TITLE OF INVENTION: SAME TO MODULATE CELL GROWTH
FILE REFERENCE: 683-112US-A
CURRENT APPLICATION NUMBER: US/09/601,144
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/073,196
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 68
LENGTH: 105
TYPE: PRT
ORGANISM: Human
US-09-601-144-68

Query Match 100.0%; Score 47; DB 2; length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 9
US-09-513-999C-8037
Sequence 8037, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 8037
LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-8037

Query Match 100.0%; Score 47; DB 2; length 105;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 10
US-08-386-729A-10
Sequence 10, Application US/08386729A
Patent No. 5753435
GENERAL INFORMATION:
APPLICANT: Aharonowitz, Yair
APPLICANT: Van Der Voort, Lucia H. M.
APPLICANT: Cohen, Gerald
APPLICANT: Bovenberg, Roelof A. L.


```

APPLICANT: Schreiber, Rachel
APPLICANT: Argaman, Anat
APPLICANT: Av-Gay, Yossef
APPLICANT: Nan, Helena M.
APPLICANT: Kaltefleiter, Alfred
APPLICANT: Pallisa, Harriet
TITLE OF INVENTION: An oxido reductase enzyme system
TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes
TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme
TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Well, Gotel & Manges
STREET: 2882 Sand Hill Road, Ste. 280
CITY: Menlo Park
STATE: CA
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/386,729A
FILING DATE: 10-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/274,043
FILING DATE: 12-JULY-1994
APPLICATION NUMBER: US 07/820,688
FILING DATE: 24-MARCH-1992
APPLICATION NUMBER: PCT/IL91/000101
FILING DATE: 18-JUNE-1991
APPLICATION NUMBER: EP 90201598.1
FILING DATE: 18-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GBRO-024/02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ. ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-386-729A-10

Query Match          100.0%; Score 47; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 11
US-07-745-382-22
Sequence 22, Application US/07/45382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.

```

```

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Caser, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-745-382-22

```

```

Query Match          100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 12
US-07-921-848-22
Sequence 22, Application US/07/921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: Lavallie, Edward
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991

```

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Caery, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G15188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-921-848-22

Query Match          100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37

RESULT 13
US-08-165-301A-22
; Sequence 22, Application US/08165301A
; Patent No. 5646016
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,301A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: G1 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-165-301A-22

Query Match          100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37
```

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Caery, Luann
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: G15188A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-921-848-22

Query Match          100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37

RESULT 14
US-08-165-301A-26
; Sequence 26, Application US/08165301A
; Patent No. 5646016
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/165,301A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: G1 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-165-301A-26

Query Match          100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37

RESULT 15
US-08-165-301A-28
; Sequence 28, Application US/08165301A
; Patent No. 5646016
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
```

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-28

Query Match 100.0%; Score 47; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

RESULT 16
US-08-810-436-22
Sequence 22, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-22

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

RESULT 17
US-08-810-436-26
Sequence 26, Application US/08810436
Patent No. 6143524
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallie, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,436
FILING DATE: 04-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/165,301
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-436-26

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 32 WCGPCK 37

Db 32 WCGPCK 37

```
RESULT 18
US-08-810-436-28
; Sequence 28, Application US/08810436
; Patent No. 6143524
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBiasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallie, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; City: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,436
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/165,301
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinel, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-436-28

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 19
US-09-485-885-17
; Sequence 17, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Gislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
```

```
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-17
```

```
Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 32 WCGPCK 37
```

```
RESULT 20
US-09-166-966E-10
; Sequence 10, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-TU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 10
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: thioredoxin
; LOCATION: 1..109
; OTHER INFORMATION: amino acid of thioredoxin
US-09-166-966E-10
```

```
Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 32 WCGPCK 37
```

```
RESULT 21
US-09-248-796A-19911
; Sequence 19911, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19911
```

LENGTH: 109
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-19911

Query Match 100.0%; Score 47; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 35 WCGPCK 40

RESULT 22
PCT-US94-14179-22
Sequence 22, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION/DOCKET NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-22

Query Match 100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 23
PCT-US94-14179-26
Sequence 26, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen

APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meinerdt, M. C.
REGISTRATION/DOCKET NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-26

Query Match 100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 24
PCT-US94-14179-28
Sequence 28, Application PC/TUS9414179
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14179
FILING DATE:
CLASSIFICATION:

```
/
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Mehnert, M. C.
/   REGISTRATION NUMBER: 33,544
/   REFERENCE/DOCKET NUMBER: GI 5188D
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (617) 876-1170
/   TELEFAX: (617) 876-5851
/   INFORMATION FOR SEQ ID NO: 28:
/   SEQUENCE CHARACTERISTICS:
/       LENGTH: 109 amino acids
/       TYPE: amino acid
/       TOPOLOGY: linear
/   MOLECULE TYPE: protein
/   PCT-US94-14179-28

Query Match      100.0%; Score 47; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      32 WCGPCK 37

RESULT 25
US-09-264-419C-6
/ Sequence 6; Application US/09264419C
/ Patent No. 6174682
/ GENERAL INFORMATION:
/ APPLICANT: Khodadoust, Mehnan
/ TITLE OF INVENTION: No. 6174682el Thioresdoxin Family Active Site Molecules and Uses
/ TITLE OF INVENTION: Therefor
/ FILE REFERENCE: MNI-076
/ CURRENT APPLICATION NUMBER: US/09/264,419C
/ CURRENT FILING DATE: 1999-03-08
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 111
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: consensus
/ OTHER INFORMATION: sequence
US-09-264-419C-6

Query Match      100.0%; Score 47; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      33 WCGPCK 38

RESULT 26
US-09-134-001C-3859
/ Sequence 3859; Application US/09134001C
/ Patent No. 6380370
/ GENERAL INFORMATION:
/ APPLICANT: Lynn Doucette-Stamm et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
/ TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007
/ CURRENT APPLICATION NUMBER: US/09/134,001C
/ CURRENT FILING DATE: 1998-08-13
/ PRIOR APPLICATION NUMBER: US 60/064,964
/ PRIOR FILING DATE: 1997-11-08
/ PRIOR APPLICATION NUMBER: US 60/055,779
/ PRIOR FILING DATE: 1997-08-14
/ NUMBER OF SEQ ID NOS: 5674
/ SEQ ID NO 3859
/ LENGTH: 111
```

```
/   TYPE: PRT
/   ORGANISM: Staphylococcus epidermidis
/   US-09-134-001C-3859

Query Match      100.0%; Score 47; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      35 WCGPCK 40

RESULT 27
US-09-882-835-5
/ Sequence 5; Application US/09882835
/ Patent No. 6462187
/ GENERAL INFORMATION:
/ APPLICANT: Bandaru, Rajasekhar
/ TITLE OF INVENTION: 22109, A NOVEL HUMAN THIOREDOXIN FAMILY
/ TITLE OF INVENTION: MEMBER AND USES THEREOF
/ FILE REFERENCE: 10448-063001
/ CURRENT APPLICATION NUMBER: US/09/882,835
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/211,673
/ PRIOR FILING DATE: 2000-06-15
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 5
/ LENGTH: 116
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: consensus sequence
US-09-882-835-5

Query Match      100.0%; Score 47; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      33 WCGPCK 38

RESULT 28
US-09-543-681A-4397
/ Sequence 4397; Application US/09543681A
/ Patent No. 6605709
/ GENERAL INFORMATION:
/ APPLICANT: GARY BRETON
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
/ TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.1002-001
/ CURRENT APPLICATION NUMBER: US/09/543,681A
/ CURRENT FILING DATE: 2000-04-05
/ PRIOR APPLICATION NUMBER: US 60/128,706
/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 8344
/ SEQ ID NO 4397
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Proteus mirabilis
/ OTHER INFORMATION:
US-09-543-681A-4397

Query Match      100.0%; Score 47; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
Db      46 WCGPCK 51
```

RESULT 29
US-09-489-039A-8017
; Sequence 8017, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8017
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8017

Query Match 100.0%; Score 47; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 47 WCGPCK 52

RESULT 30
US-09-949-016-9663
; Sequence 9663, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9663
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9663

Query Match 100.0%; Score 47; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 51 WCGPCK 56

RESULT 31
US-09-272-342B-5
; Sequence 5, Application US/09272342B
; Patent No. 6294341
; GENERAL INFORMATION:
; APPLICANT: YU, YEON-GYU
; APPLICANT: KIM, SONG-HOU
; APPLICANT: RYU, JAE-RYEON
; TITLE OF INVENTION: METHOD FOR DETECTING A SUBSTANCE HAVING AN ACTIVITY TO

; TITLE OF INVENTION: INHIBIT HIV INFECTION USING IMMUNOSSAY AND VARIANT
; TITLE OF INVENTION: PROTEIN USED FOR SAID METHOD
; FILE REFERENCE: 2901-0125-0
; CURRENT APPLICATION NUMBER: US/09/272,342B
; CURRENT FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-272-342B-5

Query Match 100.0%; Score 47; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 32
US-08-961-083-40
; Sequence 40, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: PB340P2
; TELEPHONE: (301) 309-8512
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-40

Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 61 WCGPCK 66

RESULT 33
US-09-536-784-40
; Sequence 40, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-536-784-40
Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 61 WCGPCK 66
RESULT 34
US-09-765-271-40
; Sequence 40, Application US/09765271
; Patent No. 6887663
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,271
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/536,784
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-271-40
Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5; 0; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
Db 61 WCGPCK 66
RESULT 35
US-09-765-272A-40
; Sequence 40, Application US/09765272A
; Patent No. 6929930
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigen and Vaccines
; NUMBER OF SEQUENCES: 454
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: Dell Latitude C610
; OPERATING SYSTEM: Windows 2000
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272A
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin J. Hymel
; REGISTRATION NUMBER: 45,414
; REFERENCE/DOCKET NUMBER: PB340P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 610-5790
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:

LENGTH: 137 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-09-765-272A-40

Query Match 100.0%; Score 47; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 61 WCGPCK 66

RESULT 36
US-09-328-352-5360
Sequence 5360, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5360
LENGTH: 145
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-5360

Query Match 100.0%; Score 47; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 64 WCGPCK 69

RESULT 37
US-09-166-966E-8
Sequence 8, Application US/09166966E
Patent No. 6407208
GENERAL INFORMATION:
APPLICANT: CHEN, DAVID CHANHAN
APPLICANT: HU, NIEN-TAI
APPLICANT: CHEN, YUN-JU
APPLICANT: HSEU, TSONG-HSIUNG
TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
FILE REFERENCE: 32350-150960
CURRENT APPLICATION NUMBER: US/09/166,966E
CURRENT FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: TW 86114750
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 8
LENGTH: 159
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: thioredoxin
LOCATION: 1..109
OTHER INFORMATION: Combined amino acid of thioredoxin and an artificial sequence
US-09-166-966E-8

Query Match 100.0%; Score 47; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 38
US-08-775-978-1
Sequence 1, Application US/08775978
Patent No. 5831049
GENERAL INFORMATION:
APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: NOVEL HUMAN THIOREDOXIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,978
FILING DATE: To Be Assigned
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0176 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1430906
US-08-775-978-1

Query Match 100.0%; Score 47; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 89 WCGPCK 94

RESULT 39
US-08-775-978-3
Sequence 3, Application US/08775978
Patent No. 5831049
GENERAL INFORMATION:
APPLICANT: HILLMAN, JENNIFER L.
APPLICANT: GOLI, SURYA K.
TITLE OF INVENTION: NOVEL HUMAN THIOREDOXIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,978
FILING DATE: To Be Assigned
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0176 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1545817
US-08-775-978-3

Query Match 100.0%; Score 47; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 89 WCGPCK 94

RESULT 40
US-09-741-243C-4
Sequence 4, Application US/09741243C
Patent No. 6399352
GENERAL INFORMATION:
APPLICANT: Crawford Jr., John Milton
APPLICANT: Rice, John
APPLICANT: Sevala, Veeresh
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION
FILE REFERENCE: 2022US
CURRENT APPLICATION NUMBER: US/09/741,243C
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: 60/171,785
PRIOR FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 167
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Thioresdoxin functional fragment
US-09-741-243C-4

Query Match 100.0%; Score 47; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 41
US-09-270-767-32473
Sequence 32473, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 32473
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-32473

Query Match 100.0%; Score 47; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 44 WCGPCK 49

RESULT 42
US-09-270-767-47690
Sequence 47690, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 47690
LENGTH: 170
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-47690

Query Match 100.0%; Score 47; DB 2; Length 170;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 44 WCGPCK 49

RESULT 43
US-09-272-342B-6
Sequence 6, Application US/09272342B
Patent No. 6294341
GENERAL INFORMATION:
APPLICANT: YU, YEON-GYU
APPLICANT: KIM, SUNG-HOU
APPLICANT: RU, JAB-REON
TITLE OF INVENTION: METHOD FOR DETECTING A SUBSTANCE HAVING AN ACTIVITY TO
TITLE OF INVENTION: INHIBIT HIV INFECTION USING IMMUNOASSAY AND VARIANT
FILE REFERENCE: 2901-0125-0
CURRENT APPLICATION NUMBER: US/09/272,342B

;; CURRENT FILING DATE: 1999-03-19
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 177
;; TYPE: PRT
;; ORGANISM: homo sapiens and HIV hybrid
US-09-272-342B-6

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 177;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 44
US-09-583-110-5222
; Sequence 5222, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: P4TH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5222
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5222

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 185;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 80 WCGPCK 85

RESULT 45
US-09-107-433-5104
; Sequence 5104, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/107,433
;; FILING DATE: 30-Jun-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/ 085131
;; FILING DATE: May 12, 1998
;; APPLICATION NUMBER: 60/051553
;; FILING DATE: July 2, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ariniello, Pamela Deneke
;; REGISTRATION NUMBER: 40,489
;; REFERENCE/DOCKET NUMBER: GTC-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781)893-8277
;; TELEFAX: (781)893-8277
;; INFORMATION FOR SEQ ID NO: 5104:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 194 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Streptococcus pneumoniae
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (B) LOCATION 1...194
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5104:
US-09-107-433-5104

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 194;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 89 WCGPCK 94

RESULT 46
US-09-166-966E-11
; Sequence 11, Application US/09166966E
; Patent No. 6407208
; GENERAL INFORMATION:
; APPLICANT: CHEN, DAVID CHANHAN
; APPLICANT: HU, NIEN-TAI
; APPLICANT: CHEN, YUN-JU
; APPLICANT: HSEU, TZONG-HSIUNG
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH A CELLULOSE BINDING DOMAIN
; FILE REFERENCE: 32350-150960
; CURRENT APPLICATION NUMBER: US/09/166,966E
; CURRENT FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: TW 86114750
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 11
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: Chloredoxin
; LOCATION: 1..109
; NAME/KEY: Cellulose-binding domain
; LOCATION: 162..197
; NAME/KEY: RGD
; LOCATION: 204..206
; OTHER INFORMATION: Combined amino acid sequence of chloredoxin,
; OTHER INFORMATION: artificial sequence, cellulose-binding domain, and
; OTHER INFORMATION: artificial sequence; the two artificial sequences
; OTHER INFORMATION: flanking the cellulose-binding domain contain restriction sites
US-09-166-966E-11

Query Match
Best Local Similarity 100.0%; Score 47; DB 2; Length 209;

Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 47
US-08-180-371-6
Sequence 6, Application US/08180371
Patent No. 6254861
GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived
TITLE OF INVENTION: From T Lymphocytes and Methods of Use Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,371
FILING DATE: 12-JAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 906866
FILING DATE: 01 JULY 1992
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27620/31668
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-180-371-6
Query Match 100.0%; Score 47; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 106 WCGPCK 111
RESULT 48
PCT-US92-05707-6
Sequence 6, Application PC/TUS9205707
GENERAL INFORMATION:
APPLICANT: Choudhury, Chandra
TITLE OF INVENTION: Hematopoietic Growth Factor Derived from
TITLE OF INVENTION: T Lymphocytes and Methods of Use Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell

STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05707
FILING DATE: 19920707
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 27620/30933
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 210 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-05707-6

Query Match 100.0%; Score 47; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 106 WCGPCK 111

RESULT 49
US-08-778-717-17
Sequence 17, Application US/08778717
Patent No. 6602689
GENERAL INFORMATION:
APPLICANT: UENO, EIICHI
APPLICANT: NOBUYUKI, FUJII
APPLICANT: OKADA, MASAHISA
TITLE OF INVENTION: FUSED DNA SEQUENCE, FUSED PROTEIN
TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,717
FILING DATE: 12-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 265 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: RECOMBINANT
PUBLICATION INFORMATION:
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 17: FROM 1 TO 265
US-08-778-717-17

Query Match 100.0%; Score 47; DB 2; Length 265;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 50 WCGPCK 55

RESULT 50
US-07-745-382-14
Sequence 14, Application US/07745382
Patent No. 5270181
GENERAL INFORMATION:
APPLICANT: McCoy, John
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/745,382
FILING DATE: 19910814
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-745-382-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 51
US-07-921-848-14
Sequence 14, Application US/07921848
Patent No. 5292646
GENERAL INFORMATION:
APPLICANT: McCoy, John
TITLE OF INVENTION: Peptide and Protein Fusions To
TITLE OF INVENTION: Thioedoxin and Thioedoxin-Like Molecules
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,848
FILING DATE: 19920728
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/652,531
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,382
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Geert, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: G15188A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-921-848-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 52
US-08-115-680-4
Sequence 4, Application US/08115680
Patent No. 5437863
GENERAL INFORMATION:

APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,680
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDIAUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-115-680-4

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 53
US-07-941-372-4
Sequence 4, Application US/07941372
Patent No. 5460810
GENERAL INFORMATION:
APPLICANT: Williams, David A.
APPLICANT: Clark, Steven C.
TITLE OF INVENTION: Method of Treating Cell Damage or
TITLE OF INVENTION: Depletion
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Center, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/941,372
FILING DATE: 19920902

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: INDUS1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-941-372-4

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37

RESULT 54
US-08-165-301A-14
Sequence 14, Application US/08165301A
Patent No. 5646016
GENERAL INFORMATION:
APPLICANT: McCoy, John
APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Grant, Kathleen
APPLICANT: Lavallee, Edward R.
TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/165,301A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 33,544
REFERENCE/DOCKET NUMBER: GI 5188D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-165-301A-14

Query Match 100.0%; Score 47; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No.10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 55

US-08-810-436-14
; Sequence 14, Application US/08810436
; Patent No. 6143524
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,436
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/165,301
; FILING DATE: 10-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-810-436-14

Query Match 100.0%; Score 47; DB 2; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 56
PCT-US93-08247-4
; Sequence 4, Application PC/TUS9308247
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.,
; APPLICANT: 87 Cambridgepark Drive,
; APPLICANT: Cambridge, MA 02140, USA
; TITLE OF INVENTION: Method of Treating Cell Damage or
; TITLE OF INVENTION: Depletion
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08247
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,372
FILING DATE: 02-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: IND1Apct
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 540-9206
TELEFAX: (215) 540-5818
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08247-4

Query Match 100.0%; Score 47; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 57

PCT-US94-14179-14
; Sequence 14, Application PC/TUS9414179
; GENERAL INFORMATION:
; APPLICANT: McCoy, John
; APPLICANT: DiBlasio-Smith, Elizabeth
; APPLICANT: Grant, Kathleen
; APPLICANT: Lavallee, Edward R.
; TITLE OF INVENTION: PEPTIDE AND PROTEIN FUSIONS TO
; TITLE OF INVENTION: THIOREDOXIN, THIOREDOXIN-LIKE MOLECULES, AND MODIFIED
; TITLE OF INVENTION: THIOREDOXIN-LIKE MOLECULES
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14179
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 33,544
; REFERENCE/DOCKET NUMBER: GI 5188D

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14179-14

Query Match 100.0%; Score 47; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 58
US-10-012-896-1011
Sequence 1011, Application US/10012896
GENERAL INFORMATION:
APPLICANT: Xu, Jlangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Heppler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hurai, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Roy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1011
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-896-1011

Query Match 100.0%; Score 47; DB 2; Length 355;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 59
US-08-683-007A-2

Sequence 2, Application US/08683007A
Patent No. 5858724
GENERAL INFORMATION:
APPLICANT: No. 5858724Y, Robert E
APPLICANT: Domancio, Michael
APPLICANT: Jaeger, Keith
APPLICANT: Kroeker, Warren
TITLE OF INVENTION: Recombinant Rabbit Tissue Factor
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSER: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/683,007A
FILING DATE: 16-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 740380, 90040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-683-007A-2

Query Match 100.0%; Score 47; DB 1; Length 408;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 32 WCGPCK 37

RESULT 60
US-09-513-442-2
Sequence 2, Application US/09513442
Patent No. 6387664
GENERAL INFORMATION:
APPLICANT: Ikemoto, Mitsunshi
TITLE OF INVENTION: SPARC Fusion Protein and a Process for Producing the
TITLE OF INVENTION: Same
FILE REFERENCE: HIRAKI-04218
CURRENT APPLICATION NUMBER: US/09/513,442
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 467
TYPE: PRT
ORGANISM: Mus musculus
US-09-513-442-2

Query Match 100.0%; Score 47; DB 2; Length 467;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

|||||
Db 32 WCGPCK 37

RESULT 61
US-08-260-582-77
; Sequence 77, Application US/08260582
; Patent No. 5635182
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M.
; APPLICANT: Lu, Zhijian
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND
; TITLE OF INVENTION: INTERACTIONS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/260,582
; FILING DATE: 16-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, M. C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5236
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-260-582-77
Query Match 100.0%; Score 47; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 275 WCGPCK 280
RESULT 62
PCT-US95-05471-77
; Sequence 77, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US95-05471-77

Query Match 100.0%; Score 47; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 275 WCGPCK 280

RESULT 63
US-10-057-531A-1
; Sequence 1, Application US/10057531A
; Patent No. 685332
; GENERAL INFORMATION:
; APPLICANT: Lyon, Jeffrey A.
; APPLICANT: Angov, Evelina
; TITLE OF INVENTION: Isolation and Purification of P. falciparum Merozoite
; TITLE OF INVENTION: Protein-142 Vaccine
; FILE REFERENCE: 003/241/SAP
; CURRENT APPLICATION NUMBER: US/10/057,531A
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/264,535
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/347,564
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 1
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: E. coli expressed P. falciparum MSP142 (3D7) Protein
; Patent No. 685332
US-10-057-531A-1
Query Match 100.0%; Score 47; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WCGPCK 6
|||||
Db 32 WCGPCK 37
RESULT 64
US-09-741-243C-2
; Sequence 2, Application US/09741243C
; Patent No. 6399352
; GENERAL INFORMATION:
; APPLICANT: Crawford Jr., John Milton
; APPLICANT: Rice, John
; APPLICANT: Sevala, Veeresh
; APPLICANT: Stewart, Sandy
; TITLE OF INVENTION: NOVEL PLANT PORPHOBILINOGEN AND FUSION
; TITLE OF INVENTION: PROTEIN THEREOF
; FILE REFERENCE: 2022US
; CURRENT APPLICATION NUMBER: US/09/741,243C
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/171,785
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A plant thioredoxin-porphobilinogen

OTHER INFORMATION: synthase fusion protein
US-09-741-243C-2

Query Match 100.0%; Score 47; DB 2; Length 551;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 32 WCGPCK 37

RESULT 65
US-09-252-991A-22943
Sequence 22943, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ. ID NOS: 33142
SEQ. ID NO 22943
LENGTH: 580
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22943

Query Match 100.0%; Score 47; DB 2; Length 580;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 504 WCGPCK 509

RESULT 66
US-09-626-589-3
Sequence 3, Application US/09626589
Patent No. 6326164
GENERAL INFORMATION:
APPLICANT: Rice, John
APPLICANT: Klotz, Andreas
APPLICANT: Crawford, John
APPLICANT: Lanning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: IDENTIFICATION OF MODULATORS OF DEOXYXYLULOSE 5-PHOSPHATE
FILE REFERENCE: 2037 US
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ. ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 3
LENGTH: 824
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Residues 1-165 are from the thioredoxin sequence
OTHER INFORMATION: found in the vector pET32 supplied by No. 6326164agen.
OTHER INFORMATION: Residues 166-824 represent the tdxps sequence from
OTHER INFORMATION: Arabidopsis shown in SEQ ID NO.2.
US-09-626-589-3

Query Match 100.0%; Score 47; DB 2; Length 824;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 32 WCGPCK 37

RESULT 67
US-10-237-551-92
Sequence 92, Application US/10237551
Patent No. 6821519
GENERAL INFORMATION:
APPLICANT: Day, Craig H.
APPLICANT: Hosken, Nancy A.
APPLICANT: Parsons, Joseph M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538C3
CURRENT APPLICATION NUMBER: US/10/237,551
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ. ID NOS: 254
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 92
LENGTH: 858
TYPE: PRT
ORGANISM: Homo sapiens
US-10-237-551-92

Query Match 100.0%; Score 47; DB 2; Length 858;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
| | | | |
Db 40 WCGPCK 45

RESULT 68
US-08-974-549A-600
Sequence 600, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note="fusion protein composed of
OTHER INFORMATION: enterokinase cleavable, His tagged
OTHER INFORMATION: thioresdoxin moiety and full length htrr"
US-08-974-549A-600

Query Match 100.0%; Score 47; DB 2; Length 1285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 32 WCGPCK 37

RESULT 69
US-08-912-951-314
Sequence 314, Application US/08912951
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 314:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-912-951-314

Query Match 100.0%; Score 47; DB 2; Length 1285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 32 WCGPCK 37

RESULT 70
US-09-402-181B-600
Sequence 600, Application US/09402181B
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633

```

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release# #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 600:
SEQUENCE CHARACTERISTICS:
LENGTH: 1285 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..1285
OTHER INFORMATION: /note="fusion protein composed of
enterokinase cleavable, his tagged
chlorodoxin moiety and full length hTERT"
SEQUENCE DESCRIPTION: SEQ ID NO: 600:
US-09-402-181B-600

Query Match 100.0%; Score 47; DB 2; Length 1285;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 WCGPCK 6
|||||
32 WCGPCK 37

```

Search completed: February 23, 2006, 00:43:50
Job time : 39.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:42:47 ; Search time 116.5 Seconds
(without alignments)
21.519 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WGPCPK 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	47	100.0	6	4 US-10-304-287-4	Sequence 4, Appl1
2	47	100.0	6	4 US-10-660-118A-3	Sequence 3, Appl1
3	47	100.0	6	4 US-10-735-577-4	Sequence 4, Appl1
4	47	100.0	52	3 US-09-801-260-4	Sequence 4, Appl1
5	47	100.0	52	4 US-10-145-586-43	Sequence 43, Appl1
6	47	100.0	82	4 US-10-425-115-351019	Sequence 351019,
7	47	100.0	84	4 US-10-408-765A-312	Sequence 312, App
8	47	100.0	90	4 US-10-424-599-280571	Sequence 280571,
9	47	100.0	91	4 US-10-032-201B-143	Sequence 143, App
10	47	100.0	102	4 US-10-032-201B-102	Sequence 102, App
11	47	100.0	102	4 US-10-032-201B-104	Sequence 104, App
12	47	100.0	102	4 US-10-032-201B-105	Sequence 105, App
13	47	100.0	102	4 US-10-032-201B-126	Sequence 126, App
14	47	100.0	102	4 US-10-032-201B-128	Sequence 128, App
15	47	100.0	102	5 US-10-501-282-3136	Sequence 1126, Ap
16	47	100.0	103	4 US-10-032-201B-96	Sequence 96, Appl
17	47	100.0	103	4 US-10-032-585-7785	Sequence 7785, Ap
18	47	100.0	103	4 US-10-660-118A-7	Sequence 7, Appl
19	47	100.0	103	4 US-10-451-467A-270	Sequence 450, App
20	47	100.0	103	4 US-10-451-467A-450	Sequence 470, App
21	47	100.0	103	4 US-10-451-467A-614	Sequence 614, App
22	47	100.0	104	3 US-09-954-342-62	Sequence 62, Appl
23	47	100.0	104	3 US-09-954-342-63	Sequence 63, Appl
24	47	100.0	104	3 US-09-954-342-64	Sequence 64, Appl
25	47	100.0	104	3 US-09-954-342-65	Sequence 65, Appl
26	47	100.0	104	4 US-10-032-201B-146	Sequence 146, App
27	47	100.0	104	4 US-10-032-201B-150	Sequence 150, App

28	47	100.0	104	4 US-10-032-201B-152	Sequence 152, App
29	47	100.0	104	4 US-10-032-201B-154	Sequence 154, App
30	47	100.0	104	4 US-10-032-201B-155	Sequence 155, App
31	47	100.0	104	4 US-10-032-201B-158	Sequence 158, App
32	47	100.0	104	4 US-10-032-201B-159	Sequence 159, App
33	47	100.0	104	4 US-10-032-201B-161	Sequence 161, App
34	47	100.0	104	4 US-10-032-201B-161	Sequence 161, App
35	47	100.0	104	4 US-10-032-201B-176	Sequence 276, App
36	47	100.0	104	4 US-10-424-599-282588	Sequence 282588,
37	47	100.0	104	4 US-10-451-467A-188	Sequence 188, App
38	47	100.0	105	3 US-09-954-342-61	Sequence 61, Appl
39	47	100.0	105	4 US-10-171-311-226	Sequence 226, App
40	47	100.0	105	4 US-10-316-253-291	Sequence 291, App
41	47	100.0	105	4 US-10-032-201B-47	Sequence 47, Appl
42	47	100.0	105	4 US-10-032-201B-106	Sequence 106, App
43	47	100.0	105	4 US-10-424-599-237784	Sequence 237784,
44	47	100.0	105	4 US-10-351-891-127	Sequence 127, App
45	47	100.0	105	4 US-10-408-765A-2019	Sequence 2019, Ap
46	47	100.0	105	4 US-10-660-118A-8	Sequence 8, Appl1
47	47	100.0	105	4 US-10-660-118A-9	Sequence 9, Appl1
48	47	100.0	105	4 US-10-660-118A-10	Sequence 10, Appl
49	47	100.0	105	4 US-10-660-118A-11	Sequence 11, Appl
50	47	100.0	105	4 US-10-660-118A-12	Sequence 12, Appl
51	47	100.0	105	4 US-10-451-467A-684	Sequence 684, App
52	47	100.0	105	4 US-10-699-113-32	Sequence 32, Appl
53	47	100.0	105	5 US-10-970-370-2	Sequence 2, Appl1
54	47	100.0	105	5 US-10-970-370-6	Sequence 6, Appl1
55	47	100.0	106	4 US-10-032-201B-123	Sequence 123, App
56	47	100.0	106	4 US-10-032-201B-132	Sequence 132, App
57	47	100.0	106	4 US-10-032-201B-137	Sequence 137, App
58	47	100.0	106	4 US-10-032-201B-176	Sequence 176, App
59	47	100.0	106	4 US-10-335-977-6752	Sequence 6752, Ap
60	47	100.0	106	4 US-10-628-391-1	Sequence 1, Appl1
61	47	100.0	106	4 US-10-425-115-365910	Sequence 365910,
62	47	100.0	107	6 US-11-097-143-7479	Sequence 7479, Ap
63	47	100.0	107	4 US-10-032-201B-109	Sequence 109, App
64	47	100.0	107	4 US-10-032-201B-121	Sequence 121, App
65	47	100.0	107	4 US-10-032-201B-151	Sequence 151, App
66	47	100.0	107	4 US-10-335-977-6753	Sequence 6753, Ap
67	47	100.0	107	6 US-11-097-143-8826	Sequence 8826, Ap
68	47	100.0	108	3 US-09-812-777-16	Sequence 16, Appl
69	47	100.0	108	4 US-10-032-201B-117	Sequence 117, App
70	47	100.0	108	4 US-10-032-201B-133	Sequence 133, App
71	47	100.0	108	4 US-10-032-201B-142	Sequence 142, App
72	47	100.0	109	4 US-10-000-903-17	Sequence 17, Appl
73	47	100.0	109	4 US-10-128-714-3073	Sequence 3073, Ap
74	47	100.0	109	4 US-10-128-714-8073	Sequence 8073, Ap
75	47	100.0	109	4 US-10-194-885-24	Sequence 24, Appl
76	47	100.0	109	4 US-10-032-201B-93	Sequence 43, Appl
77	47	100.0	109	4 US-10-032-201B-93	Sequence 93, Appl
78	47	100.0	109	4 US-10-460-524-11	Sequence 11, Appl
79	47	100.0	109	4 US-10-424-999-22	Sequence 22, Appl
80	47	100.0	109	4 US-10-660-118A-4	Sequence 4, Appl1
81	47	100.0	109	4 US-10-767-701-51831	Sequence 51831, A
82	47	100.0	109	5 US-10-899-771-17	Sequence 17, Appl
83	47	100.0	109	5 US-10-970-370-4	Sequence 4, Appl1
84	47	100.0	111	6 US-10-724-972A-5631	Sequence 5631, Ap
85	47	100.0	111	6 US-11-097-143-6207	Sequence 6207, Ap
86	47	100.0	112	4 US-10-032-201B-87	Sequence 87, App
87	47	100.0	112	4 US-10-032-201B-129	Sequence 129, App
88	47	100.0	112	4 US-10-767-701-33511	Sequence 33511, A
89	47	100.0	112	4 US-10-425-115-201579	Sequence 201579,
90	47	100.0	113	3 US-09-963-333-8	Sequence 8, Appl1
91	47	100.0	113	4 US-10-145-586-57	Sequence 57, Appl
92	47	100.0	115	4 US-10-032-201B-130	Sequence 130, App
93	47	100.0	115	4 US-10-032-201B-148	Sequence 148, App
94	47	100.0	116	3 US-09-963-333-7	Sequence 7, Appl1
95	47	100.0	116	4 US-10-087-192-1311	Sequence 1311, Ap
96	47	100.0	116	4 US-10-145-586-49	Sequence 49, Appl
97	47	100.0	117	4 US-10-145-586-56	Sequence 56, Appl
98	47	100.0	118	4 US-10-032-201B-98	Sequence 98, Appl
99	47	100.0	121	4 US-10-032-201B-82	Sequence 82, Appl
100	47	100.0	124	3 US-10-424-599-158010	Sequence 158010,
				US-09-738-626-6919	Sequence 6919, Ap

101	47	100.0	124	5	US-10-494-541-34	Sequence 34, Appl	174	47	100.0	221	4	US-10-424-999-36	Sequence 36, Appl
102	47	100.0	125	4	US-10-087-192-1314	Sequence 1314, Ap	175	47	100.0	222	4	US-10-425-114-53092	Sequence 53092, A
103	47	100.0	126	4	US-10-424-599-250281	Sequence 250281,	176	47	100.0	225	4	US-10-425-000-64	Sequence 64, Appl
104	47	100.0	127	5	US-10-032-201B-131	Sequence 131, App	177	47	100.0	247	5	US-10-450-763-55922	Sequence 55922, A
105	47	100.0	127	5	US-10-450-763-48663	Sequence 48663, A	178	47	100.0	252	4	US-10-423-155-7	Sequence 7, Appl
106	47	100.0	128	4	US-10-424-599-224915	Sequence 224915,	179	47	100.0	252	4	US-10-423-155-8	Sequence 8, Appl
107	47	100.0	129	4	US-10-320-797-3005	Sequence 3005, Ap	180	47	100.0	263	4	US-10-108-260A-2809	Sequence 2809, Ap
108	47	100.0	130	4	US-10-032-201B-136	Sequence 136, App	181	47	100.0	263	5	US-10-732-923-13421	Sequence 13421, A
109	47	100.0	132	4	US-10-425-000-48	Sequence 48, Appl	182	47	100.0	265	4	US-10-457-372-17	GENERAL INFORNA
110	47	100.0	133	4	US-10-424-599-194117	Sequence 194117,	183	47	100.0	271	4	US-10-417-922-4	Sequence 4, Appl
111	47	100.0	133	4	US-10-425-115-311941	Sequence 311941,	184	47	100.0	274	5	US-10-888-805-24	Sequence 24, Appl
112	47	100.0	134	4	US-10-424-599-237789	Sequence 237789,	185	47	100.0	274	5	US-10-888-805-26	Sequence 26, Appl
113	47	100.0	135	4	US-10-424-599-201417	Sequence 201417,	186	47	100.0	283	5	US-10-888-805-28	Sequence 28, Appl
114	47	100.0	137	3	US-09-765-272-40	Sequence 40, Appl	187	47	100.0	283	5	US-10-888-805-30	Sequence 30, Appl
115	47	100.0	137	4	US-10-424-599-182536	Sequence 182536,	188	47	100.0	283	5	US-10-888-805-32	Sequence 32, Appl
116	47	100.0	137	4	US-10-424-599-259824	Sequence 259824,	189	47	100.0	283	5	US-10-888-805-34	Sequence 34, Appl
117	47	100.0	137	6	US-11-106-649-40	Sequence 40, Appl	190	47	100.0	284	4	US-10-032-201B-189	Sequence 189, App
118	47	100.0	138	4	US-10-424-599-157666	Sequence 157666,	191	47	100.0	287	4	US-10-032-201B-190	Sequence 190, App
119	47	100.0	138	4	US-10-437-963-161970	Sequence 161970,	192	47	100.0	287	6	US-11-097-143-11535	Sequence 11535, A
120	47	100.0	139	4	US-10-424-599-237785	Sequence 237785,	193	47	100.0	290	4	US-10-032-201B-186	Sequence 186, App
121	47	100.0	140	4	US-10-032-201B-163	Sequence 163, App	194	47	100.0	323	4	US-10-141-531-28	Sequence 28, Appl
122	47	100.0	145	4	US-10-032-201B-108	Sequence 108, App	195	47	100.0	323	4	US-10-290-072-28	Sequence 28, Appl
123	47	100.0	147	4	US-10-424-599-282587	Sequence 282587,	196	47	100.0	330	4	US-10-250-615-23	Sequence 23, Appl
124	47	100.0	160	4	US-10-425-115-314782	Sequence 314782,	197	47	100.0	330	5	US-10-732-922-13423	Sequence 13423, A
125	47	100.0	164	4	US-10-264-049-2874	Sequence 2874, Ap	198	47	100.0	342	3	US-09-938-864-332	Sequence 332, App
126	47	100.0	165	4	US-10-417-923-20	Sequence 20, Appl	199	47	100.0	342	3	US-09-785-019-332	Sequence 332, App
127	47	100.0	166	4	US-10-032-201B-147	Sequence 147, App	200	47	100.0	342	4	US-10-125-633A-332	Sequence 332, App
128	47	100.0	166	4	US-10-032-201B-153	Sequence 153, App	201	47	100.0	342	4	US-10-002-603-332	Sequence 332, App
129	47	100.0	166	4	US-10-032-201B-156	Sequence 156, App	202	47	100.0	342	4	US-10-195-835-332	Sequence 332, App
130	47	100.0	166	4	US-10-032-201B-160	Sequence 160, App	203	47	100.0	342	4	US-10-286-333-332	Sequence 332, App
131	47	100.0	166	4	US-10-264-049-3110	Sequence 3110, Ap	204	47	100.0	342	4	US-10-244-830-332	Sequence 332, App
132	47	100.0	166	5	US-10-970-370-8	Sequence 8, Appl	205	47	100.0	342	4	US-10-427-717-332	Sequence 332, App
133	47	100.0	167	4	US-10-767-701-46297	Sequence 46297, A	206	47	100.0	342	4	US-10-648-780-332	Sequence 332, App
134	47	100.0	173	4	US-10-437-963-108195	Sequence 108195,	207	47	100.0	355	4	US-10-012-896-1011	Sequence 1011, Ap
135	47	100.0	173	4	US-10-425-115-187390	Sequence 187390,	208	47	100.0	355	4	US-10-144-678A-1011	Sequence 1011, Ap
136	47	100.0	173	4	US-10-425-115-187392	Sequence 187392,	209	47	100.0	365	5	US-10-294-025-1011	Sequence 1011, Ap
137	47	100.0	177	4	US-10-032-201B-63	Sequence 63, Appl	210	47	100.0	366	5	US-10-928-992-162	Sequence 162, App
138	47	100.0	178	4	US-10-032-201B-52	Sequence 52, Appl	211	47	100.0	410	3	US-09-938-864-333	Sequence 333, App
139	47	100.0	179	4	US-10-323-362-4	Sequence 4, Appl	212	47	100.0	410	3	US-09-785-019-333	Sequence 333, App
140	47	100.0	179	4	US-10-032-201B-59	Sequence 59, Appl	213	47	100.0	410	4	US-10-125-633A-333	Sequence 333, App
141	47	100.0	180	4	US-10-425-115-314784	Sequence 314784,	214	47	100.0	410	4	US-10-002-603-333	Sequence 333, App
142	47	100.0	181	4	US-10-032-201B-68	Sequence 68, Appl	215	47	100.0	410	4	US-10-195-835-333	Sequence 333, App
143	47	100.0	181	4	US-10-424-599-280573	Sequence 280573,	216	47	100.0	410	4	US-10-286-333-333	Sequence 333, App
144	47	100.0	182	4	US-10-032-201B-54	Sequence 54, Appl	217	47	100.0	410	4	US-10-244-830-333	Sequence 333, App
145	47	100.0	182	4	US-10-032-201B-56	Sequence 56, Appl	218	47	100.0	410	4	US-10-427-717-333	Sequence 333, App
146	47	100.0	182	4	US-10-425-115-256661	Sequence 256661,	219	47	100.0	410	4	US-10-648-780-333	Sequence 333, App
147	47	100.0	182	4	US-10-425-115-314786	Sequence 314786,	220	47	100.0	421	4	US-10-296-672-7	Sequence 7, Appl
148	47	100.0	185	4	US-10-032-201B-53	Sequence 53, Appl	221	47	100.0	437	4	US-10-290-072-222	Sequence 222, App
149	47	100.0	185	5	US-10-739-930-6217	Sequence 6217, Ap	222	47	100.0	438	4	US-10-290-072-218	Sequence 218, App
150	47	100.0	185	5	US-10-739-930-6865	Sequence 6865, Ap	223	47	100.0	438	4	US-10-290-072-220	Sequence 220, App
151	47	100.0	185	5	US-10-472-928-1980	Sequence 1980, App	224	47	100.0	438	4	US-10-290-072-224	Sequence 224, App
152	47	100.0	186	4	US-10-032-201B-60	Sequence 60, Appl	225	47	100.0	457	4	US-10-141-531-174	Sequence 174, App
153	47	100.0	187	4	US-10-437-963-183458	Sequence 183458,	226	47	100.0	457	4	US-10-290-072-174	Sequence 174, App
154	47	100.0	190	4	US-10-032-201B-57	Sequence 57, Appl	227	47	100.0	458	4	US-10-141-531-67	Sequence 67, Appl
155	47	100.0	191	4	US-10-032-201B-55	Sequence 55, Appl	228	47	100.0	458	4	US-10-141-531-84	Sequence 84, Appl
156	47	100.0	191	4	US-10-474-776-661	Sequence 661, App	229	47	100.0	458	4	US-10-141-531-93	Sequence 93, Appl
157	47	100.0	192	4	US-10-767-701-46126	Sequence 46126, A	230	47	100.0	458	4	US-10-141-531-102	Sequence 102, App
158	47	100.0	194	4	US-10-437-963-104327	Sequence 104327,	231	47	100.0	458	4	US-10-141-531-111	Sequence 111, App
159	47	100.0	194	5	US-10-617-320-5104	Sequence 5104, Ap	232	47	100.0	458	4	US-10-141-531-120	Sequence 120, App
160	47	100.0	196	4	US-10-180-120-2	Sequence 2, Appl	233	47	100.0	458	4	US-10-141-531-129	Sequence 129, App
161	47	100.0	209	4	US-10-425-000-54	Sequence 54, Appl	234	47	100.0	458	4	US-10-141-531-138	Sequence 138, App
162	47	100.0	213	4	US-10-425-000-62	Sequence 62, Appl	235	47	100.0	458	4	US-10-141-531-147	Sequence 147, App
163	47	100.0	214	4	US-10-425-000-58	Sequence 58, Appl	236	47	100.0	458	4	US-10-141-531-156	Sequence 156, App
164	47	100.0	214	4	US-10-425-000-66	Sequence 66, Appl	237	47	100.0	458	4	US-10-141-531-165	Sequence 165, App
165	47	100.0	215	4	US-10-425-000-56	Sequence 56, Appl	238	47	100.0	458	4	US-10-141-531-183	Sequence 183, App
166	47	100.0	217	4	US-10-425-000-70	Sequence 70, Appl	239	47	100.0	458	4	US-10-141-531-192	Sequence 192, App
167	47	100.0	217	4	US-10-424-999-38	Sequence 38, Appl	240	47	100.0	458	4	US-10-141-531-201	Sequence 201, Appl
168	47	100.0	218	4	US-10-425-000-50	Sequence 50, Appl	241	47	100.0	458	4	US-10-032-201B-36	Sequence 36, Appl
169	47	100.0	219	4	US-10-425-000-52	Sequence 52, Appl	242	47	100.0	458	4	US-10-032-201B-51	Sequence 51, Appl
170	47	100.0	219	4	US-10-425-000-60	Sequence 60, Appl	243	47	100.0	458	4	US-10-032-201B-127	Sequence 127, App
171	47	100.0	219	4	US-10-425-000-72	Sequence 72, Appl	244	47	100.0	458	4	US-10-032-201B-214	Sequence 214, App
172	47	100.0	219	4	US-10-424-999-40	Sequence 40, Appl	245	47	100.0	458	4	US-10-290-072-67	Sequence 67, Appl
173	47	100.0	221	4	US-10-424-999-34	Sequence 34, Appl	246	47	100.0	458	4	US-10-290-072-84	Sequence 84, Appl

247	47	100.0	458	4	US-10-290-072-93	Sequence 93, Appl	320	44	93.6	105	4	US-10-032-201B-94	Sequence 94, Appl
248	47	100.0	458	4	US-10-290-072-102	Sequence 102, App	321	44	93.6	105	4	US-10-032-201B-113	Sequence 114, App
249	47	100.0	458	4	US-10-290-072-111	Sequence 111, App	322	44	93.6	105	4	US-10-032-201B-135	Sequence 135, App
250	47	100.0	458	4	US-10-290-072-120	Sequence 120, App	323	44	93.6	106	4	US-10-032-201B-58	Sequence 58, Appl
251	47	100.0	458	4	US-10-290-072-129	Sequence 129, App	324	44	93.6	106	4	US-10-032-201B-70	Sequence 70, Appl
252	47	100.0	458	4	US-10-290-072-138	Sequence 138, App	325	44	93.6	106	4	US-10-032-201B-113	Sequence 111, App
253	47	100.0	458	4	US-10-290-072-147	Sequence 147, App	326	44	93.6	106	4	US-10-032-201B-140	Sequence 140, App
254	47	100.0	458	4	US-10-290-072-156	Sequence 156, App	327	44	93.6	107	4	US-10-032-201B-171	Sequence 71, Appl
255	47	100.0	458	4	US-10-290-072-183	Sequence 183, App	328	44	93.6	107	4	US-10-032-201B-75	Sequence 75, Appl
256	47	100.0	458	4	US-10-290-072-185	Sequence 185, App	329	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
257	47	100.0	458	4	US-10-290-072-182	Sequence 182, App	330	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
258	47	100.0	458	4	US-10-290-072-201	Sequence 201, App	331	44	93.6	107	4	US-10-032-201B-139	Sequence 139, App
259	47	100.0	462	4	US-10-425-000-68	Sequence 68, Appl	332	44	93.6	109	4	US-10-032-201B-73	Sequence 73, Appl
260	47	100.0	513	3	US-10-032-201B-32	Sequence 32, Appl	333	44	93.6	109	4	US-10-032-201B-141	Sequence 141, App
261	47	100.0	516	3	US-09-804-626-4	Sequence 4, Appl	334	44	93.6	109	4	US-10-032-201B-185	Sequence 185, App
262	47	100.0	518	3	US-09-804-626-2	Sequence 2, Appl	335	44	93.6	110	4	US-10-156-761-11840	Sequence 11840, A
263	47	100.0	522	4	US-10-296-770-2	Sequence 2, Appl	336	44	93.6	110	4	US-10-032-201B-138	Sequence 138, App
264	47	100.0	530	4	US-10-296-770-5	Sequence 5, Appl	337	44	93.6	110	4	US-10-424-599-265070	Sequence 265070, A
265	47	100.0	546	4	US-10-057-531A-1	Sequence 1, Appl	338	44	93.6	112	3	US-09-954-342-32	Sequence 32, Appl
266	47	100.0	546	4	US-10-057-531A-1	Sequence 1, Appl	339	44	93.6	112	4	US-10-425-115-106849	Sequence 306849, A
267	47	100.0	591	3	US-09-785-019-334	Sequence 334, App	340	44	93.6	114	3	US-09-897-898-6	Sequence 6, Appl
268	47	100.0	591	3	US-09-785-019-334	Sequence 334, App	341	44	93.6	114	3	US-09-897-898-6	Sequence 6, Appl
269	47	100.0	591	4	US-10-125-635A-334	Sequence 334, App	342	44	93.6	114	4	US-10-194-885-23	Sequence 23, Appl
270	47	100.0	591	4	US-10-002-603-334	Sequence 334, App	343	44	93.6	114	4	US-10-032-201B-15	Sequence 15, Appl
271	47	100.0	591	4	US-10-195-835-334	Sequence 334, App	344	44	93.6	114	4	US-10-032-201B-39	Sequence 39, Appl
272	47	100.0	591	4	US-10-286-333-334	Sequence 334, App	345	44	93.6	114	4	US-10-032-201B-76	Sequence 76, Appl
273	47	100.0	591	4	US-10-244-830-334	Sequence 334, App	346	44	93.6	114	5	US-10-611-330-2930	Sequence 2930, App
274	47	100.0	591	4	US-10-427-717-334	Sequence 334, App	347	44	93.6	114	5	US-10-978-538-11	Sequence 11, Appl
275	47	100.0	591	4	US-10-648-780-334	Sequence 334, App	348	44	93.6	116	4	US-10-032-201B-88	Sequence 88, Appl
276	47	100.0	602	4	US-10-290-072-226	Sequence 226, App	349	44	93.6	117	4	US-10-424-599-261511	Sequence 261511, A
277	47	100.0	602	4	US-10-290-072-228	Sequence 228, App	350	44	93.6	117	4	US-10-424-599-283863	Sequence 283863, A
278	47	100.0	602	4	US-10-290-072-230	Sequence 230, App	351	44	93.6	118	4	US-10-032-201B-91	Sequence 91, Appl
279	47	100.0	602	4	US-10-290-072-232	Sequence 232, App	352	44	93.6	118	4	US-10-767-701-46089	Sequence 46089, A
280	47	100.0	710	4	US-10-296-770-4	Sequence 4, Appl	353	44	93.6	118	4	US-10-425-115-200792	Sequence 200792, A
281	47	100.0	824	4	US-10-046-583A-3	Sequence 3, Appl	354	44	93.6	118	4	US-10-425-115-316523	Sequence 316523, A
282	47	100.0	858	4	US-10-121-988-92	Sequence 92, Appl	355	44	93.6	118	5	US-10-978-538-4	Sequence 4, Appl
283	47	100.0	858	4	US-10-200-556-92	Sequence 92, Appl	356	44	93.6	118	5	US-10-978-538-10	Sequence 10, Appl
284	47	100.0	858	4	US-10-237-551-92	Sequence 92, Appl	357	44	93.6	118	5	US-10-978-538-13	Sequence 13, Appl
285	47	100.0	858	5	US-10-945-050-92	Sequence 92, Appl	358	44	93.6	119	4	US-10-032-201B-175	Sequence 175, App
286	47	100.0	1285	4	US-10-044-693-314	Sequence 314, App	359	44	93.6	119	4	US-10-424-599-227977	Sequence 227977, A
287	47	100.0	1285	4	US-10-044-533-314	Sequence 314, App	360	44	93.6	120	4	US-10-424-599-190543	Sequence 190543, A
288	47	100.0	1285	4	US-10-325-810-600	Sequence 600, App	361	44	93.6	120	4	US-10-425-115-283653	Sequence 283653, A
289	47	100.0	1285	5	US-10-877-124-600	Sequence 600, App	362	44	93.6	120	5	US-10-978-538-6	Sequence 6, Appl
290	47	100.0	1285	5	US-10-877-124-600	Sequence 600, App	363	44	93.6	121	4	US-10-437-963-117121	Sequence 117121, A
291	47	100.0	1285	5	US-10-877-146-600	Sequence 600, App	364	44	93.6	121	4	US-10-425-115-283697	Sequence 283697, A
292	47	93.6	1285	3	US-09-963-339-10	Sequence 10, Appl	365	44	93.6	122	4	US-10-194-885-9	Sequence 9, Appl
293	47	93.6	19	4	US-10-145-386-59	Sequence 59, Appl	366	44	93.6	122	4	US-10-194-885-19	Sequence 19, Appl
294	47	93.6	32	4	US-10-424-599-160512	Sequence 160512, A	367	44	93.6	122	4	US-10-194-885-21	Sequence 21, Appl
295	47	93.6	49	4	US-10-425-115-334172	Sequence 334172, A	368	44	93.6	122	4	US-10-091-841-2	Sequence 84, Appl
296	47	93.6	55	4	US-10-425-115-307743	Sequence 307743, A	369	44	93.6	122	4	US-10-032-201B-89	Sequence 89, Appl
297	47	93.6	56	4	US-10-425-115-219153	Sequence 219153, A	370	44	93.6	122	4	US-10-425-115-280336	Sequence 280336, A
298	47	93.6	59	4	US-10-424-599-176362	Sequence 176362, A	371	44	93.6	122	4	US-10-425-115-280338	Sequence 280338, A
299	47	93.6	61	4	US-10-425-115-336734	Sequence 336734, A	372	44	93.6	122	4	US-10-425-115-280382	Sequence 280382, A
300	47	93.6	71	3	US-09-764-875-1015	Sequence 1015, App	373	44	93.6	122	5	US-10-810-160-25	Sequence 25, Appl
301	47	93.6	89	4	US-10-437-963-147189	Sequence 147189, A	374	44	93.6	122	5	US-10-978-538-2	Sequence 2, Appl
302	47	93.6	81	4	US-10-425-115-311489	Sequence 311489, A	375	44	93.6	123	4	US-10-425-115-283692	Sequence 283692, A
303	47	93.6	83	4	US-10-425-115-243739	Sequence 243739, A	376	44	93.6	123	4	US-10-425-115-283655	Sequence 283655, A
304	47	93.6	88	4	US-10-032-201B-115	Sequence 115, App	377	44	93.6	123	5	US-10-978-538-8	Sequence 8, Appl
305	47	93.6	88	4	US-10-032-201B-116	Sequence 116, App	378	44	93.6	124	4	US-10-425-115-312480	Sequence 312480, A
306	47	93.6	96	4	US-10-425-115-286533	Sequence 286533, A	379	44	93.6	125	4	US-10-194-885-20	Sequence 20, Appl
307	47	93.6	96	4	US-10-425-115-334150	Sequence 334150, A	380	44	93.6	125	4	US-10-032-201B-90	Sequence 90, Appl
308	47	93.6	102	4	US-10-032-201B-72	Sequence 72, Appl	381	44	93.6	125	4	US-10-437-963-135318	Sequence 135318, A
309	47	93.6	102	4	US-10-032-201B-103	Sequence 103, App	382	44	93.6	126	4	US-10-194-885-22	Sequence 22, Appl
310	47	93.6	102	4	US-10-289-762-697	Sequence 697, App	383	44	93.6	126	4	US-10-032-201B-79	Sequence 79, Appl
311	47	93.6	103	5	US-10-275-652-20	Sequence 20, Appl	384	44	93.6	126	4	US-10-032-201B-92	Sequence 92, Appl
312	47	93.6	103	4	US-10-032-201B-124	Sequence 124, App	385	44	93.6	126	5	US-10-978-538-12	Sequence 12, Appl
313	47	93.6	103	4	US-10-660-118A-6	Sequence 6, Appl	386	44	93.6	127	4	US-10-091-841-4	Sequence 4, Appl
314	47	93.6	103	4	US-10-425-115-243742	Sequence 243742, A	387	44	93.6	127	4	US-10-425-114-60505	Sequence 60505, A
315	47	93.6	103	4	US-10-425-115-280404	Sequence 280404, A	388	44	93.6	128	4	US-10-425-115-200323	Sequence 200323, A
316	47	93.6	104	4	US-10-032-201B-134	Sequence 134, App	389	44	93.6	129	4	US-10-156-761-14876	Sequence 14876, A
317	47	93.6	104	4	US-10-474-776-712	Sequence 712, App	390	44	93.6	130	4	US-10-091-841-6	Sequence 6, Appl
318	47	93.6	104	4	US-10-660-118A-5	Sequence 5, Appl	391	44	93.6	130	4	US-10-425-115-244247	Sequence 244247, A
319	47	93.6	104	5	US-10-472-928-3670	Sequence 3670, App	392	44	93.6	131	4	US-10-032-201B-170	Sequence 170, App

393	44	93.6	131	4	US-10-032-201B-171	Sequence 171, App	466	44	93.6	180	4	US-10-425-114-66813	Sequence 66813, A
394	44	93.6	131	4	US-10-032-201B-172	Sequence 172, App	467	44	93.6	180	4	US-10-437-963-17191	Sequence 147191, A
395	44	93.6	131	4	US-10-032-201B-174	Sequence 174, App	468	44	93.6	181	4	US-10-424-599-178291	Sequence 178291, A
396	44	93.6	131	4	US-10-032-201B-193	Sequence 193, App	469	44	93.6	181	4	US-10-424-599-273435	Sequence 273435, A
397	44	93.6	131	4	US-10-424-599-231070	Sequence 231070, A	470	44	93.6	181	4	US-10-437-963-204686	Sequence 204686, A
398	44	93.6	131	4	US-10-425-115-320098	Sequence 320098, A	471	44	93.6	182	4	US-10-424-599-250227	Sequence 250227, A
399	44	93.6	132	4	US-10-425-115-317382	Sequence 317382, A	472	44	93.6	182	4	US-10-425-114-67114	Sequence 67114, A
400	44	93.6	133	4	US-10-032-201B-80	Sequence 80, App1	473	44	93.6	182	4	US-10-767-701-46296	Sequence 46296, A
401	44	93.6	133	4	US-10-425-114-61995	Sequence 61995, A	474	44	93.6	183	4	US-10-767-701-42070	Sequence 42070, A
402	44	93.6	133	4	US-10-767-701-43666	Sequence 43666, A	475	44	93.6	188	4	US-10-425-115-360038	Sequence 360038, A
403	44	93.6	134	4	US-10-660-118A-13	Sequence 13, App1	476	44	93.6	189	4	US-10-437-963-204658	Sequence 204658, A
404	44	93.6	134	4	US-10-425-115-247611	Sequence 247611, A	477	44	93.6	191	4	US-10-424-599-275952	Sequence 275952, A
405	44	93.6	135	4	US-10-425-115-237035	Sequence 237035, A	478	44	93.6	193	4	US-10-032-201B-62	Sequence 62, App1
406	44	93.6	136	4	US-10-425-114-624530	Sequence 624530, A	479	44	93.6	194	4	US-10-437-963-204634	Sequence 204634, A
407	44	93.6	137	4	US-10-425-114-48233	Sequence 48233, A	480	44	93.6	204	4	US-10-425-114-47113	Sequence 47113, A
408	44	93.6	137	4	US-10-425-114-53102	Sequence 53102, A	481	44	93.6	216	4	US-10-425-114-66365	Sequence 66365, A
409	44	93.6	137	4	US-10-425-114-60594	Sequence 60594, A	482	44	93.6	229	4	US-10-425-115-207582	Sequence 207582, A
410	44	93.6	137	4	US-10-425-114-64437	Sequence 64437, A	483	44	93.6	232	4	US-09-897-898-11	Sequence 11, App1
411	44	93.6	137	4	US-10-425-114-65475	Sequence 65475, A	484	44	93.6	232	3	US-09-897-425-46	Sequence 46, App1
412	44	93.6	137	4	US-10-425-115-272549	Sequence 272549, A	485	44	93.6	232	4	US-10-032-201B-20	Sequence 20, App1
413	44	93.6	137	4	US-10-425-115-272551	Sequence 272551, A	486	44	93.6	264	4	US-10-767-701-47316	Sequence 47316, A
414	44	93.6	139	4	US-10-032-201B-119	Sequence 119, App	487	44	93.6	318	5	US-10-732-923-9556	Sequence 9556, App
415	44	93.6	139	4	US-10-425-114-66598	Sequence 66598, A	488	44	93.6	329	5	US-10-732-923-9551	Sequence 9551, App
416	44	93.6	140	4	US-10-032-201B-64	Sequence 64, App1	489	44	93.6	330	4	US-10-437-963-154386	Sequence 154386, A
417	44	93.6	140	4	US-10-425-114-60597	Sequence 60597, A	490	44	93.6	345	5	US-10-732-923-9550	Sequence 9550, App
418	44	93.6	141	4	US-10-425-114-48043	Sequence 48043, A	491	44	93.6	375	5	US-10-732-923-9537	Sequence 9537, App
419	44	93.6	141	4	US-10-425-114-48133	Sequence 48133, A	492	44	93.6	375	5	US-10-732-923-9538	Sequence 9538, App
420	44	93.6	141	4	US-10-425-114-60598	Sequence 60598, A	493	44	93.6	379	4	US-10-424-599-160099	Sequence 160099, A
421	44	93.6	141	4	US-10-425-114-61985	Sequence 61985, A	494	44	93.6	380	5	US-10-732-923-9531	Sequence 9531, App
422	44	93.6	142	4	US-10-378-029-75	Sequence 75, App1	495	44	93.6	380	5	US-10-732-923-9532	Sequence 9532, App
423	44	93.6	143	4	US-10-425-115-247344	Sequence 247344, A	496	44	93.6	385	5	US-10-732-923-9524	Sequence 9524, App
424	44	93.6	144	4	US-10-425-115-247348	Sequence 247348, A	497	44	93.6	385	5	US-10-732-923-9542	Sequence 9542, App
425	44	93.6	149	3	US-10-425-114-49225	Sequence 49225, A	498	44	93.6	446	4	US-10-290-072-212	Sequence 212, App
426	44	93.6	149	3	US-09-738-626-67935	Sequence 67935, App	499	44	93.6	446	4	US-10-290-072-214	Sequence 214, App
427	44	93.6	150	4	US-10-425-114-65385	Sequence 65385, A	500	44	93.6	447	4	US-10-290-072-216	Sequence 216, App
428	44	93.6	150	4	US-10-767-701-41404	Sequence 41404, A	501	44	93.6	447	4	US-10-290-072-210	Sequence 210, App
429	44	93.6	151	4	US-10-156-761-14771	Sequence 14771, A	502	44	93.6	447	4	US-10-290-072-229	Sequence 239, App
430	44	93.6	152	4	US-10-425-114-62447	Sequence 62447, A	503	44	93.6	469	5	US-10-511-699-18	Sequence 18, App1
431	44	93.6	153	4	US-10-424-599-178292	Sequence 178292, A	504	44	93.6	471	4	US-10-032-201B-37	Sequence 37, App1
432	44	93.6	153	4	US-10-425-114-50553	Sequence 50553, A	505	44	93.6	483	5	US-10-511-699-17	Sequence 17, App1
433	44	93.6	155	4	US-10-425-115-196289	Sequence 196289, A	506	44	93.6	486	3	US-09-963-339-5	Sequence 5, App1
434	44	93.6	160	4	US-10-032-201B-181	Sequence 181, App	507	44	93.6	486	4	US-10-145-586-54	Sequence 54, App1
435	44	93.6	163	4	US-10-425-114-41500	Sequence 41500, A	508	44	93.6	518	4	US-10-032-201B-35	Sequence 35, App1
436	44	93.6	163	4	US-10-425-114-52657	Sequence 52657, A	509	44	93.6	549	4	US-10-424-599-250228	Sequence 250228, A
437	44	93.6	165	4	US-10-437-963-131521	Sequence 131521, A	510	44	93.6	553	4	US-10-108-260A-4505	Sequence 4505, App
438	44	93.6	167	4	US-10-032-201B-65	Sequence 65, App1	511	44	93.6	569	4	US-10-437-963-132372	Sequence 132372, A
439	44	93.6	167	4	US-10-437-963-137652	Sequence 137652, A	512	44	93.6	588	5	US-10-408-766A-907	Sequence 907, App
440	44	93.6	167	4	US-10-660-118A-14	Sequence 14, App1	513	44	93.6	588	4	US-10-732-923-13420	Sequence 13420, A
441	44	93.6	167	4	US-10-425-115-196292	Sequence 196292, A	514	44	93.6	588	5	US-10-732-923-13422	Sequence 13422, A
442	44	93.6	168	4	US-10-425-115-196290	Sequence 196290, A	515	44	93.6	596	4	US-10-114-087-17	Sequence 17, App1
443	44	93.6	169	3	US-09-897-898-9	Sequence 9, App1	516	44	93.6	596	4	US-10-712-124-44	Sequence 44, App1
444	44	93.6	169	3	US-09-897-425-44	Sequence 44, App1	517	44	93.6	606	5	US-10-511-699-16	Sequence 16, App1
445	44	93.6	169	4	US-10-032-201B-18	Sequence 18, App1	518	44	93.6	629	5	US-10-723-860-19	Sequence 19, App1
446	44	93.6	169	4	US-10-424-599-176516	Sequence 176516, A	519	44	93.6	629	4	US-10-437-963-119462	Sequence 119462, A
447	44	93.6	172	4	US-10-032-201B-66	Sequence 66, App1	520	44	93.6	981	4	US-10-437-963-127070	Sequence 127070, A
448	44	93.6	172	4	US-10-032-201B-67	Sequence 67, App1	521	44	93.6	105	4	US-10-032-201B-118	Sequence 118, App
449	44	93.6	172	4	US-10-437-963-137025	Sequence 137025, A	522	44	93.6	105	4	US-10-032-201B-184	Sequence 184, App1
450	44	93.6	172	4	US-10-660-118A-15	Sequence 15, App1	523	44	93.6	110	4	US-10-032-201B-77	Sequence 77, App1
451	44	93.6	173	4	US-10-032-201B-61	Sequence 61, App1	524	44	93.6	111	4	US-10-437-963-182983	Sequence 182983, A
452	44	93.6	174	4	US-10-767-701-32096	Sequence 32096, A	525	44	93.6	126	5	US-10-741-601-389	Sequence 389, App
453	44	93.6	174	4	US-10-425-115-317875	Sequence 317875, A	526	44	93.6	126	5	US-10-741-601-1162	Sequence 1162, App
454	44	93.6	175	4	US-10-032-201B-69	Sequence 69, App1	527	44	93.6	151	4	US-10-032-201B-168	Sequence 168, App
455	44	93.6	175	4	US-10-032-201B-156	Sequence 156, App	528	44	93.6	167	4	US-10-425-115-249338	Sequence 249338, A
456	44	93.6	175	4	US-10-424-599-177899	Sequence 177899, A	529	44	93.6	177	4	US-10-425-114-41212	Sequence 41212, A
457	44	93.6	175	4	US-10-424-599-282483	Sequence 282483, A	530	44	93.6	183	4	US-10-424-599-225032	Sequence 225032, A
458	44	93.6	175	4	US-10-425-114-50857	Sequence 50857, A	531	44	93.6	327	4	US-10-032-585-7827	Sequence 7827, App
459	44	93.6	175	4	US-10-767-701-40803	Sequence 40803, A	532	44	93.6	459	5	US-10-450-766-48425	Sequence 48425, A
460	44	93.6	177	4	US-10-425-115-349412	Sequence 349412, A	533	44	93.6	570	5	US-10-424-599-21821	Sequence 21821, A
461	44	93.6	179	4	US-10-425-114-62266	Sequence 62266, A	534	44	93.6	706	6	US-11-097-143-26871	Sequence 26871, A
462	44	93.6	179	4	US-10-425-114-66811	Sequence 66811, A	535	44	93.6	747	3	US-09-978-295A-459	Sequence 459, App
463	44	93.6	179	4	US-10-425-115-280370	Sequence 280370, A	536	44	93.6	747	3	US-09-938-418-9	Sequence 9, App1
464	44	93.6	180	4	US-10-425-114-48070	Sequence 48070, A	537	44	93.6	747	3	US-09-978-697-459	Sequence 459, App
465	44	93.6	180	4	US-10-425-114-52471	Sequence 52471, A	538	44	93.6	747	3	US-09-978-192A-459	Sequence 459, App

539	43	91.5	747	3	US-09-999-832A-459	Sequence 459, App	612	43	91.5	747	4	US-10-131-818A-426	Sequence 426, App
540	43	91.5	747	3	US-09-978-189-459	Sequence 459, App	613	43	91.5	747	4	US-10-131-823A-426	Sequence 426, App
541	43	91.5	747	3	US-09-978-608A-459	Sequence 459, App	614	43	91.5	747	4	US-10-131-824A-426	Sequence 426, App
542	43	91.5	747	3	US-09-978-585A-459	Sequence 459, App	615	43	91.5	747	4	US-10-131-830A-426	Sequence 426, App
543	43	91.5	747	3	US-09-978-191A-459	Sequence 459, App	616	43	91.5	747	4	US-10-131-837A-426	Sequence 426, App
544	43	91.5	747	3	US-09-978-403A-459	Sequence 459, App	617	43	91.5	747	4	US-10-137-872A-426	Sequence 426, App
545	43	91.5	747	3	US-09-978-564A-459	Sequence 459, App	618	43	91.5	747	4	US-10-147-500-426	Sequence 426, App
546	43	91.5	747	3	US-09-999-833A-459	Sequence 459, App	619	43	91.5	747	4	US-10-147-502-426	Sequence 426, App
547	43	91.5	747	3	US-09-981-915A-459	Sequence 459, App	620	43	91.5	747	4	US-10-147-515-426	Sequence 426, App
548	43	91.5	747	3	US-09-978-824-459	Sequence 459, App	621	43	91.5	747	4	US-10-147-517-426	Sequence 426, App
549	43	91.5	747	3	US-09-918-585A-459	Sequence 459, App	622	43	91.5	747	4	US-10-147-526-426	Sequence 426, App
550	43	91.5	747	3	US-09-999-834A-459	Sequence 459, App	623	43	91.5	747	4	US-10-147-527-426	Sequence 426, App
551	43	91.5	747	3	US-09-978-423A-459	Sequence 459, App	624	43	91.5	747	4	US-10-121-041-426	Sequence 426, App
552	43	91.5	747	3	US-09-978-193A-459	Sequence 459, App	625	43	91.5	747	4	US-10-121-043-426	Sequence 426, App
553	43	91.5	747	3	US-09-999-830A-459	Sequence 459, App	626	43	91.5	747	4	US-10-121-047-426	Sequence 426, App
554	43	91.5	747	3	US-09-978-757A-459	Sequence 459, App	627	43	91.5	747	4	US-10-123-215-426	Sequence 426, App
555	43	91.5	747	3	US-09-978-187B-459	Sequence 459, App	628	43	91.5	747	4	US-10-123-902-426	Sequence 426, App
556	43	91.5	747	3	US-09-978-643A-459	Sequence 459, App	629	43	91.5	747	4	US-10-123-908-426	Sequence 426, App
557	43	91.5	747	3	US-09-978-375A-459	Sequence 459, App	630	43	91.5	747	4	US-10-123-909-426	Sequence 426, App
558	43	91.5	747	3	US-09-978-298A-459	Sequence 459, App	631	43	91.5	747	4	US-10-123-910-426	Sequence 426, App
559	43	91.5	747	3	US-09-978-188A-459	Sequence 459, App	632	43	91.5	747	4	US-10-124-813-426	Sequence 426, App
560	43	91.5	747	3	US-09-978-681A-459	Sequence 459, App	633	43	91.5	747	4	US-10-124-817-426	Sequence 426, App
561	43	91.5	747	3	US-09-978-194A-459	Sequence 459, App	634	43	91.5	747	4	US-10-125-922-426	Sequence 426, App
562	43	91.5	747	3	US-09-999-823A-459	Sequence 459, App	635	43	91.5	747	4	US-10-125-924-426	Sequence 426, App
563	43	91.5	747	3	US-09-978-299A-459	Sequence 459, App	636	43	91.5	747	4	US-10-140-860-426	Sequence 426, App
564	43	91.5	747	3	US-09-978-544A-459	Sequence 459, App	637	43	91.5	747	4	US-10-142-417-426	Sequence 426, App
565	43	91.5	747	3	US-09-978-654A-459	Sequence 459, App	638	43	91.5	747	4	US-10-142-419-426	Sequence 426, App
566	43	91.5	747	3	US-09-978-802A-459	Sequence 459, App	639	43	91.5	747	4	US-10-147-519-426	Sequence 426, App
567	43	91.5	747	3	US-09-999-831A-459	Sequence 459, App	640	43	91.5	747	4	US-10-152-395-426	Sequence 426, App
568	43	91.5	747	3	US-09-978-824-459	Sequence 459, App	641	43	91.5	747	4	US-10-125-926A-426	Sequence 426, App
569	43	91.5	747	4	US-10-028-072-426	Sequence 426, App	642	43	91.5	747	4	US-10-125-930A-426	Sequence 426, App
570	43	91.5	747	4	US-10-140-808-426	Sequence 426, App	643	43	91.5	747	4	US-10-127-831A-426	Sequence 426, App
571	43	91.5	747	4	US-10-121-904-426	Sequence 426, App	644	43	91.5	747	4	US-10-127-837A-426	Sequence 426, App
572	43	91.5	747	4	US-10-123-904-426	Sequence 426, App	645	43	91.5	747	4	US-10-127-839B-426	Sequence 426, App
573	43	91.5	747	4	US-10-140-470-426	Sequence 426, App	646	43	91.5	747	4	US-10-127-842A-426	Sequence 426, App
574	43	91.5	747	4	US-10-175-746-426	Sequence 426, App	647	43	91.5	747	4	US-10-127-843A-426	Sequence 426, App
575	43	91.5	747	4	US-10-176-918-426	Sequence 426, App	648	43	91.5	747	4	US-10-127-845A-426	Sequence 426, App
576	43	91.5	747	4	US-10-176-921-426	Sequence 426, App	649	43	91.5	747	4	US-10-127-846A-426	Sequence 426, App
577	43	91.5	747	4	US-10-137-865-426	Sequence 426, App	650	43	91.5	747	4	US-10-127-848A-426	Sequence 426, App
578	43	91.5	747	4	US-10-140-474-426	Sequence 426, App	651	43	91.5	747	4	US-10-127-849A-426	Sequence 426, App
579	43	91.5	747	4	US-10-142-431-426	Sequence 426, App	652	43	91.5	747	4	US-10-127-850A-426	Sequence 426, App
580	43	91.5	747	4	US-10-143-114-426	Sequence 426, App	653	43	91.5	747	4	US-10-127-851A-426	Sequence 426, App
581	43	91.5	747	4	US-10-142-419-426	Sequence 426, App	654	43	91.5	747	4	US-10-128-688A-426	Sequence 426, App
582	43	91.5	747	4	US-10-017-081A-459	Sequence 459, App	655	43	91.5	747	4	US-10-128-686A-426	Sequence 426, App
583	43	91.5	747	4	US-10-123-262-426	Sequence 426, App	656	43	91.5	747	4	US-10-128-690A-426	Sequence 426, App
584	43	91.5	747	4	US-10-142-423-426	Sequence 426, App	657	43	91.5	747	4	US-10-128-691A-426	Sequence 426, App
585	43	91.5	747	4	US-10-121-050-426	Sequence 426, App	658	43	91.5	747	4	US-10-131-819A-426	Sequence 426, App
586	43	91.5	747	4	US-10-141-755-426	Sequence 426, App	659	43	91.5	747	4	US-10-131-829A-426	Sequence 426, App
587	43	91.5	747	4	US-10-167-749-459	Sequence 459, App	660	43	91.5	747	4	US-10-131-836A-426	Sequence 426, App
588	43	91.5	747	4	US-10-143-033-426	Sequence 426, App	661	43	91.5	747	4	US-10-146-729-426	Sequence 426, App
589	43	91.5	747	4	US-10-013-921A-459	Sequence 459, App	662	43	91.5	747	4	US-10-146-729-426	Sequence 426, App
590	43	91.5	747	4	US-10-123-108-426	Sequence 426, App	663	43	91.5	747	4	US-10-147-488-426	Sequence 426, App
591	43	91.5	747	4	US-10-123-236-426	Sequence 426, App	664	43	91.5	747	4	US-10-147-508-426	Sequence 426, App
592	43	91.5	747	4	US-10-123-261-426	Sequence 426, App	665	43	91.5	747	4	US-10-147-512-426	Sequence 426, App
593	43	91.5	747	4	US-10-140-921-426	Sequence 426, App	666	43	91.5	747	4	US-10-175-735-426	Sequence 426, App
594	43	91.5	747	4	US-10-140-928-426	Sequence 426, App	667	43	91.5	747	4	US-10-121-040-426	Sequence 426, App
595	43	91.5	747	4	US-10-013-929A-459	Sequence 459, App	668	43	91.5	747	4	US-10-121-056-426	Sequence 426, App
596	43	91.5	747	4	US-10-016-177A-459	Sequence 459, App	669	43	91.5	747	4	US-10-121-061-426	Sequence 426, App
597	43	91.5	747	4	US-10-121-045-426	Sequence 426, App	670	43	91.5	747	4	US-10-123-225-426	Sequence 426, App
598	43	91.5	747	4	US-10-123-292-426	Sequence 426, App	671	43	91.5	747	4	US-10-124-818-426	Sequence 426, App
599	43	91.5	747	4	US-10-123-903-426	Sequence 426, App	672	43	91.5	747	4	US-10-137-868-426	Sequence 426, App
600	43	91.5	747	4	US-10-124-819-426	Sequence 426, App	673	43	91.5	747	4	US-10-147-492-426	Sequence 426, App
601	43	91.5	747	4	US-10-124-822-426	Sequence 426, App	674	43	91.5	747	4	US-10-158-782-426	Sequence 426, App
602	43	91.5	747	4	US-10-140-925-426	Sequence 426, App	675	43	91.5	747	4	US-10-123-905-426	Sequence 426, App
603	43	91.5	747	4	US-10-160-498-426	Sequence 426, App	676	43	91.5	747	4	US-10-123-907-426	Sequence 426, App
604	43	91.5	747	4	US-10-124-824-426	Sequence 426, App	677	43	91.5	747	4	US-10-124-815-426	Sequence 426, App
605	43	91.5	747	4	US-10-127-825A-426	Sequence 426, App	678	43	91.5	747	4	US-10-125-921A-426	Sequence 426, App
606	43	91.5	747	4	US-10-127-829A-426	Sequence 426, App	679	43	91.5	747	4	US-10-127-822A-426	Sequence 426, App
607	43	91.5	747	4	US-10-127-835A-426	Sequence 426, App	680	43	91.5	747	4	US-10-127-821A-426	Sequence 426, App
608	43	91.5	747	4	US-10-127-839A-426	Sequence 426, App	681	43	91.5	747	4	US-10-127-824A-426	Sequence 426, App
609	43	91.5	747	4	US-10-127-901A-426	Sequence 426, App	682	43	91.5	747	4	US-10-127-826A-426	Sequence 426, App
610	43	91.5	747	4	US-10-128-693A-426	Sequence 426, App	683	43	91.5	747	4	US-10-127-827A-426	Sequence 426, App
611	43	91.5	747	4	US-10-131-813A-426	Sequence 426, App	684	43	91.5	747	4	US-10-127-827A-426	Sequence 426, App

685	43	91.5	747	4	US-10-127-828A-426	Sequence 426, App	758	43	91.5	747	4	US-10-147-529-426	Sequence 426, App
686	43	91.5	747	4	US-10-127-830A-426	Sequence 426, App	759	43	91.5	747	4	US-10-152-397-426	Sequence 426, App
687	43	91.5	747	4	US-10-127-832A-426	Sequence 426, App	760	43	91.5	747	4	US-10-153-588-426	Sequence 426, App
688	43	91.5	747	4	US-10-127-833A-426	Sequence 426, App	761	43	91.5	747	4	US-10-158-788-426	Sequence 426, App
689	43	91.5	747	4	US-10-127-834A-426	Sequence 426, App	762	43	91.5	747	4	US-10-143-031A-459	Sequence 459, App
690	43	91.5	747	4	US-10-127-836A-426	Sequence 426, App	763	43	91.5	747	4	US-10-137-870-426	Sequence 426, App
691	43	91.5	747	4	US-10-127-841A-426	Sequence 426, App	764	43	91.5	747	4	US-10-140-018-426	Sequence 426, App
692	43	91.5	747	4	US-10-127-844A-426	Sequence 426, App	765	43	91.5	747	4	US-10-140-021-426	Sequence 426, App
693	43	91.5	747	4	US-10-128-687A-426	Sequence 426, App	766	43	91.5	747	4	US-10-140-477-426	Sequence 426, App
694	43	91.5	747	4	US-10-128-688A-426	Sequence 426, App	767	43	91.5	747	4	US-10-140-922-426	Sequence 426, App
695	43	91.5	747	4	US-10-128-689A-426	Sequence 426, App	768	43	91.5	747	4	US-10-145-631-426	Sequence 426, App
696	43	91.5	747	4	US-10-128-694A-426	Sequence 426, App	769	43	91.5	747	4	US-10-145-633-426	Sequence 426, App
697	43	91.5	747	4	US-10-131-825A-426	Sequence 426, App	770	43	91.5	747	4	US-10-158-788-426	Sequence 426, App
698	43	91.5	747	4	US-10-230-817-426	Sequence 426, App	771	43	91.5	747	4	US-10-140-278-426	Sequence 426, App
699	43	91.5	747	4	US-10-131-815A-426	Sequence 426, App	772	43	91.5	747	4	US-10-143-030A-459	Sequence 459, App
700	43	91.5	747	4	US-10-131-817A-426	Sequence 426, App	773	43	91.5	747	4	US-10-002-967A-459	Sequence 459, App
701	43	91.5	747	4	US-10-131-821A-426	Sequence 426, App	774	43	91.5	747	4	US-10-017-082A-459	Sequence 426, App
702	43	91.5	747	4	US-10-131-822A-426	Sequence 426, App	775	43	91.5	747	4	US-10-140-019-426	Sequence 426, App
703	43	91.5	747	4	US-10-131-828A-426	Sequence 426, App	776	43	91.5	747	4	US-10-140-022-426	Sequence 426, App
704	43	91.5	747	4	US-10-131-835A-426	Sequence 426, App	777	43	91.5	747	4	US-10-140-861-426	Sequence 426, App
705	43	91.5	747	4	US-10-137-864A-426	Sequence 426, App	778	43	91.5	747	4	US-10-140-862-426	Sequence 426, App
706	43	91.5	747	4	US-10-137-869A-426	Sequence 426, App	779	43	91.5	747	4	US-10-141-697-426	Sequence 426, App
707	43	91.5	747	4	US-10-147-523-426	Sequence 426, App	780	43	91.5	747	4	US-10-141-700-426	Sequence 426, App
708	43	91.5	747	4	US-10-158-785-426	Sequence 426, App	781	43	91.5	747	4	US-10-141-705-426	Sequence 426, App
709	43	91.5	747	4	US-10-121-051-426	Sequence 426, App	782	43	91.5	747	4	US-10-141-753-426	Sequence 426, App
710	43	91.5	747	4	US-10-121-042-426	Sequence 426, App	783	43	91.5	747	4	US-10-141-758-426	Sequence 426, App
711	43	91.5	747	4	US-10-123-912-426	Sequence 426, App	784	43	91.5	747	4	US-10-142-418-426	Sequence 426, App
712	43	91.5	747	4	US-10-223-085-114	Sequence 114, App	785	43	91.5	747	4	US-10-142-422-426	Sequence 426, App
713	43	91.5	747	4	US-10-166-709A-459	Sequence 459, App	786	43	91.5	747	4	US-10-142-422-426	Sequence 426, App
714	43	91.5	747	4	US-10-192-007-426	Sequence 426, App	787	43	91.5	747	4	US-10-142-427-426	Sequence 426, App
715	43	91.5	747	4	US-10-194-359-426	Sequence 426, App	788	43	91.5	747	4	US-10-142-760-426	Sequence 426, App
716	43	91.5	747	4	US-10-223-084-114	Sequence 114, App	789	43	91.5	747	4	US-10-145-821-426	Sequence 426, App
717	43	91.5	747	4	US-10-223-088-114	Sequence 114, App	790	43	91.5	747	4	US-10-152-531-426	Sequence 426, App
718	43	91.5	747	4	US-10-223-090-114	Sequence 114, App	791	43	91.5	747	4	US-10-127-840A-426	Sequence 426, App
719	43	91.5	747	4	US-10-127-087-114	Sequence 114, App	792	43	91.5	747	4	US-10-142-424-426	Sequence 426, App
720	43	91.5	747	4	US-10-127-847A-426	Sequence 426, App	793	43	91.5	747	4	US-10-142-761-426	Sequence 426, App
721	43	91.5	747	4	US-10-223-083-114	Sequence 114, App	794	43	91.5	747	4	US-10-142-763-426	Sequence 426, App
722	43	91.5	747	4	US-10-223-089-114	Sequence 114, App	795	43	91.5	747	4	US-10-142-765-426	Sequence 426, App
723	43	91.5	747	4	US-10-137-866-426	Sequence 426, App	796	43	91.5	747	4	US-10-142-882-426	Sequence 426, App
724	43	91.5	747	4	US-10-146-726-426	Sequence 426, App	797	43	91.5	747	4	US-10-142-888-426	Sequence 426, App
725	43	91.5	747	4	US-10-146-727-426	Sequence 426, App	798	43	91.5	747	4	US-10-143-034-426	Sequence 426, App
726	43	91.5	747	4	US-10-146-788-426	Sequence 426, App	799	43	91.5	747	4	US-10-143-116-426	Sequence 426, App
727	43	91.5	747	4	US-10-152-380-426	Sequence 426, App	800	43	91.5	747	4	US-10-144-957-426	Sequence 426, App
728	43	91.5	747	4	US-10-153-934-426	Sequence 426, App	801	43	91.5	747	4	US-10-144-992-426	Sequence 426, App
729	43	91.5	747	4	US-10-140-807-426	Sequence 426, App	802	43	91.5	747	4	US-10-145-015-426	Sequence 426, App
730	43	91.5	747	4	US-10-140-924-426	Sequence 426, App	803	43	91.5	747	4	US-10-145-019-426	Sequence 426, App
731	43	91.5	747	4	US-10-140-926-426	Sequence 426, App	804	43	91.5	747	4	US-10-145-091-426	Sequence 426, App
732	43	91.5	747	4	US-10-141-698-426	Sequence 426, App	805	43	91.5	747	4	US-10-145-128A-459	Sequence 459, App
733	43	91.5	747	4	US-10-141-702-426	Sequence 426, App	806	43	91.5	747	4	US-10-145-629-426	Sequence 426, App
734	43	91.5	747	4	US-10-141-704-426	Sequence 426, App	807	43	91.5	747	4	US-10-145-630-426	Sequence 426, App
735	43	91.5	747	4	US-10-142-421-426	Sequence 426, App	808	43	91.5	747	4	US-10-145-747-426	Sequence 426, App
736	43	91.5	747	4	US-10-142-432-426	Sequence 426, App	809	43	91.5	747	4	US-10-145-752-426	Sequence 426, App
737	43	91.5	747	4	US-10-142-767-426	Sequence 426, App	810	43	91.5	747	4	US-10-145-754-426	Sequence 426, App
738	43	91.5	747	4	US-10-143-033-426	Sequence 426, App	811	43	91.5	747	4	US-10-145-755-426	Sequence 426, App
739	43	91.5	747	4	US-10-144-594-426	Sequence 426, App	812	43	91.5	747	4	US-10-145-818-426	Sequence 426, App
740	43	91.5	747	4	US-10-145-628-426	Sequence 426, App	813	43	91.5	747	4	US-10-145-820-426	Sequence 426, App
741	43	91.5	747	4	US-10-145-746-426	Sequence 426, App	814	43	91.5	747	4	US-10-145-872-426	Sequence 426, App
742	43	91.5	747	4	US-10-145-748-426	Sequence 426, App	815	43	91.5	747	4	US-10-145-873-426	Sequence 426, App
743	43	91.5	747	4	US-10-145-823-426	Sequence 426, App	816	43	91.5	747	4	US-10-145-874-426	Sequence 426, App
744	43	91.5	747	4	US-10-145-826-426	Sequence 426, App	817	43	91.5	747	4	US-10-147-482-426	Sequence 426, App
745	43	91.5	747	4	US-10-145-870-426	Sequence 426, App	818	43	91.5	747	4	US-10-147-503-426	Sequence 426, App
746	43	91.5	747	4	US-10-145-876-426	Sequence 426, App	819	43	91.5	747	4	US-10-147-522-426	Sequence 426, App
747	43	91.5	747	4	US-10-145-899-426	Sequence 426, App	820	43	91.5	747	4	US-10-152-441-426	Sequence 426, App
748	43	91.5	747	4	US-10-146-724-426	Sequence 426, App	821	43	91.5	747	4	US-10-157-783-426	Sequence 426, App
749	43	91.5	747	4	US-10-146-725-426	Sequence 426, App	822	43	91.5	747	4	US-10-158-792-426	Sequence 426, App
750	43	91.5	747	4	US-10-146-795-426	Sequence 426, App	823	43	91.5	747	4	US-10-158-862-426	Sequence 426, App
751	43	91.5	747	4	US-10-147-495-426	Sequence 426, App	824	43	91.5	747	4	US-10-143-031-426	Sequence 426, App
752	43	91.5	747	4	US-10-147-501-426	Sequence 426, App	825	43	91.5	747	4	US-10-143-031-426	Sequence 426, App
753	43	91.5	747	4	US-10-147-504-426	Sequence 426, App	826	43	91.5	747	4	US-10-145-822-426	Sequence 426, App
754	43	91.5	747	4	US-10-147-506-426	Sequence 426, App	827	43	91.5	747	4	US-10-145-824-426	Sequence 426, App
755	43	91.5	747	4	US-10-147-509-426	Sequence 426, App	828	43	91.5	747	4	US-10-145-827-426	Sequence 426, App
756	43	91.5	747	4	US-10-147-510-426	Sequence 426, App	829	43	91.5	747	4	US-10-145-869-426	Sequence 426, App
757	43	91.5	747	4	US-10-147-511-426	Sequence 426, App	830	43	91.5	747	4	US-10-145-875-426	Sequence 426, App

831	43	91.5	747	4	US-10-145-877-426	Sequence 426, App	904	43	91.5	747	4	US-10-123-154-426	Sequence 426, App
832	43	91.5	747	4	US-10-145-958-426	Sequence 426, App	905	43	91.5	747	4	US-10-123-157-426	Sequence 426, App
833	43	91.5	747	4	US-10-146-787-426	Sequence 426, App	906	43	91.5	747	4	US-10-123-906-426	Sequence 426, App
834	43	91.5	747	4	US-10-146-790-426	Sequence 426, App	907	43	91.5	747	4	US-10-124-814-426	Sequence 426, App
835	43	91.5	747	4	US-10-146-793-426	Sequence 426, App	908	43	91.5	747	4	US-10-124-816-426	Sequence 426, App
836	43	91.5	747	4	US-10-147-480-426	Sequence 426, App	909	43	91.5	747	4	US-10-124-820-426	Sequence 426, App
837	43	91.5	747	4	US-10-147-485-426	Sequence 426, App	910	43	91.5	747	4	US-10-125-704-426	Sequence 426, App
838	43	91.5	747	4	US-10-147-486-426	Sequence 426, App	911	43	91.5	747	4	US-10-125-927-426	Sequence 426, App
839	43	91.5	747	4	US-10-147-487-426	Sequence 426, App	912	43	91.5	747	4	US-10-125-927-426	Sequence 426, App
840	43	91.5	747	4	US-10-147-490-426	Sequence 426, App	913	43	91.5	747	4	US-10-145-087A-459	Sequence 459, App
841	43	91.5	747	4	US-10-147-494-426	Sequence 426, App	914	43	91.5	747	4	US-10-017-086A-459	Sequence 459, App
842	43	91.5	747	4	US-10-147-498-426	Sequence 426, App	915	43	91.5	747	4	US-10-142-889-426	Sequence 426, App
843	43	91.5	747	4	US-10-147-514-426	Sequence 426, App	916	43	91.5	747	4	US-10-145-874-426	Sequence 426, App
844	43	91.5	747	4	US-10-147-524-426	Sequence 426, App	917	43	91.5	747	4	US-10-147-794-426	Sequence 426, App
845	43	91.5	747	4	US-10-152-379-426	Sequence 426, App	918	43	91.5	747	4	US-10-152-371-426	Sequence 426, App
846	43	91.5	747	4	US-10-152-394-426	Sequence 426, App	919	43	91.5	747	4	US-10-152-374-426	Sequence 426, App
847	43	91.5	747	4	US-10-152-406-426	Sequence 426, App	920	43	91.5	747	4	US-10-152-375-426	Sequence 426, App
848	43	91.5	747	4	US-10-156-847-426	Sequence 426, App	921	43	91.5	747	4	US-10-152-377-426	Sequence 426, App
849	43	91.5	747	4	US-10-157-778-426	Sequence 426, App	922	43	91.5	747	4	US-10-152-386-426	Sequence 426, App
850	43	91.5	747	4	US-10-157-799-426	Sequence 426, App	923	43	91.5	747	4	US-10-152-391-426	Sequence 426, App
851	43	91.5	747	4	US-10-160-504-426	Sequence 426, App	924	43	91.5	747	4	US-10-152-399-426	Sequence 426, App
852	43	91.5	747	4	US-10-017-191A-459	Sequence 459, App	925	43	91.5	747	4	US-10-156-848-426	Sequence 426, App
853	43	91.5	747	4	US-10-145-634-426	Sequence 426, App	926	43	91.5	747	4	US-10-157-789-426	Sequence 426, App
854	43	91.5	747	4	US-10-147-520-426	Sequence 426, App	927	43	91.5	747	4	US-10-157-794-426	Sequence 426, App
855	43	91.5	747	4	US-10-157-781-426	Sequence 426, App	928	43	91.5	747	4	US-10-157-796-426	Sequence 426, App
856	43	91.5	747	4	US-10-176-989-426	Sequence 426, App	929	43	91.5	747	4	US-10-160-500-426	Sequence 426, App
857	43	91.5	747	4	US-10-147-491-426	Sequence 426, App	930	43	91.5	747	4	US-10-164-829A-459	Sequence 459, App
858	43	91.5	747	4	US-10-152-378-426	Sequence 426, App	931	43	91.5	747	4	US-10-164-929A-459	Sequence 459, App
859	43	91.5	747	4	US-10-152-382-426	Sequence 426, App	932	43	91.5	747	4	US-10-121-046-426	Sequence 426, App
860	43	91.5	747	4	US-10-152-384-426	Sequence 426, App	933	43	91.5	747	4	US-10-121-046-426	Sequence 426, App
861	43	91.5	747	4	US-10-152-384-426	Sequence 426, App	934	43	91.5	747	4	US-10-123-214-426	Sequence 426, App
862	43	91.5	747	4	US-10-152-387-426	Sequence 426, App	935	43	91.5	747	4	US-10-125-805-426	Sequence 426, App
863	43	91.5	747	4	US-10-152-389-426	Sequence 426, App	936	43	91.5	747	4	US-10-013-922A-459	Sequence 459, App
864	43	91.5	747	4	US-10-152-390-426	Sequence 426, App	937	43	91.5	747	4	US-10-020-445A-459	Sequence 459, App
865	43	91.5	747	4	US-10-152-392-426	Sequence 426, App	938	43	91.5	747	4	US-10-013-924A-459	Sequence 459, App
866	43	91.5	747	4	US-10-153-756-426	Sequence 426, App	939	43	91.5	747	4	US-10-124-821-426	Sequence 426, App
867	43	91.5	747	4	US-10-157-784-426	Sequence 426, App	940	43	91.5	747	4	US-10-152-385-426	Sequence 426, App
868	43	91.5	747	4	US-10-157-797-426	Sequence 426, App	941	43	91.5	747	4	US-10-152-393-426	Sequence 426, App
869	43	91.5	747	4	US-10-158-491-426	Sequence 426, App	942	43	91.5	747	4	US-10-152-396-426	Sequence 426, App
870	43	91.5	747	4	US-10-143-028A-459	Sequence 459, App	943	43	91.5	747	4	US-10-153-552-426	Sequence 426, App
871	43	91.5	747	4	US-10-143-029A-459	Sequence 459, App	944	43	91.5	747	4	US-10-153-840-426	Sequence 426, App
872	43	91.5	747	4	US-10-142-764-426	Sequence 426, App	945	43	91.5	747	4	US-10-156-841-426	Sequence 426, App
873	43	91.5	747	4	US-10-142-764-426	Sequence 426, App	946	43	91.5	747	4	US-10-156-842-426	Sequence 426, App
874	43	91.5	747	4	US-10-142-766-426	Sequence 426, App	947	43	91.5	747	4	US-10-156-844-426	Sequence 426, App
875	43	91.5	747	4	US-10-145-089A-459	Sequence 459, App	948	43	91.5	747	4	US-10-156-845-426	Sequence 426, App
876	43	91.5	747	4	US-10-145-625-426	Sequence 426, App	949	43	91.5	747	4	US-10-156-846-426	Sequence 426, App
877	43	91.5	747	4	US-10-145-627-426	Sequence 426, App	950	43	91.5	747	4	US-10-121-048-426	Sequence 426, App
878	43	91.5	747	4	US-10-145-960-426	Sequence 426, App	951	43	91.5	747	4	US-10-121-052-426	Sequence 426, App
879	43	91.5	747	4	US-10-145-962-426	Sequence 426, App	952	43	91.5	747	4	US-10-121-053-426	Sequence 426, App
880	43	91.5	747	4	US-10-146-789-426	Sequence 426, App	953	43	91.5	747	4	US-10-121-054-426	Sequence 426, App
881	43	91.5	747	4	US-10-147-483-426	Sequence 426, App	954	43	91.5	747	4	US-10-121-054-426	Sequence 426, App
882	43	91.5	747	4	US-10-147-496-426	Sequence 426, App	955	43	91.5	747	4	US-10-123-212-426	Sequence 426, App
883	43	91.5	747	4	US-10-147-505-426	Sequence 426, App	956	43	91.5	747	4	US-10-123-213-426	Sequence 426, App
884	43	91.5	747	4	US-10-147-516-426	Sequence 426, App	957	43	91.5	747	4	US-10-123-221-426	Sequence 426, App
885	43	91.5	747	4	US-10-152-398-426	Sequence 426, App	958	43	91.5	747	4	US-10-123-322-426	Sequence 426, App
886	43	91.5	747	4	US-10-139-980-426	Sequence 426, App	959	43	91.5	747	4	US-10-123-771-426	Sequence 426, App
887	43	91.5	747	4	US-10-165-067A-459	Sequence 459, App	960	43	91.5	747	4	US-10-123-911-426	Sequence 426, App
888	43	91.5	747	4	US-10-145-017A-459	Sequence 459, App	961	43	91.5	747	4	US-10-124-823-426	Sequence 426, App
889	43	91.5	747	4	US-10-145-750-426	Sequence 426, App	962	43	91.5	747	4	US-10-124-824-426	Sequence 426, App
890	43	91.5	747	4	US-10-152-373-426	Sequence 426, App	963	43	91.5	747	4	US-10-125-932-426	Sequence 426, App
891	43	91.5	747	4	US-10-164-728A-459	Sequence 459, App	964	43	91.5	747	4	US-10-017-084A-459	Sequence 459, App
892	43	91.5	747	4	US-10-223-081-114	Sequence 114, App	965	43	91.5	747	4	US-10-127-852A-426	Sequence 426, App
893	43	91.5	747	4	US-10-013-925A-459	Sequence 459, App	966	43	91.5	747	4	US-10-127-900A-426	Sequence 426, App
894	43	91.5	747	4	US-10-165-247A-459	Sequence 459, App	967	43	91.5	747	4	US-10-128-655A-426	Sequence 426, App
895	43	91.5	747	4	US-10-145-124A-459	Sequence 459, App	968	43	91.5	747	4	US-10-131-862A-426	Sequence 426, App
896	43	91.5	747	4	US-10-160-502A-459	Sequence 459, App	969	43	91.5	747	4	US-10-142-886-426	Sequence 426, App
897	43	91.5	747	4	US-10-121-044-426	Sequence 426, App	970	43	91.5	747	4	US-10-145-016A-459	Sequence 459, App
898	43	91.5	747	4	US-10-121-055-426	Sequence 426, App	971	43	91.5	747	4	US-10-145-088A-459	Sequence 459, App
899	43	91.5	747	4	US-10-121-057-426	Sequence 426, App	972	43	91.5	747	4	US-10-145-092A-459	Sequence 459, App
900	43	91.5	747	4	US-10-121-058-426	Sequence 426, App	973	43	91.5	747	4	US-10-146-129A-459	Sequence 459, App
901	43	91.5	747	4	US-10-121-059-426	Sequence 426, App	974	43	91.5	747	4	US-10-146-728-426	Sequence 426, App
902	43	91.5	747	4	US-10-121-060-426	Sequence 426, App	975	43	91.5	747	4	US-10-146-766-426	Sequence 426, App
903	43	91.5	747	4	US-10-123-109-426	Sequence 426, App	976	43	91.5	747	4	US-10-147-499-426	Sequence 426, App

```
977 43 91.5 747 4 US-10-157-798-426 Sequence 426, App
978 43 91.5 747 4 US-10-165-038A-459 Sequence 459, App
979 43 91.5 747 4 US-10-165-353A-459 Sequence 459, App
980 43 91.5 747 4 US-10-167-600-459 Sequence 459, App
981 43 91.5 747 4 US-10-170-81A-459 Sequence 459, App
982 43 91.5 747 4 US-10-172-039A-459 Sequence 459, App
983 43 91.5 747 4 US-10-210-028-459 Sequence 426, App
984 43 91.5 747 4 US-10-123-913-426 Sequence 426, App
985 43 91.5 747 4 US-10-017-085A-459 Sequence 459, App
986 43 91.5 747 4 US-10-013-916A-459 Sequence 459, App
987 43 91.5 747 4 US-10-140-873-426 Sequence 426, App
988 43 91.5 747 4 US-10-140-806-426 Sequence 426, App
989 43 91.5 747 4 US-10-140-810-426 Sequence 426, App
990 43 91.5 747 4 US-10-140-863-426 Sequence 426, App
991 43 91.5 747 4 US-10-141-699-426 Sequence 426, App
992 43 91.5 747 4 US-10-141-703-426 Sequence 426, App
993 43 91.5 747 4 US-10-141-706-426 Sequence 426, App
994 43 91.5 747 4 US-10-141-757-426 Sequence 426, App
995 43 91.5 747 4 US-10-141-762-426 Sequence 426, App
996 43 91.5 747 4 US-10-142-428-426 Sequence 426, App
997 43 91.5 747 4 US-10-142-429-426 Sequence 426, App
998 43 91.5 747 4 US-10-142-884-426 Sequence 426, App
999 43 91.5 747 4 US-10-143-027-426 Sequence 426, App
1000 43 91.5 747 4 US-10-143-115-426 Sequence 426, App
```

ALIGNMENTS

```
RESULT 1
US-10-304-287-4
; Sequence 4, Application US/10304287
; Publication No. US2003008323A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; APPLICANT: Kwon, Myung
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304,287
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: US 60/333,866
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-304-287-4
```

```
Query Match          100.0%; Score 47; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WCGPCK 6
        |||||
Db      1 WCGPCK 6
```

```
RESULT 2
US-10-660-118A-3
; Sequence 3, Application US/10660118A
; Publication No. US2004013160A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
; FILE REFERENCE: 2879-98
; CURRENT APPLICATION NUMBER: US/10/660,118A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
```

```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-10-660-118A-3
```

```
Query Match          100.0%; Score 47; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WCGPCK 6
        |||||
Db      1 WCGPCK 6
```

```
RESULT 3
US-10-735-577-4
; Sequence 4, Application US/10735577
; Publication No. US20040142897A1
; GENERAL INFORMATION:
; APPLICANT: Waisman, David M.
; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastasis
; FILE REFERENCE: ME03-009
; CURRENT APPLICATION NUMBER: US/10/735,577
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: US 60/433,140
; PRIOR FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Microsoft Word
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: mammalian
US-10-735-577-4
```

```
Query Match          100.0%; Score 47; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 WCGPCK 6
        |||||
Db      1 WCGPCK 6
```

```
RESULT 4
US-09-801-260-4
; Sequence 4, Application US/09801260
; Patent No. US20020034801A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: 22105, A NOVEL HUMAN THIOREDOXIN FAMILY
; FILE REFERENCE: 10448-022001
; CURRENT APPLICATION NUMBER: US/09/801,260
; CURRENT FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 60/187,447
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-260-4
```

```
Query Match          100.0%; Score 47; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 7.1;
```

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

Db 20 WCGPCK 25

RESULT 5

US-10-145-586-43

/ Sequence 43, Application US/10145586

/ Publication No. US20030138890A1

/ GENERAL INFORMATION:

/ APPLICANT: Alexandra Glucksmann, Maria

/ APPLICANT: Silos-Santiago, Imaculada

/ APPLICANT: M. Galvin, Katherine

/ APPLICANT: Weich, Nadine

/ APPLICANT: Curtis, Rory A.J.

/ APPLICANT: Bandaru, Rajasekhar

/ APPLICANT: Kapeller-Libermann, Rosana

/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,

/ TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LEUCINE-RICH

/ TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER

/ FILE REFERENCE: 10448-188001

/ CURRENT APPLICATION NUMBER: US/10/145,586

/ CURRENT FILING DATE: 2002-05-14

/ Prior Application removed - See File Wrapper or Palm

/ NUMBER OF SEQ ID NOS: 95

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 43

/ LENGTH: 52

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: consensus sequence

US-10-145-586-43

Query Match 100.0%; Score 47; DB 4; Length 52;

Best Local Similarity 100.0%; Pred. No. 7.1;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

Db 20 WCGPCK 25

RESULT 6

US-10-425-115-351019

/ Sequence 351019, Application US/10425115

/ Publication No. US20040214272A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J.

/ APPLICANT: Kovalic, David K.

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants

/ FILE REFERENCE: 38-21(53222)B

/ CURRENT APPLICATION NUMBER: US/10/425,115

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 369326

/ SEQ ID NO 351019

/ LENGTH: 82

/ TYPE: PRT

/ ORGANISM: Zea mays

/ FEATURE:

/ OTHER INFORMATION: Clone ID: MRT4577_83299C.1.pep

US-10-425-115-351019

Query Match 100.0%; Score 47; DB 4; Length 82;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 5 WCGPCK 10
|||||

RESULT 7

US-10-408-765A-312

/ Sequence 312, Application US/10408765A

/ Publication No. US20040101874A1

/ GENERAL INFORMATION:

/ APPLICANT: Ghosh, Soumitra S.

/ APPLICANT: Fahy, Bojn D.

/ APPLICANT: Zhang, Bing

/ APPLICANT: Gibson, Bradford W.

/ APPLICANT: Taylor, Steven W.

/ APPLICANT: Glenn, Gary M.

/ APPLICANT: Warnock, Dale E.

/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

/ TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

/ FILE REFERENCE: 660088.465

/ CURRENT APPLICATION NUMBER: US/10/408,765A

/ CURRENT FILING DATE: 2003-04-04

/ NUMBER OF SEQ ID NOS: 3077

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 312

/ LENGTH: 84

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-408-765A-312

Query Match 100.0%; Score 47; DB 4; Length 84;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

Db 30 WCGPCK 35

RESULT 8

US-10-424-599-280571

/ Sequence 280571, Application US/10424599

/ Publication No. US20040031072A1

/ GENERAL INFORMATION:

/ APPLICANT: La Rosa, Thomas J

/ APPLICANT: Kovalic, David K

/ APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

/ FILE REFERENCE: 38-21(53223)B

/ CURRENT APPLICATION NUMBER: US/10/424,599

/ CURRENT FILING DATE: 2003-04-28

/ NUMBER OF SEQ ID NOS: 285684

/ SEQ ID NO 280571

/ LENGTH: 90

/ TYPE: PRT

/ ORGANISM: Glycine max

/ FEATURE:

/ NAME/KEY: unsure

/ LOCATION: (1)..(90)

/ OTHER INFORMATION: unsure at all Xaa locations

/ FEATURE:

/ OTHER INFORMATION: Clone ID: PAT_MRT3847_95379C.1.pep

US-10-424-599-280571

Query Match 100.0%; Score 47; DB 4; Length 90;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||

Db 13 WCGPCK 18

```
RESULT 9
US-10-032-201B-143
; Sequence 143, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Thiocapsa roseopersicina
US-10-032-201B-143
```

```
Query Match          100.0%; Score 47; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       32 WCGPCK 37
```

```
RESULT 10
US-10-032-201B-102
; Sequence 102, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia muridarum
US-10-032-201B-102
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 11
US-10-032-201B-104
```

```
; Sequence 104, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Paiticaci
US-10-032-201B-104
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 12
US-10-032-201B-105
; Sequence 105, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-10-032-201B-105
```

```
Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       27 WCGPCK 32
```

```
RESULT 13
US-10-032-201B-126
; Sequence 126, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma genitalium
US-10-032-201B-126
```

```

Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      29 WCGPCK 34
```

```

RESULT 14
US-10-032-201B-128
; Sequence 128, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Mycoplasma pneumoniae
US-10-032-201B-128
```

```

Query Match          100.0%; Score 47; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      29 WCGPCK 34
```

```

RESULT 15
US-10-501-282-3126
; Sequence 3126, Application US/10501282
; Publication No. US20050203280A1
; GENERAL INFORMATION:
; APPLICANT: MCWITCHEL, JOHN CALHOUN
; APPLICANT: ZAGORSKY, ROBERT JOHN
; APPLICANT: RUSSELL, DAVID PARRISH
```

```

; APPLICANT: FLETCHER, LEAH DIANE
; TITLE OF INVENTION: ALLOTOCOCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
; FILE REFERENCE: AM100780 L2
; CURRENT APPLICATION NUMBER: US/10/501,282
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/333,777
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/426,742
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/36123
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 6653
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3126
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Alloiococcus otitidis
US-10-501-282-3126
```

```

Query Match          100.0%; Score 47; DB 5; Length 102;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      27 WCGPCK 32
```

```

RESULT 16
US-10-032-201B-96
; Sequence 96, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-032-201B-96
```

```

Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      27 WCGPCK 32
```

```

RESULT 17
US-10-032-585-7785
; Sequence 7785, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jitang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
```

```
/ TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
/ FILE REFERENCE: 10182-005-999
/ CURRENT APPLICATION NUMBER: US/10/032,585
/ CURRENT FILING DATE: 2001-12-20
/ NUMBER OF SEQ ID NOS: 8000
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7785
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-10-032-585-7785
```

```
Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```
RESULT 18
US-10-660-118a-7
/ Sequence 7, Application US/10660118A
/ Publication No. US20040131606A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
/ FILE REFERENCE: 2879-98
/ CURRENT APPLICATION NUMBER: US/10/660,118A
/ CURRENT FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 7
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-660-118a-7
```

```
Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```
RESULT 19
US-10-451-467a-270
/ Sequence 270, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 732
```

```
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 270
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-451-467a-270
```

```
Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```
RESULT 20
US-10-451-467a-450
/ Sequence 450, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
/ NUMBER OF SEQ ID NOS: 732
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 450
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-10-451-467a-450
```

```
Query Match          100.0%; Score 47; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       29 WCGPCK 34
```

```
RESULT 21
US-10-451-467a-614
/ Sequence 614, Application US/10451467A
/ Publication No. US20040161840A1
/ GENERAL INFORMATION:
/ APPLICANT: CONTRERAS, ROLAND HENRI
/ APPLICANT: EBERHARDT, INES
/ APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
/ APPLICANT: REEKMAN, RIEKA JOSEPHINA
/ TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
/ FILE REFERENCE: JAB-1667
/ CURRENT APPLICATION NUMBER: US/10/451,467A
/ CURRENT FILING DATE: 2003-06-19
/ PRIOR APPLICATION NUMBER: EP 00870318.3
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: EP 01870002.1
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: EP 01870003.9
/ PRIOR FILING DATE: 2001-01-09
```


NUMBER OF SEQ ID NOS: 732
SOFTWARE: PatentIn version 3.1
SEQ ID NO 614
LENGTH: 103
TYPE: PRT
ORGANISM: Candida albicans
US-10-451-467A-614

Query Match
Best Local Similarity 100.0%; Score 47; DB 4; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 22
US-09-954-342-62
Sequence 62, Application US/09954342
Publication No. US20030170838A1
GENERAL INFORMATION:
APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTER, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: VERNET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: GORMAN, LINDA
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: SHENOY, SURESH
APPLICANT: PADIGARU, MURALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: MILLET, ISABELLE
APPLICANT: PEYMAN, JOHN
APPLICANT: STONE, DAVID
APPLICANT: GUNTHER, ERIK
APPLICANT: ELLERMAN, KAREN
APPLICANT: LI, LI
APPLICANT: RASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,382
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/240,498
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/260,284
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/260,973
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/264,794
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 60/238,398
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/232,675
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/274,862
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/233,801
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,676
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/233,402
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/233,521
PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/233,522
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,679
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 104
TYPE: PRT
ORGANISM: Ovis aries
US-09-954-342-62

Query Match
Best Local Similarity 100.0%; Score 47; DB 3; Length 104;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 23
US-09-954-342-63
Sequence 63, Application US/09954342
Publication No. US20030170838A1
GENERAL INFORMATION:
APPLICANT: MISHRA, VISHNU S.
APPLICANT: SPYTER, KIMBERLY ANN
APPLICANT: TAUPIER, RAYMOND J.
APPLICANT: VERNET, CORINE A.
APPLICANT: COLMAN, STEVEN D.
APPLICANT: GORMAN, LINDA
APPLICANT: TCHERNEV, VELIZAR T.
APPLICANT: MALYANKAR, URIEL M.
APPLICANT: SHENOY, SURESH
APPLICANT: PADIGARU, MURALIDHARA
APPLICANT: GERLACH, VALERIE L.
APPLICANT: MACDOUGALL, JOHN R.
APPLICANT: SMITHSON, GLENNDA
APPLICANT: MILLET, ISABELLE
APPLICANT: PEYMAN, JOHN
APPLICANT: STONE, DAVID
APPLICANT: GUNTHER, ERIK
APPLICANT: ELLERMAN, KAREN
APPLICANT: LI, LI
APPLICANT: RASTELLI, LUCA
APPLICANT: ZERHUSEN, BRYAN
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
FILE REFERENCE: 21402-114
CURRENT APPLICATION NUMBER: US/09/954,342
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/233,382
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 60/240,498
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: 60/260,284
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/232,675
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/264,794
PRIOR FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/238,398
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/232,675
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/274,862
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/233,801
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 60/232,676
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 60/233,960
PRIOR FILING DATE: 2000-09-20

;; PRIOR APPLICATION NUMBER: 60/233,402
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/233,521
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/233,522
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/232,679
;; PRIOR FILING DATE: 2000-09-15
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 63
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Bos taurus
US-09-954-342-63

Query Match 100.0%; Score 47; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 24
US-09-954-342-64
;; Sequence 64, Application US/09954342
;; Publication No. US20030170838A1
;; GENERAL INFORMATION:
;; APPLICANT: MISHRA, VISHNU S.
;; APPLICANT: SPYTER, KIMBERLY ANN
;; APPLICANT: TAUPIER, RAYMOND J.
;; APPLICANT: VERNET, CORINE A.
;; APPLICANT: COLMAN, STEVEN D.
;; APPLICANT: GORMAN, LINDA
;; APPLICANT: TCHERNEY, VELIZAR T.
;; APPLICANT: MALYANKAR, URIEL M.
;; APPLICANT: SHENOY, SURESH
;; APPLICANT: PADIGARU, MURALIDHARA
;; APPLICANT: GERLACH, VALERIE L.
;; APPLICANT: MACDOUGALL, JOHN R.
;; APPLICANT: SMITHSON, GLENDA
;; APPLICANT: MILLER, ISABELLE
;; APPLICANT: PEYMAN, JOHN
;; APPLICANT: STONE, DAVID
;; APPLICANT: GUNTER, ERIK
;; APPLICANT: ELLERMAN, KAREN
;; APPLICANT: LI, LI
;; APPLICANT: RASTELLI, LUCA
;; APPLICANT: ZERHUSEN, BRYAN
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;; FILE REFERENCE: 21402-114
;; CURRENT APPLICATION NUMBER: US/09/954,342
;; PRIOR FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: 60/233,382
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/240,498
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/260,284
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: 60/260,973
;; PRIOR FILING DATE: 2001-01-11
;; PRIOR APPLICATION NUMBER: 60/264,794
;; PRIOR FILING DATE: 2001-01-29
;; PRIOR APPLICATION NUMBER: 60/238,398
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/232,675
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/274,862
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 60/233,801
;; PRIOR FILING DATE: 2000-09-19

;; PRIOR APPLICATION NUMBER: 60/232,676
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/233,960
;; PRIOR FILING DATE: 2000-09-20
;; PRIOR APPLICATION NUMBER: 60/233,402
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/233,521
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/233,522
;; PRIOR FILING DATE: 2000-09-19
;; PRIOR APPLICATION NUMBER: 60/232,679
;; PRIOR FILING DATE: 2000-09-15
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 64
;; LENGTH: 104
;; TYPE: PRT
;; ORGANISM: Macaca mulatta
US-09-954-342-64

Query Match 100.0%; Score 47; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 30 WCGPCK 35

RESULT 25
US-09-954-342-65
;; Sequence 65, Application US/09954342
;; Publication No. US20030170838A1
;; GENERAL INFORMATION:
;; APPLICANT: MISHRA, VISHNU S.
;; APPLICANT: SPYTER, KIMBERLY ANN
;; APPLICANT: TAUPIER, RAYMOND J.
;; APPLICANT: VERNET, CORINE A.
;; APPLICANT: COLMAN, STEVEN D.
;; APPLICANT: GORMAN, LINDA
;; APPLICANT: TCHERNEY, VELIZAR T.
;; APPLICANT: MALYANKAR, URIEL M.
;; APPLICANT: SHENOY, SURESH
;; APPLICANT: PADIGARU, MURALIDHARA
;; APPLICANT: GERLACH, VALERIE L.
;; APPLICANT: MACDOUGALL, JOHN R.
;; APPLICANT: SMITHSON, GLENDA
;; APPLICANT: MILLER, ISABELLE
;; APPLICANT: PEYMAN, JOHN
;; APPLICANT: STONE, DAVID
;; APPLICANT: GUNTER, ERIK
;; APPLICANT: ELLERMAN, KAREN
;; APPLICANT: LI, LI
;; APPLICANT: RASTELLI, LUCA
;; APPLICANT: ZERHUSEN, BRYAN
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
;; FILE REFERENCE: 21402-114
;; CURRENT APPLICATION NUMBER: US/09/954,342
;; PRIOR FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: 60/233,382
;; PRIOR FILING DATE: 2000-09-18
;; PRIOR APPLICATION NUMBER: 60/240,498
;; PRIOR FILING DATE: 2000-10-13
;; PRIOR APPLICATION NUMBER: 60/260,284
;; PRIOR FILING DATE: 2001-01-08
;; PRIOR APPLICATION NUMBER: 60/260,973
;; PRIOR FILING DATE: 2001-01-11
;; PRIOR APPLICATION NUMBER: 60/264,794
;; PRIOR FILING DATE: 2001-01-29
;; PRIOR APPLICATION NUMBER: 60/238,398
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 60/232,675
;; PRIOR FILING DATE: 2000-09-15

```
/ PRIOR APPLICATION NUMBER: 60/274,862
/ PRIOR FILING DATE: 2001-03-09
/ PRIOR APPLICATION NUMBER: 60/233,801
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/232,676
/ PRIOR FILING DATE: 2000-09-15
/ PRIOR APPLICATION NUMBER: 60/233,960
/ PRIOR FILING DATE: 2000-09-20
/ PRIOR APPLICATION NUMBER: 60/233,402
/ PRIOR FILING DATE: 2000-09-18
/ PRIOR APPLICATION NUMBER: 60/233,521
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/233,522
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 60/232,679
/ PRIOR FILING DATE: 2000-09-15
/ NUMBER OF SEQ ID NOS: 104
/ SOFTWARE: PatentIn Ver. 2.1
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-09-954-342-65
```

```
Query Match          100.0%; Score 47; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      30 WCGPCK 35
```

```
RESULT 26
US-10-032-201B-146
/ Sequence 146, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gtjs
/ APPLICANT: Deckers, Harm
/ APPLICANT: Helfetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 146
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Bos taurus
US-10-032-201B-146
```

```
Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      30 WCGPCK 35
```

```
RESULT 27
US-10-032-201B-150
/ Sequence 150, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Van Rooijen, Gtjs
/ APPLICANT: Deckers, Harm
/ APPLICANT: Helfetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 150
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Gallus gallus
US-10-032-201B-150
```

```
Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      30 WCGPCK 35
```

```
RESULT 28
US-10-032-201B-152
/ Sequence 152, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gtjs
/ APPLICANT: Deckers, Harm
/ APPLICANT: Helfetz, Peter Bernard
/ APPLICANT: Briggs, Steven
/ APPLICANT: Dalma, Bipin Kumar
/ APPLICANT: Del Val, Greg
/ APPLICANT: Zaplachinski, Steve
/ APPLICANT: Moloney, Maurice
/ TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
/ FILE REFERENCE: 38814 351B
/ CURRENT APPLICATION NUMBER: US/10/032,201B
/ CURRENT FILING DATE: 2001-12-19
/ NUMBER OF SEQ ID NOS: 313
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 152
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-10-032-201B-152
```

```
Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db      30 WCGPCK 35
```

```
RESULT 29
US-10-032-201B-154
/ Sequence 154, Application US/10032201B
/ Publication No. US20030167524A1
/ GENERAL INFORMATION:
/ APPLICANT: Van Rooijen, Gtjs
/ APPLICANT: Deckers, Harm
/ APPLICANT: Helfetz, Peter Bernard
```

```

; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-032-201B-154

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 30 WCGPCK 35

```

```

RESULT 30
US-10-032-201B-155
; Sequence 155, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-032-201B-155

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 30 WCGPCK 35

```

```

RESULT 31
US-10-032-201B-158
; Sequence 158, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg

```

```

; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-032-201B-158

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 30 WCGPCK 35

```

```

RESULT 32
US-10-032-201B-159
; Sequence 159, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-032-201B-159

```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 30 WCGPCK 35

```

```

RESULT 33
US-10-032-201B-161
; Sequence 161, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED

```

```

; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Ovis aries
US-10-032-201B-161
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
DB      30 WCGPCK 35
```

```

RESULT 34
US-10-032-201B-276
; Sequence 276, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggas, Steven
; APPLICANT: Dalmaia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-10-032-201B-276
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
DB      28 WCGPCK 33
```

```

RESULT 35
US-10-424-599-282588
; Sequence 282588, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285664
; SEQ ID NO 282588
; LENGTH: 104
```

```

; TYPE: PRF
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_97199C.1.pep
US-10-424-599-282588
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
DB      54 WCGPCK 59
```

```

RESULT 36
US-10-451-467A-188
; Sequence 188, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEMANS, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 104
; TYPE: PRF
; ORGANISM: Saccharomyces cerevisiae
US-10-451-467A-188
```

```

Query Match          100.0%; Score 47; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
DB      30 WCGPCK 35
```

```

RESULT 37
US-09-954-342-61
; Sequence 61, Application US/09954342
; Publication No. US20030170838A1
; GENERAL INFORMATION:
; APPLICANT: MISHRA, VISHNU S.
; APPLICANT: SPYTER, KIMBERLY ANN
; APPLICANT: TAUPIER, RAYMOND J.
; APPLICANT: VERNET, CORINE A.
; APPLICANT: COLMAN, STEVEN D.
; APPLICANT: GORMAN, LINDA
; APPLICANT: TCHERNIEV, VELIZAR T.
; APPLICANT: MALYANKAR, URIEL M.
; APPLICANT: SHENOY, SURESH
; APPLICANT: PADIGARU, MURALIDHARA
; APPLICANT: GERLACH, VALERIE L.
; APPLICANT: MACDONALD, JOHN R.
; APPLICANT: SMITHSON, GLENDA
; APPLICANT: WILLET, ISABELLE
; APPLICANT: PEYMAN, JOHN
; APPLICANT: STONE, DAVID
```

```
; APPLICANT: GUNTHER, ERIK
; APPLICANT: ELLERMAN, KAREN
; APPLICANT: LI, LI
; APPLICANT: RASTELLI, LUCA
; APPLICANT: ZERHUSEN, BRYAN
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY
; FILE REFERENCE: 21402-114
; CURRENT APPLICATION NUMBER: US/09/954,342
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/233,382
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/240,498
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/260,284
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/260,973
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/264,794
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/238,398
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/232,675
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/274,862
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/233,801
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,676
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/233,960
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 60/233,402
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/233,521
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/233,522
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 60/232,679
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Equus caballus
US-09-954-342-61

Query Match          100.0%; Score 47; DB 3; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 31 WCGPCK 36
```

RESULT 38
US-10-171-311-226

```
; Sequence 226, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamathkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Ganavarampu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
```

```
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 226
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-226

Query Match          100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 31 WCGPCK 36
```

RESULT 39
US-10-316-253-291

```
; Sequence 291, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Peng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865M
; CURRENT APPLICATION NUMBER: US/10/316,253
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 291
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-291
```

```
Query Match          100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 WCGPCK 6
Db 31 WCGPCK 36
```

RESULT 40
US-10-032-201B-47

```
; Sequence 47, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Heileitz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalwala, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: COMPOSITIONS
```

FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 47
LENGTH: 105
TYPE: PRT
ORGANISM: Homo Sapien
US-10-032-201B-47

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 41

US-10-032-201B-106
Sequence 106, Application US/10032201B
Publication No. US20030167524A1
GENERAL INFORMATION:
APPLICANT: Van Rooijen, G.J.s
APPLICANT: Deckers, Harm
APPLICANT: Heifetz, Peter Bernard
APPLICANT: Briggs, Steven
APPLICANT: Dalmla, Bipin Kumar
APPLICANT: Del Val, Greg
APPLICANT: Zaplachinski, Steve
APPLICANT: Moloney, Maurice
TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 38814 351B
CURRENT APPLICATION NUMBER: US/10/032,201B
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 313
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 106
LENGTH: 105
TYPE: PRT
ORGANISM: Corynebacterium nephridii
US-10-032-201B-106

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 29 WCGPCK 34

RESULT 42

US-10-424-599-237784
Sequence 237784, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237784
LENGTH: 105
TYPE: PRT

ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(105)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56744C.1.dep
US-10-424-599-237784

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 57 WCGPCK 62

RESULT 43

US-10-351-891-127
Sequence 127, Application US/10351891
Publication No. US20040048311A1
GENERAL INFORMATION:
APPLICANT: PAUL D. KASSNER
APPLICANT: DANA ADLT-RICHER
TITLE OF INVENTION: USE OF COLLECTIONS OF BINDING SITES FOR SAMPLE PROFILING AND OTH
TITLE OF INVENTION: APPLICATIONS
FILE REFERENCE: 25885-1753
CURRENT APPLICATION NUMBER: US/10/351,891
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: US 60/352,011
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 127
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank BAA04881
DATABASE ENTRY DATE: 2002-12-25
US-10-351-891-127

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 44

US-10-408-765A-2019
Sequence 2019, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Bojn D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2019
LENGTH: 105

TYPE: PRT
ORGANISM: Homo sapiens
US-10-408-765A-2019

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 45
US-10-660-118A-8
Sequence 8, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Gallus gallus
US-10-660-118A-8

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 46
US-10-660-118A-9
Sequence 9, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
US-10-660-118A-9

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 47
US-10-660-118A-10
Sequence 10, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 105
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-660-118A-10

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 48
US-10-660-118A-11
Sequence 11, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 105
TYPE: PRT
ORGANISM: Bos taurus
US-10-660-118A-11

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 31 WCGPCK 36

RESULT 49
US-10-660-118A-12
Sequence 12, Application US/10660118A
Publication No. US20040131606A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
TITLE OF INVENTION: Product and Process for Liquefaction of Mucus or Sputum
FILE REFERENCE: 2879-98
CURRENT APPLICATION NUMBER: US/10/660,118A

;; CURRENT FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/409,960
;; PRIOR FILING DATE: 2002-09-10
;; PRIOR APPLICATION NUMBER: 60/462,082
;; PRIOR FILING DATE: 2003-04-11
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-660-118a-12

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
Db 31 WCGPCK 36

RESULT 50
US-10-451-467a-684
; Sequence 684, Application US/10451467a
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RIEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467a
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 684
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-451-467a-684

Query Match 100.0%; Score 47; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
Db 31 WCGPCK 36

RESULT 51
US-10-699-113-32
; Sequence 32, Application US/106599113
; Publication No. US200402411748A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Kumble, Krishanand
; APPLICANT: Schultz, Rainer
; APPLICANT: Schultz, Kenneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
; FILE REFERENCE: 25885-1755
; CURRENT APPLICATION NUMBER: US/10/699,113
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/446,687

;; PRIOR FILING DATE: 2003-02-10
;; NUMBER OF SEQ ID NOS: 948
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 32
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank BAA04881
; DATABASE ENTRY DATE: 2002-12-25
US-10-699-113-32

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
Db 31 WCGPCK 36

RESULT 52
US-10-970-370-2
; Sequence 2, Application US/10970370
; Publication No. US20050208037A1
; GENERAL INFORMATION:
; APPLICANT: DASHNAMOORTHY, RAVI
; APPLICANT: DAS, KUMUDA C.
; TITLE OF INVENTION: THIORDOXIN INCREASES REDOX-CYCLING OF ANTICANCER
; TITLE OF INVENTION: AGENTS THEREBY SENSITIZES CANCER CELLS TO APOPTOSIS
; FILE REFERENCE: UTSN:025US
; CURRENT APPLICATION NUMBER: US/10/970,370
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/513,134
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-970-370-2

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
 |||||
Db 31 WCGPCK 36

RESULT 53
US-10-970-370-6
; Sequence 6, Application US/10970370
; Publication No. US20050208037A1
; GENERAL INFORMATION:
; APPLICANT: DASHNAMOORTHY, RAVI
; APPLICANT: DAS, KUMUDA C.
; TITLE OF INVENTION: THIORDOXIN INCREASES REDOX-CYCLING OF ANTICANCER
; TITLE OF INVENTION: AGENTS THEREBY SENSITIZES CANCER CELLS TO APOPTOSIS
; FILE REFERENCE: UTSN:025US
; CURRENT APPLICATION NUMBER: US/10/970,370
; CURRENT FILING DATE: 2004-10-21
; PRIOR APPLICATION NUMBER: 60/513,134
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-10-970-370-6

Query Match 100.0%; Score 47; DB 5; Length 105;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 54

US-10-032-201B-123
; Sequence 123, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 123
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-032-201B-123

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 29 WCGPCK 34

RESULT 55

US-10-032-201B-132
; Sequence 132, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Penicillium chrysogenum
US-10-032-201B-132

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 56

US-10-032-201B-137
; Sequence 137, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Streptomyces aureofaciens
US-10-032-201B-137

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 30 WCGPCK 35

RESULT 57

US-10-032-201B-176
; Sequence 176, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
; APPLICANT: Helfetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalma, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Manduca sexta
US-10-032-201B-176

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6

Db 31 WCGPCK 36

RESULT 58

US-10-335-977-6752
; Sequence 6752, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6752:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1..106
; SEQUENCE DESCRIPTION: SEQ ID NO: 6752:
US-10-335-977-6752

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 59

US-10-628-391-1
; Sequence 1, Application US/10628391
; Publication No. US20040146526A1
; GENERAL INFORMATION:
; APPLICANT: WINDLE, Henry J.
; APPLICANT: O'TOOLE, Dermot
; APPLICANT: KELLEHER, Dermot
; APPLICANT: ABDEL-LATIF, Mohamed M.
; TITLE OF INVENTION: INHIBITION OF NF-kappaB ACTIVATION

; FILE REFERENCE: P69048US0
; CURRENT APPLICATION NUMBER: US/10/628,391
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/IE02/00011
; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 106
; TYPE: PRT
; ORGANISM: H. pylori
US-10-628-391-1

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 60
US-10-425-115-365910
; Sequence 365910, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: LA ROSA, Thomas J.
; APPLICANT: KOVALIC, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 365910
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_96874C.1.pep
US-10-425-115-365910

Query Match 100.0%; Score 47; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 61
US-11-097-143-7479
; Sequence 7479, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28

```
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7479
; LENGTH: 106
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-7479
```

```
Query Match          100.0%; Score 47; DB 6; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 62

```
US-10-032-201B-109
; Sequence 109, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmla, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Chromatium vinosum
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 17, 38, 42, 55, 58, 60, 72, 107
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-032-201B-109
```

```
Query Match          100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 63

```
US-10-032-201B-121
; Sequence 121, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Deckers, Harm
```

```
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmla, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-10-032-201B-121
```

```
Query Match          100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       31 WCGPCK 36
```

RESULT 64

```
US-10-032-201B-151
; Sequence 151, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gijb
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmla, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-032-201B-151
```

```
Query Match          100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
        |||||
Db       30 WCGPCK 35
```

RESULT 65

```
US-10-335-977-6753
; Sequence 6753, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 28 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: CD-ROM ISO9660
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: Windows NT 4.0
;; SOFTWARE: UNIX
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/335,977
;; FILING DATE: 30-Dec-2002
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/993,002
;; FILING DATE: 17-DEC-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mandragouras, Amy E.
;; REGISTRATION NUMBER: 36,207
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 6753:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHEetical: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Helicobacter pylori
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (B) LOCATION 1...107
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6753:
US-10-335-977-6753
;
Query Match 100.0%; Score 47; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 WCGPCK 6
|||
Db 30 WCGPCK 35
;
RESULT 66
US-11-097-143-8226
;; Sequence 8226, Application US/11097143
;; Publication No. US2005020858A1
;; GENERAL INFORMATION:
;; APPLICANT: Venter, J. Craig
;; APPLICANT: et al.
;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
;; FILE REFERENCE: CL000728
;; CURRENT APPLICATION NUMBER: US/11/097,143
;; CURRENT FILING DATE: 2005-04-04
;; PRIOR APPLICATION NUMBER: 60/157,832
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: 60/160,191
;; PRIOR FILING DATE: 1999-10-19
;; PRIOR APPLICATION NUMBER: 60/161,932
;; PRIOR FILING DATE: 1999-10-28
;; PRIOR APPLICATION NUMBER: 60/164,769
;; PRIOR FILING DATE: 1999-11-12
;; PRIOR APPLICATION NUMBER: 60/173,383
;; PRIOR FILING DATE: 1999-12-28
;; PRIOR APPLICATION NUMBER: 60/175,693
;

;; PRIOR FILING DATE: 2000-01-12
;; PRIOR APPLICATION NUMBER: 60/184,831
;; PRIOR FILING DATE: 2000-02-24
;; PRIOR APPLICATION NUMBER: 60/191,637
;; PRIOR FILING DATE: 2000-03-23
;; NUMBER OF SEQ ID NOS: 43008
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 8226
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: DROSOPHILA
US-11-097-143-8226
;
Query Match 100.0%; Score 47; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 WCGPCK 6
|||
Db 30 WCGPCK 35
;
RESULT 67
US-09-812-777-16
;; Sequence 16, Application US/09812777
;; Patent No. US20020115827A1
;; GENERAL INFORMATION:
;; APPLICANT: KIM, KEY-SUN
;; APPLICANT: LEE, DUCK YEON
;; TITLE OF INVENTION: A METHOD OF PROTEIN STABILIZATION
;; FILE REFERENCE: 05823, 0195-0000
;; CURRENT APPLICATION NUMBER: US/09/812,777
;; CURRENT FILING DATE: 2001-03-18
;; PRIOR APPLICATION NUMBER: KR 00-63596
;; PRIOR FILING DATE: 2000-10-27
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 16
;; LENGTH: 108
;; TYPE: PRT
;; ORGANISM: Escherichia coli
US-09-812-777-16
;
Query Match 100.0%; Score 47; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 WCGPCK 6
|||
Db 31 WCGPCK 36
;
RESULT 68
US-10-032-201B-117
;; Sequence 117, Application US/10032201B
;; Publication No. US20030167524A1
;; GENERAL INFORMATION:
;; APPLICANT: Van Rooijen, Gij's
;; APPLICANT: Deckers, Harm
;; APPLICANT: Helfetz, Peter Bernard
;; APPLICANT: Briggs, Steven
;; APPLICANT: Dalmia, Bipin Kumar
;; APPLICANT: Del Val, Greg
;; APPLICANT: Zapiachinski, Steve
;; APPLICANT: Moloney, Maurice
;; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
;; FILE REFERENCE: 38814 351B
;; CURRENT APPLICATION NUMBER: US/10/032,201B
;; CURRENT FILING DATE: 2001-12-19
;; NUMBER OF SEQ ID NOS: 313
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 117
;

; LENGTH: 108
; TYPE: PRT
; ORGANISM: E coli, salmonella typhimurium
US-10-032-201B-117

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 69
US-10-032-201B-133

; Sequence 133, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-032-201B-133

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

RESULT 70
US-10-032-201B-142

; Sequence 142, Application US/10032201B
; Publication No. US20030167524A1
; GENERAL INFORMATION:
; APPLICANT: Van Rooijen, Gij's
; APPLICANT: Deckers, Harm
; APPLICANT: Heifetz, Peter Bernard
; APPLICANT: Briggs, Steven
; APPLICANT: Dalmia, Bipin Kumar
; APPLICANT: Del Val, Greg
; APPLICANT: Zaplachinski, Steve
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF MULTIMERIC PROTEINS, AND RELATED
; FILE REFERENCE: 38814 351B
; CURRENT APPLICATION NUMBER: US/10/032,201B
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Thioacillus ferrooxidans

US-10-032-201B-142

Query Match 100.0%; Score 47; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
Db 32 WCGPCK 37

Search completed: February 23, 2006, 00:47:55
Job time : 125.5 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 00:44:02 ; Search time 11.5 Seconds
(without alignments)
7.767 Million cell updates/sec

Title: US-10-660-118A-3

Perfect score: 47

Sequence: 1 WCGPCK 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Published Applications AA.New.*

1: /cgn2_6/protdata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/protdata/2/pubppaa/US06_NEW_PUB.pep.*
3: /cgn2_6/protdata/2/pubppaa/US07_NEW_PUB.pep.*
4: /cgn2_6/protdata/2/pubppaa/US09_NEW_PUB.pep.*
5: /cgn2_6/protdata/2/pubppaa/US10_NEW_PUB.pep.*
6: /cgn2_6/protdata/2/pubppaa/US11_NEW_PUB.pep.*
7: /cgn2_6/protdata/2/pubppaa/US60_NEW_PUB.pep.*
8: /cgn2_6/protdata/2/pubppaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	6	US-11-090-916-3	Sequence 3, Appl1
2	47	100.0	75	US-11-131-744-2	Sequence 2, Appl1
3	47	100.0	91	US-11-131-744-1	Sequence 1, Appl1
4	47	100.0	103	US-11-074-176-286	Sequence 286, App
5	47	100.0	103	US-11-090-916-7	Sequence 7, Appl1
6	47	100.0	105	US-10-821-234-1371	Sequence 1371, Ap
7	47	100.0	105	US-11-090-916-8	Sequence 8, Appl1
8	47	100.0	105	US-11-090-916-9	Sequence 9, Appl1
9	47	100.0	105	US-11-090-916-10	Sequence 10, Appl
10	47	100.0	105	US-11-090-916-11	Sequence 11, Appl
11	47	100.0	105	US-11-090-916-12	Sequence 12, Appl
12	47	100.0	105	US-11-106-796-13	Sequence 13, Appl
13	47	100.0	105	US-11-144-301A-9	Sequence 10, Appl
14	47	100.0	105	US-11-144-301A-10	Sequence 10, Appl
15	47	100.0	105	US-11-032-773-943	Sequence 943, App
16	47	100.0	109	US-11-090-916-4	Sequence 4, Appl
17	47	100.0	127	US-11-106-796-11	Sequence 11, Appl
18	47	100.0	127	US-11-106-796-12	Sequence 12, Appl
19	47	100.0	129	US-10-467-657-4354	Sequence 4354, Ap
20	47	100.0	177	US-11-131-744-3	Sequence 3, Appl1
21	47	100.0	273	US-11-131-744-6	Sequence 6, Appl1
22	47	100.0	440	US-11-131-744-7	Sequence 7, Appl1
23	44	93.6	103	US-11-090-916-6	Sequence 6, Appl1
24	44	93.6	104	US-11-090-916-5	Sequence 5, Appl1
25	44	93.6	107	US-11-098-686-10612	Sequence 10612, A

99	33	70.2	1218	7	US-11-078-735-20	Sequence 20, Appl	172	31	66.0	232	7	US-11-211-724-5	Sequence 5, Appl1
100	33	70.2	1218	7	US-11-050-346-65	Sequence 65, Appl	173	31	66.0	232	7	US-11-233-119-7	Sequence 91, Appl1
101	33	70.2	1218	7	US-11-103-077-20	Sequence 20, Appl	174	31	66.0	232	7	US-11-075-047A-91	Sequence 9, Appl1
102	33	70.2	1218	7	US-11-072-175-155	Sequence 155, App	175	31	66.0	291	6	US-10-511-538-225	Sequence 225, App
103	33	70.2	1218	7	US-11-022-478-4	Sequence 4, Appl1	176	31	66.0	300	7	US-11-154-257-2	Sequence 2, Appl1
104	33	70.2	1503	7	US-11-087-100-6	Sequence 6, Appl1	177	31	66.0	325	5	US-09-978-360A-406	Sequence 406, App
105	33	70.2	1503	7	US-11-087-084-6	Sequence 6, Appl1	178	31	66.0	430	7	US-11-072-512-2204	Sequence 2204, Ap
106	33	70.2	1503	7	US-11-087-085-6	Sequence 6, Appl1	179	31	66.0	447	6	US-10-967-527A-14	Sequence 14, Appl1
107	33	70.2	2059	7	US-11-087-100-4	Sequence 4, Appl1	180	31	66.0	448	6	US-10-967-527A-16	Sequence 16, Appl1
108	33	70.2	2059	7	US-11-087-084-4	Sequence 4, Appl1	181	31	66.0	448	7	US-11-182-016-24	Sequence 24, Appl1
109	33	70.2	2059	7	US-11-087-085-4	Sequence 4, Appl1	182	31	66.0	509	7	US-11-124-367A-447	Sequence 447, App
110	33	70.2	2144	7	US-11-043-889-2	Sequence 2, Appl1	183	31	66.0	539	7	US-11-043-788-464	Sequence 464, App
111	32	68.1	46	7	US-11-000-463-844	Sequence 844, App	184	31	66.0	549	7	US-11-043-788-467	Sequence 467, App
112	32	68.1	51	7	US-11-172-571-29	Sequence 29, Appl	185	31	66.0	549	7	US-11-043-788-468	Sequence 468, App
113	32	68.1	76	7	US-11-172-571-28	Sequence 28, Appl	186	31	66.0	574	6	US-10-763-712A-1	Sequence 1, Appl1
114	32	68.1	282	7	US-11-186-284-85	Sequence 85, Appl	187	31	66.0	574	6	US-10-763-712A-6	Sequence 6, Appl1
115	32	68.1	371	7	US-11-186-284-16	Sequence 16, Appl	188	31	66.0	574	6	US-10-763-712A-102	Sequence 102, App
116	32	68.1	410	6	US-10-467-657-2312	Sequence 2312, Ap	189	31	66.0	612	7	US-11-098-686-10678	Sequence 10678, A
117	32	68.1	450	7	US-11-186-284-14	Sequence 14, Appl	190	31	66.0	654	6	US-10-510-947-6	Sequence 6, Appl1
118	32	68.1	502	6	US-10-966-483-23	Sequence 23, Appl	191	31	66.0	780	6	US-10-878-556A-197	Sequence 197, App
119	32	68.1	502	7	US-11-021-441-7	Sequence 7, Appl1	192	31	66.0	884	7	US-11-098-686-11426	Sequence 11426, A
120	32	68.1	563	6	US-10-966-483-25	Sequence 25, Appl	193	31	66.0	885	6	US-10-467-657-2302	Sequence 2302, Ap
121	32	68.1	563	7	US-11-021-441-9	Sequence 9, Appl1	194	31	66.0	905	7	US-11-072-512-2728	Sequence 2728, Ap
122	32	68.1	574	6	US-10-966-483-31	Sequence 31, Appl	195	31	66.0	954	6	US-10-467-962B-31	Sequence 31, Appl
123	32	68.1	574	6	US-11-021-441-15	Sequence 15, Appl	196	31	66.0	1238	7	US-11-078-735-21	Sequence 21, Appl
124	32	68.1	581	6	US-10-966-483-27	Sequence 27, Appl	197	31	66.0	1238	7	US-11-050-346-66	Sequence 66, Appl
125	32	68.1	581	6	US-10-966-483-29	Sequence 29, Appl	198	31	66.0	1238	7	US-11-103-077-21	Sequence 21, Appl
126	32	68.1	581	7	US-11-021-441-11	Sequence 11, Appl	199	31	66.0	1257	7	US-11-022-478-6	Sequence 6, Appl1
127	32	68.1	581	7	US-11-021-441-13	Sequence 13, Appl	200	30	63.8	37	6	US-10-467-657-1382	Sequence 1382, Ap
128	32	68.1	755	7	US-11-067-121-16	Sequence 6, Appl1	201	30	63.8	58	7	US-11-123-896-228	Sequence 228, App
129	32	68.1	757	7	US-11-067-121-16	Sequence 16, Appl	202	30	63.8	58	7	US-11-123-896-231	Sequence 231, App
130	32	68.1	757	7	US-11-186-284-41	Sequence 41, Appl	203	30	63.8	58	7	US-11-123-896-234	Sequence 234, App
131	32	68.1	976	6	US-10-966-483-2	Sequence 2, Appl1	204	30	63.8	86	7	US-11-123-896-227	Sequence 227, App
132	32	68.1	976	6	US-10-511-273-1	Sequence 1, Appl1	205	30	63.8	86	7	US-11-123-896-230	Sequence 230, App
133	32	68.1	976	7	US-11-233-796-2	Sequence 2, Appl1	206	30	63.8	86	7	US-11-123-896-233	Sequence 233, App
134	32	68.1	976	7	US-11-072-175-138	Sequence 138, App	207	30	63.8	134	7	US-11-188-281-13	Sequence 13, Appl
135	32	68.1	1035	6	US-10-966-483-20	Sequence 20, Appl	208	30	63.8	217	7	US-11-188-281-18	Sequence 18, Appl
136	32	68.1	1035	7	US-11-021-441-4	Sequence 4, Appl1	209	30	63.8	227	6	US-10-515-720A-2	Sequence 2, Appl1
137	32	68.1	1075	7	US-11-174-150-34	Sequence 34, Appl	210	30	63.8	230	6	US-10-515-720A-1	Sequence 1, Appl1
138	32	68.1	1114	7	US-11-174-150-35	Sequence 35, Appl	211	30	63.8	230	7	US-11-188-281-4	Sequence 4, Appl1
139	31.5	67.0	294	7	US-11-055-822-480	Sequence 480, App	212	30	63.8	514	6	US-10-498-026-97	Sequence 97, Appl
140	31.5	67.0	294	7	US-11-055-822-880	Sequence 880, App	213	30	63.8	514	6	US-10-498-026-98	Sequence 98, Appl
141	31	66.0	4	7	US-11-090-916-1	Sequence 1, Appl1	214	30	63.8	1049	6	US-10-131-826A-358	Sequence 358, App
142	31	66.0	4	7	US-11-144-301A-8	Sequence 8, Appl1	215	30	63.8	1398	6	US-10-055-877-46	Sequence 46, Appl
143	31	66.0	4	7	US-11-223-405-1	Sequence 1, Appl1	216	30	63.8	1398	6	US-10-453-372-872	Sequence 872, App
144	31	66.0	4	7	US-11-223-547-1	Sequence 1, Appl1	217	30	63.8	1403	6	US-10-055-877-52	Sequence 52, Appl
145	31	66.0	4	7	US-11-058-926-2	Sequence 2, Appl1	218	30	63.8	1403	6	US-10-453-372-878	Sequence 878, App
146	31	66.0	6	7	US-11-090-916-2	Sequence 2, Appl1	219	30	63.8	1404	6	US-10-053-877-44	Sequence 44, Appl
147	31	66.0	27	6	US-10-995-064-1084	Sequence 1084, Ap	220	30	63.8	1404	6	US-10-453-372-870	Sequence 870, App
148	31	66.0	27	7	US-11-129-741-1084	Sequence 1084, Ap	221	30	63.8	1433	7	US-11-114-962-1	Sequence 1, Appl1
149	31	66.0	84	6	US-10-467-657-5372	Sequence 5372, Ap	222	30	63.8	1547	6	US-10-453-372-886	Sequence 886, App
150	31	66.0	113	7	US-11-072-512-3199	Sequence 3199, Ap	223	30	63.8	1577	6	US-10-055-877-54	Sequence 54, Appl
151	31	66.0	137	7	US-11-098-686-11212	Sequence 11212, A	224	30	63.8	1577	6	US-10-453-372-882	Sequence 882, App
152	31	66.0	143	5	US-09-978-360A-641	Sequence 641, App	225	30	63.8	1577	6	US-10-453-372-884	Sequence 884, App
153	31	66.0	146	6	US-11-226-657-47	Sequence 47, Appl	226	30	63.8	1594	6	US-10-453-372-860	Sequence 860, App
154	31	66.0	189	6	US-10-995-561-643	Sequence 643, App	227	30	63.8	1820	6	US-10-453-372-868	Sequence 868, App
155	31	66.0	191	6	US-10-995-561-642	Sequence 642, App	228	30	63.8	1853	6	US-10-453-372-866	Sequence 866, App
156	31	66.0	191	7	US-11-064-774A-2	Sequence 2, Appl1	229	30	63.8	2256	7	US-11-050-346-67	Sequence 67, Appl
157	31	66.0	191	7	US-11-075-400-2	Sequence 2, Appl1	230	29	61.7	63	7	US-11-183-914-1	Sequence 1, Appl1
158	31	66.0	191	7	US-11-226-005-4	Sequence 4, Appl1	231	29	61.7	155	7	US-11-013-592-24	Sequence 24, Appl
159	31	66.0	191	7	US-11-129-076-9	Sequence 9, Appl1	232	29	61.7	253	7	US-11-179-977-13	Sequence 13, Appl
160	31	66.0	191	7	US-11-145-494-2	Sequence 2, Appl1	233	29	61.7	262	7	US-11-072-512-2276	Sequence 2276, Ap
161	31	66.0	191	7	US-11-075-047A-81	Sequence 81, Appl	234	29	61.7	279	7	US-11-098-686-10882	Sequence 10882, A
162	31	66.0	197	7	US-11-098-686-11017	Sequence 11017, A	235	29	61.7	523	7	US-11-072-512-2046	Sequence 2046, Ap
163	31	66.0	209	6	US-10-995-561-640	Sequence 640, App	236	29	61.7	613	6	US-10-467-657-5796	Sequence 5796, Ap
164	31	66.0	215	6	US-10-995-561-645	Sequence 645, App	237	29	61.7	838	7	US-11-072-512-2819	Sequence 2819, Ap
165	31	66.0	215	6	US-10-995-561-646	Sequence 646, App	238	29	61.7	1026	7	US-11-072-512-2509	Sequence 2509, Ap
166	31	66.0	215	7	US-11-149-462-3	Sequence 3, Appl1	239	29	61.7	1150	6	US-10-821-234-1083	Sequence 1083, Ap
167	31	66.0	234	7	US-11-072-512-3343	Sequence 3343, Ap	240	28	59.6	16	6	US-10-929-988-108	Sequence 108, App
168	31	66.0	232	6	US-10-995-561-642	Sequence 641, App	241	28	59.6	53	6	US-10-914-391A-7	Sequence 7, Appl1
169	31	66.0	232	6	US-10-995-561-644	Sequence 644, App	242	28	59.6	58	7	US-11-068-783-54	Sequence 54, Appl
170	31	66.0	232	7	US-11-153-880-7	Sequence 7, Appl1	243	28	59.6	70	6	US-10-506-192-8	Sequence 8, Appl1
171	31	66.0	232	7	US-11-064-774A-147	Sequence 147, App	244	28	59.6	81	6	US-10-131-826A-150	Sequence 150, App

245	28	59.6	106	7	US-11-074-176-288	Sequence 288, App	318	27	57.4	72	7	US-11-114-979-2	Sequence 2, Appli
246	28	59.6	126	7	US-11-195-459-14	Sequence 17, Appl	319	27	57.4	88	6	US-10-467-657-6627	Sequence 8627, Ap
247	28	59.6	134	6	US-10-498-025-37	Sequence 34, Appl	320	27	57.4	96	6	US-10-467-657-1198	Sequence 4198, Ap
248	28	59.6	155	7	US-11-098-686-10859	Sequence 10859, A	321	27	57.4	102	7	US-11-000-463-327	Sequence 327, App
249	28	59.6	188	7	US-11-024-953-304	Sequence 304, App	322	27	57.4	121	5	US-09-978-360A-614	Sequence 614, App
250	28	59.6	188	7	US-11-024-959-307	Sequence 307, App	323	27	57.4	132	6	US-10-821-234-1676	Sequence 1676, Ap
251	28	59.6	233	7	US-11-150-533-45	Sequence 45, Appl	324	27	57.4	135	6	US-10-467-657-8348	Sequence 8348, Ap
252	28	59.6	236	7	US-11-008-727-4	Sequence 4, Appli	325	27	57.4	142	6	US-10-856-751-37	Sequence 37, Appl
253	28	59.6	249	7	US-11-072-512-2058	Sequence 2058, Ap	326	27	57.4	162	5	US-09-978-360A-615	Sequence 615, App
254	28	59.6	303	7	US-11-186-284-133	Sequence 193, App	327	27	57.4	167	7	US-11-072-512-3290	Sequence 3290, Ap
255	28	59.6	309	6	US-10-714-887-42	Sequence 42, Appl	328	27	57.4	202	7	US-11-072-512-3917	Sequence 3917, Ap
256	28	59.6	318	7	US-11-021-305-168	Sequence 168, App	329	27	57.4	225	6	US-10-670-009-5	Sequence 5, Appli
257	28	59.6	336	6	US-10-467-657-4390	Sequence 4390, Ap	330	27	57.4	226	6	US-10-670-009-6	Sequence 6, Appli
258	28	59.6	365	7	US-11-087-177-5	Sequence 5, Appli	331	27	57.4	226	7	US-11-148-010-2	Sequence 2, Appli
259	28	59.6	390	6	US-10-467-657-3212	Sequence 3212, Ap	332	27	57.4	227	6	US-10-670-009-4	Sequence 4, Appli
260	28	59.6	438	7	US-11-183-136-40	Sequence 40, Appl	333	27	57.4	227	6	US-10-670-009-7	Sequence 7, Appli
261	28	59.6	470	7	US-11-008-727-20	Sequence 20, Appl	334	27	57.4	228	6	US-10-670-009-2	Sequence 2, Appli
262	28	59.6	470	7	US-11-121-438-35	Sequence 35, Appl	335	27	57.4	229	7	US-11-014-629-1	Sequence 1, Appli
263	28	59.6	476	7	US-11-008-727-22	Sequence 22, Appl	336	27	57.4	232	7	US-11-072-512-3111	Sequence 3111, Ap
264	28	59.6	490	6	US-10-763-712A-65	Sequence 65, Appl	337	27	57.4	249	7	US-11-010-239-107	Sequence 107, App
265	28	59.6	490	7	US-11-072-512-2640	Sequence 2640, Ap	338	27	57.4	255	6	US-10-660-499A-2	Sequence 2, Appli
266	28	59.6	509	7	US-11-008-727-16	Sequence 16, Appl	339	27	57.4	273	7	US-11-072-512-2703	Sequence 2703, Ap
267	28	59.6	513	7	US-11-000-463-458	Sequence 458, App	340	27	57.4	276	7	US-11-183-555-5	Sequence 5, Appli
268	28	59.6	519	7	US-11-033-039-442	Sequence 442, App	341	27	57.4	280	6	US-10-967-457-75	Sequence 75, Appl
269	28	59.6	530	7	US-11-183-136-44	Sequence 44, Appl	342	27	57.4	284	7	US-11-037-243-112	Sequence 112, App
270	28	59.6	539	7	US-11-183-136-38	Sequence 38, Appl	343	27	57.4	304	6	US-10-821-234-1540	Sequence 1540, Ap
271	28	59.6	578	7	US-11-083-800-2	Sequence 2, Appli	344	27	57.4	307	5	US-09-978-360A-550	Sequence 550, App
272	28	59.6	673	7	US-11-072-512-2774	Sequence 2774, Ap	345	27	57.4	307	5	US-09-978-360A-693	Sequence 693, App
273	28	59.6	710	7	US-11-169-041-203	Sequence 203, App	346	27	57.4	327	7	US-11-098-666-10271	Sequence 10271, A
274	28	59.6	742	6	US-10-658-986-2	Sequence 2, Appli	347	27	57.4	344	7	US-11-052-554A-43	Sequence 43, Appl
275	28	59.6	746	6	US-10-828-831-5	Sequence 5, Appli	348	27	57.4	349	6	US-10-131-826A-424	Sequence 424, App
276	28	59.6	777	6	US-10-658-986-4	Sequence 4, Appli	349	27	57.4	372	6	US-10-131-826A-106	Sequence 106, App
277	28	59.6	801	6	US-10-793-626-90	Sequence 90, Appl	350	27	57.4	378	7	US-11-244-219-7	Sequence 7, Appli
278	28	59.6	837	7	US-11-094-519A-43	Sequence 43, Appl	351	27	57.4	398	6	US-10-544-501-4	Sequence 4, Appli
279	28	59.6	844	6	US-10-453-372-852	Sequence 852, App	352	27	57.4	398	6	US-11-024-959-336	Sequence 336, App
280	28	59.6	845	6	US-10-453-372-856	Sequence 856, App	353	27	57.4	399	7	US-11-077-386-18	Sequence 18, Appl
281	28	59.6	845	6	US-11-094-519A-42	Sequence 42, Appl	354	27	57.4	400	7	US-11-183-205-46	Sequence 46, Appl
282	28	59.6	1011	6	US-10-877-346-127	Sequence 127, App	355	27	57.4	415	7	US-11-183-246-6	Sequence 6, Appli
283	28	59.6	1041	6	US-10-828-831-9	Sequence 9, Appli	356	27	57.4	416	6	US-10-821-234-1375	Sequence 1375, Ap
284	28	59.6	1198	6	US-10-877-346-35	Sequence 35, Appl	357	27	57.4	435	7	US-11-077-386-19	Sequence 19, Appl
285	28	59.6	1275	6	US-10-877-346-36	Sequence 36, Appl	358	27	57.4	450	7	US-11-077-386-20	Sequence 20, Appl
286	28	59.6	1306	6	US-10-467-657-5406	Sequence 5406, Ap	359	27	57.4	458	6	US-10-763-712A-32	Sequence 32, Appl
287	28	59.6	1428	6	US-10-877-346-33	Sequence 33, Appl	360	27	57.4	459	7	US-11-014-842A-23	Sequence 23, Appl
288	28	59.6	1428	6	US-10-877-346-34	Sequence 34, Appl	361	27	57.4	491	7	US-11-195-739-20	Sequence 20, Appl
289	28	59.6	1616	6	US-10-821-234-1497	Sequence 1497, Ap	362	27	57.4	502	7	US-11-226-701-4	Sequence 4, Appli
290	28	59.6	3712	7	US-11-019-711-48	Sequence 48, Appl	363	27	57.4	515	7	US-11-124-367A-180	Sequence 480, App
291	28	59.6	3712	7	US-11-019-711-51	Sequence 51, Appl	364	27	57.4	529	7	US-11-033-039-487	Sequence 487, App
292	28	59.6	4128	6	US-10-770-726-77	Sequence 77, Appl	365	27	57.4	529	7	US-11-155-288-1	Sequence 1, Appli
293	27.5	58.5	140	6	US-10-055-877-332	Sequence 332, App	366	27	57.4	560	7	US-11-040-218-7	Sequence 7, Appli
294	27	57.4	8	7	US-11-045-024-463	Sequence 463, App	367	27	57.4	566	7	US-11-065-695-2	Sequence 2, Appli
295	27	57.4	8	7	US-11-045-024-6174	Sequence 6174, Ap	368	27	57.4	576	7	US-11-040-218-9	Sequence 9, Appli
296	27	57.4	8	7	US-11-045-024-10930	Sequence 10930, A	369	27	57.4	580	7	US-11-183-136-6	Sequence 6, Appli
297	27	57.4	9	7	US-11-045-024-5123	Sequence 5123, Ap	370	27	57.4	580	7	US-11-046-653-2	Sequence 2, Appli
298	27	57.4	9	7	US-11-045-024-7020	Sequence 7020, Ap	371	27	57.4	581	7	US-11-236-198-7	Sequence 7, Appli
299	27	57.4	27	7	US-11-045-024-13608	Sequence 13608, A	372	27	57.4	589	7	US-11-183-136-42	Sequence 42, Appl
300	27	57.4	10	7	US-11-045-024-777	Sequence 777, App	373	27	57.4	589	7	US-11-040-218-5	Sequence 5, Appli
301	27	57.4	11	7	US-11-045-024-917	Sequence 917, App	374	27	57.4	595	6	US-10-510-386-240	Sequence 240, App
302	27	57.4	11	7	US-11-045-024-6135	Sequence 6135, Ap	375	27	57.4	601	7	US-11-065-695-8	Sequence 8, Appli
303	27	57.4	15	6	US-10-939-890-200	Sequence 200, App	376	27	57.4	602	6	US-10-493-909-51	Sequence 51, Appl
304	27	57.4	15	6	US-10-939-890-367	Sequence 367, App	377	27	57.4	630	7	US-11-236-198-5	Sequence 5, Appli
305	27	57.4	15	6	US-10-939-890-707	Sequence 707, App	378	27	57.4	649	7	US-11-236-198-3	Sequence 3, Appli
306	27	57.4	17	7	US-11-045-024-12952	Sequence 12952, A	379	27	57.4	682	7	US-11-072-512-2390	Sequence 2390, Ap
307	27	57.4	21	6	US-11-129-741-3980	Sequence 3980, Ap	380	27	57.4	682	7	US-11-072-512-2390	Sequence 2390, Ap
308	27	57.4	23	6	US-10-939-890-549	Sequence 549, App	381	27	57.4	684	6	US-10-714-781A-55	Sequence 55, Appl
309	27	57.4	23	6	US-10-939-890-321	Sequence 321, App	382	27	57.4	684	6	US-10-714-781A-57	Sequence 57, Appl
310	27	57.4	23	6	US-10-939-890-323	Sequence 323, App	383	27	57.4	684	6	US-10-714-781A-61	Sequence 61, Appl
311	27	57.4	23	6	US-10-939-890-367	Sequence 367, App	384	27	57.4	703	6	US-10-714-781A-59	Sequence 59, Appl
312	27	57.4	23	6	US-10-939-890-708	Sequence 708, App	385	27	57.4	703	6	US-10-821-234-1412	Sequence 1412, Ap
313	27	57.4	23	6	US-10-939-890-710	Sequence 710, App	386	27	57.4	703	7	US-11-065-695-4	Sequence 4, Appli
314	27	57.4	23	6	US-10-939-890-711	Sequence 711, App	387	27	57.4	708	7	US-11-107-028-2	Sequence 2, Appli
315	27	57.4	23	6	US-10-939-890-838	Sequence 838, App	388	27	57.4	830	6	US-10-995-561-899	Sequence 899, App
316	27	57.4	52	7	US-11-111-900-4	Sequence 4, Appli	389	27	57.4	833	6	US-10-537-971-2	Sequence 2, Appli
317	27	57.4	56	7	US-11-145-861-166	Sequence 166, App	390	27	57.4	938	7	US-11-109-157A-18	Sequence 18, Appl

391	27	57.4	1001	7	US-11-132-285-40	Sequence 40, Appl	464	26	55.3	55	6	US-10-467-657-5614	Sequence 5614, Ap
392	27	57.4	1013	6	US-10-131-826A-38	Sequence 38, Appl	465	26	55.3	57	7	US-11-000-463-710	Sequence 710, App
393	27	57.4	1047	7	US-11-124-367A-388	Sequence 388, Appl	466	26	55.3	57	7	US-11-000-463-883	Sequence 883, App
394	27	57.4	1058	7	US-11-124-367A-386	Sequence 386, App	467	26	55.3	58	6	US-10-467-657-5394	Sequence 5394, Ap
395	27	57.4	1062	7	US-11-124-367A-387	Sequence 387, Appl	468	26	55.3	75	7	US-11-174-968A-57	Sequence 57, Appl
396	27	57.4	1184	7	US-11-065-695-10	Sequence 10, Appl	469	26	55.3	86	5	US-09-978-360A-96	Sequence 496, Appl
397	27	57.4	1196	6	US-10-613-744-9	Sequence 10, Appl	470	26	55.3	85	5	US-09-978-360A-612	Sequence 612, App
398	27	57.4	1221	7	US-11-109-157A-17	Sequence 17, Appl	471	26	55.3	88	7	US-11-018-868-8	Sequence 8, Appl
399	27	57.4	1330	6	US-10-453-372-260	Sequence 260, App	472	26	55.3	93	6	US-10-467-657-6162	Sequence 6162, Ap
400	27	57.4	1342	6	US-10-453-372-258	Sequence 258, App	473	26	55.3	103	6	US-10-467-657-2150	Sequence 2150, Ap
401	27	57.4	1442	6	US-10-453-372-266	Sequence 266, App	474	26	55.3	104	7	US-11-072-512-2562	Sequence 2562, Ap
402	27	57.4	1542	6	US-10-453-372-280	Sequence 280, App	475	26	55.3	106	7	US-11-072-512-2218	Sequence 2218, Ap
403	27	57.4	1566	7	US-11-124-367A-481	Sequence 481, App	476	26	55.3	107	7	US-11-072-512-2122	Sequence 2122, App
404	27	57.4	3433	6	US-10-714-781A-67	Sequence 67, Appl	477	26	55.3	109	6	US-10-467-657-562	Sequence 562, App
405	26	55.3	8	7	US-11-045-024-3194	Sequence 3194, Ap	478	26	55.3	116	6	US-10-467-657-7486	Sequence 7486, Ap
406	26	55.3	8	7	US-11-045-024-3195	Sequence 3195, Ap	479	26	55.3	117	7	US-11-103-957-74	Sequence 74, Appl
407	26	55.3	8	7	US-11-045-024-4415	Sequence 4415, Ap	480	26	55.3	118	7	US-11-073-605-7	Sequence 7, Appl
408	26	55.3	8	7	US-11-045-024-4416	Sequence 4416, Ap	481	26	55.3	118	7	US-11-140-284-19	Sequence 19, Appl
409	26	55.3	8	7	US-11-045-024-5812	Sequence 5812, Ap	482	26	55.3	126	7	US-11-098-688-81	Sequence 81, Appl
410	26	55.3	8	7	US-11-045-024-9768	Sequence 9768, Ap	483	26	55.3	137	7	US-11-124-367A-509	Sequence 509, Appl
411	26	55.3	8	7	US-11-045-024-10009	Sequence 10009, A	484	26	55.3	140	7	US-11-084-591-4	Sequence 4, Appl
412	26	55.3	8	7	US-11-045-024-11748	Sequence 11748, A	485	26	55.3	146	7	US-11-226-657-80	Sequence 80, Appl
413	26	55.3	8	7	US-11-045-024-11916	Sequence 11916, A	486	26	55.3	146	7	US-11-072-512-3316	Sequence 3316, Ap
414	26	55.3	8	7	US-11-045-024-12718	Sequence 12718, A	487	26	55.3	158	7	US-11-072-512-3047	Sequence 3047, Ap
415	26	55.3	8	7	US-11-045-024-12754	Sequence 12754, A	488	26	55.3	159	7	US-11-072-512-3714	Sequence 3714, Ap
416	26	55.3	9	7	US-11-045-024-1989	Sequence 1989, Ap	489	26	55.3	162	7	US-11-033-037-246	Sequence 246, App
417	26	55.3	9	7	US-11-045-024-1990	Sequence 1990, Ap	490	26	55.3	170	6	US-10-467-657-104	Sequence 104, App
418	26	55.3	9	7	US-11-045-024-4558	Sequence 4558, Ap	491	26	55.3	170	6	US-10-467-657-8078	Sequence 8078, Ap
419	26	55.3	9	7	US-11-045-024-4559	Sequence 4559, Ap	492	26	55.3	172	7	US-11-098-686-10841	Sequence 10841, A
420	26	55.3	9	7	US-11-045-024-4560	Sequence 4560, Ap	493	26	55.3	174	7	US-11-009-658-16	Sequence 16, Appl
421	26	55.3	9	7	US-11-045-024-4561	Sequence 4561, Ap	494	26	55.3	178	7	US-11-072-512-3886	Sequence 3886, Ap
422	26	55.3	9	7	US-11-045-024-5871	Sequence 5871, Ap	495	26	55.3	179	6	US-10-467-657-1122	Sequence 1122, App
423	26	55.3	9	7	US-11-045-024-12712	Sequence 12712, A	496	26	55.3	179	6	US-10-467-657-3138	Sequence 3138, Ap
424	26	55.3	9	7	US-11-045-024-12752	Sequence 12752, A	497	26	55.3	179	6	US-10-467-657-3138	Sequence 3138, Ap
425	26	55.3	9	7	US-11-045-024-13842	Sequence 13842, A	498	26	55.3	179	6	US-10-467-657-3752	Sequence 3752, Ap
426	26	55.3	9	7	US-11-045-024-13899	Sequence 13899, A	499	26	55.3	182	6	US-10-467-657-3510	Sequence 3510, Ap
427	26	55.3	10	7	US-11-045-024-2224	Sequence 2224, Ap	500	26	55.3	193	7	US-11-072-512-3833	Sequence 3833, Ap
428	26	55.3	10	7	US-11-045-024-2225	Sequence 2225, Ap	501	26	55.3	202	6	US-10-467-657-8154	Sequence 8154, Ap
429	26	55.3	10	7	US-11-045-024-4709	Sequence 4709, Ap	502	26	55.3	206	7	US-11-072-512-2066	Sequence 2066, Ap
430	26	55.3	10	7	US-11-045-024-4710	Sequence 4710, Ap	503	26	55.3	208	6	US-10-467-657-3050	Sequence 3050, Ap
431	26	55.3	10	7	US-11-045-024-4711	Sequence 4711, Ap	504	26	55.3	208	7	US-11-072-512-2002	Sequence 2002, Ap
432	26	55.3	10	7	US-11-045-024-4712	Sequence 4712, Ap	505	26	55.3	213	6	US-10-467-657-7468	Sequence 7468, Ap
433	26	55.3	10	7	US-11-045-024-5377	Sequence 5377, Ap	506	26	55.3	214	7	US-11-098-686-11115	Sequence 11115, A
434	26	55.3	10	7	US-11-045-024-5378	Sequence 5378, Ap	507	26	55.3	217	6	US-10-467-657-2356	Sequence 2356, Ap
435	26	55.3	10	7	US-11-045-024-5675	Sequence 5675, Ap	508	26	55.3	217	6	US-10-467-657-8046	Sequence 8044, Ap
436	26	55.3	10	7	US-11-045-024-10000	Sequence 10000, A	509	26	55.3	232	7	US-11-072-512-3777	Sequence 3777, Ap
437	26	55.3	10	7	US-11-045-024-11679	Sequence 11679, A	510	26	55.3	244	7	US-11-072-512-3205	Sequence 3205, Ap
438	26	55.3	10	7	US-11-045-024-11909	Sequence 11909, A	511	26	55.3	248	7	US-11-152-811-7	Sequence 7, Appl
439	26	55.3	10	7	US-11-045-024-12715	Sequence 12715, A	512	26	55.3	251	7	US-11-072-175-223	Sequence 223, App
440	26	55.3	10	7	US-11-045-024-12753	Sequence 12753, A	513	26	55.3	255	7	US-11-009-658-42	Sequence 42, Appl
441	26	55.3	11	7	US-11-045-024-368	Sequence 368, App	514	26	55.3	257	7	US-11-140-284-40	Sequence 40, Appl
442	26	55.3	11	7	US-11-045-024-369	Sequence 369, App	515	26	55.3	258	7	US-11-058-924-6	Sequence 6, Appl
443	26	55.3	11	7	US-11-045-024-4871	Sequence 4871, Ap	516	26	55.3	258	7	US-11-072-512-3590	Sequence 3590, Ap
444	26	55.3	11	7	US-11-045-024-4872	Sequence 4872, Ap	517	26	55.3	263	6	US-10-821-234-1403	Sequence 1403, Ap
445	26	55.3	11	7	US-11-045-024-5411	Sequence 5411, Ap	518	26	55.3	263	6	US-10-954-468-45	Sequence 45, Appl
446	26	55.3	11	7	US-11-045-024-5411	Sequence 5411, Ap	519	26	55.3	263	6	US-11-102-883-36	Sequence 36, Appl
447	26	55.3	11	7	US-11-045-024-7639	Sequence 7639, Ap	520	26	55.3	263	7	US-11-102-883-36	Sequence 2, Appl
448	26	55.3	11	7	US-11-045-024-7794	Sequence 7794, Ap	521	26	55.3	266	6	US-11-155-114A-2	Sequence 2, Appl
449	26	55.3	14	7	US-11-188-552-6	Sequence 6, Appl	522	26	55.3	266	6	US-10-063-703-2	Sequence 2, Appl
450	26	55.3	15	7	US-11-045-024-13186	Sequence 13186, A	523	26	55.3	267	7	US-11-102-240-2	Sequence 2, Appl
451	26	55.3	15	7	US-11-045-024-13243	Sequence 13243, A	524	26	55.3	267	5	US-09-978-360A-702	Sequence 702, App
452	26	55.3	16	6	US-10-929-988-81	Sequence 81, Appl	525	26	55.3	274	7	US-11-102-883-34	Sequence 34, Appl
453	26	55.3	17	6	US-10-939-890-108	Sequence 108, App	526	26	55.3	282	7	US-11-058-924-9	Sequence 9, Appl
454	26	55.3	17	7	US-11-149-757-23	Sequence 23, Appl	527	26	55.3	284	6	US-10-467-657-3920	Sequence 3920, Ap
455	26	55.3	25	7	US-11-119-293-27	Sequence 27, Appl	528	26	55.3	286	6	US-10-853-807A-8	Sequence 8, Appl
456	26	55.3	28	7	US-11-129-741-3998	Sequence 3998, App	529	26	55.3	290	7	US-11-240-769-65	Sequence 65, Appl
457	26	55.3	29	6	US-10-986-501-269	Sequence 269, App	530	26	55.3	293	6	US-10-527-500-47	Sequence 47, Appl
458	26	55.3	33	7	US-11-121-301-78	Sequence 78, Appl	531	26	55.3	296	7	US-10-527-500-77	Sequence 77, Appl
459	26	55.3	33	7	US-11-121-301-79	Sequence 79, Appl	532	26	55.3	300	7	US-11-102-978-7	Sequence 7, Appl
460	26	55.3	39	7	US-11-145-861-307	Sequence 307, App	533	26	55.3	306	7	US-11-058-924-7	Sequence 7, Appl
461	26	55.3	51	5	US-09-978-360A-625	Sequence 625, App	534	26	55.3	305	7	US-11-000-463-391	Sequence 391, App
462	26	55.3	51	6	US-10-467-657-1730	Sequence 1730, App	535	26	55.3	305	7	US-11-000-463-863	Sequence 863, App
463	26	55.3	54	7	US-11-196-670-64	Sequence 64, Appl	536	26	55.3	308	7	US-11-098-686-10572	Sequence 10572, A

537	26	55.3	308	7	US-11-072-512-3715	Sequence 3715, Ap	610	26	55.3	557	6	US-10-718-264-8	Sequence 8, Appl1
538	26	55.3	315	7	US-11-037-243-60	Sequence 60, Appl	611	26	55.3	557	6	US-10-718-264-8	Sequence 8, Appl1
539	26	55.3	317	6	US-10-954-468-43	Sequence 43, Appl	612	26	55.3	557	6	US-11-072-512-33214	Sequence 3214, Ap
540	26	55.3	317	7	US-11-155-114A-3	Sequence 3, Appl1	613	26	55.3	576	7	US-11-098-686-10763	Sequence 10763, A
541	26	55.3	318	7	US-11-072-512-3654	Sequence 3654, Ap	614	26	55.3	615	7	US-11-231-599-57	Sequence 57, Appl
542	26	55.3	320	6	US-10-467-657-424	Sequence 424, App	615	26	55.3	622	7	US-11-199-124-12	Sequence 12, Appl
543	26	55.3	320	7	US-11-052-554A-219	Sequence 219, App	616	26	55.3	636	7	US-11-072-512-3366	Sequence 3666, Ap
544	26	55.3	322	7	US-11-073-605-4	Sequence 4, Appl1	617	26	55.3	642	6	US-10-995-561-631	Sequence 631, App
545	26	55.3	322	7	US-11-140-284-6	Sequence 6, Appl1	618	26	55.3	644	7	US-11-120-544B-2	Sequence 2, Appl1
546	26	55.3	323	6	US-10-525-674-8	Sequence 8, Appl1	619	26	55.3	647	7	US-11-072-512-2845	Sequence 2945, Ap
547	26	55.3	332	6	US-10-131-826A-386	Sequence 386, App	620	26	55.3	657	6	US-10-995-561-622	Sequence 622, App
548	26	55.3	334	7	US-11-055-822-644	Sequence 644, App	621	26	55.3	657	7	US-11-193-561-27	Sequence 27, Appl
549	26	55.3	341	7	US-11-156-084-127	Sequence 127, App	622	26	55.3	657	7	US-11-193-717-27	Sequence 27, Appl
550	26	55.3	342	7	US-11-072-512-2985	Sequence 2985, Ap	623	26	55.3	657	7	US-11-193-788-27	Sequence 27, Appl
551	26	55.3	344	7	US-11-120-308-100	Sequence 100, App	624	26	55.3	657	7	US-11-193-806-27	Sequence 27, Appl
552	26	55.3	345	6	US-10-131-826A-286	Sequence 286, App	625	26	55.3	657	7	US-11-193-857-27	Sequence 27, Appl
553	26	55.3	345	7	US-11-073-605-6	Sequence 6, Appl1	626	26	55.3	660	7	US-11-186-284-125	Sequence 125, App
554	26	55.3	345	7	US-11-064-774A-149	Sequence 149, App	627	26	55.3	682	7	US-11-098-686-10487	Sequence 10487, A
555	26	55.3	345	7	US-11-075-400-12	Sequence 12, Appl	628	26	55.3	688	7	US-11-131-035-2	Sequence 2, Appl1
556	26	55.3	345	7	US-11-076-427A-22	Sequence 22, Appl	629	26	55.3	693	7	US-11-098-686-11343	Sequence 11343, A
557	26	55.3	345	7	US-11-098-686-10120	Sequence 10120, A	630	26	55.3	702	6	US-10-467-657-7230	Sequence 7230, Ap
558	26	55.3	345	7	US-11-072-175-191	Sequence 191, App	631	26	55.3	708	6	US-10-821-234-917	Sequence 917, App
559	26	55.3	345	7	US-11-075-047A-103	Sequence 103, App	632	26	55.3	712	6	US-10-995-561-984	Sequence 984, App
560	26	55.3	345	7	US-11-140-284-32	Sequence 32, Appl	633	26	55.3	743	7	US-11-149-513-2	Sequence 2, Appl1
561	26	55.3	347	6	US-10-131-826A-18	Sequence 18, Appl	634	26	55.3	746	7	US-11-024-959-346	Sequence 346, App
562	26	55.3	348	6	US-10-878-556A-111	Sequence 111, App	635	26	55.3	750	7	US-11-070-627-1	Sequence 1, Appl1
563	26	55.3	349	7	US-11-098-686-10115	Sequence 10115, A	636	26	55.3	750	7	US-11-070-627-2	Sequence 2, Appl1
564	26	55.3	362	7	US-11-152-569-16	Sequence 16, Appl	637	26	55.3	750	7	US-11-070-627-3	Sequence 3, Appl1
565	26	55.3	364	6	US-10-131-826A-186	Sequence 186, App	638	26	55.3	750	7	US-11-070-627-4	Sequence 4, Appl1
566	26	55.3	364	7	US-11-140-284-38	Sequence 38, Appl	639	26	55.3	750	7	US-11-070-627-6	Sequence 6, Appl1
567	26	55.3	370	7	US-11-073-605-2	Sequence 2, Appl1	640	26	55.3	751	6	US-10-821-234-1007	Sequence 1007, Ap
568	26	55.3	370	7	US-11-075-400-14	Sequence 14, Appl	641	26	55.3	763	7	US-11-144-985-6	Sequence 6, Appl1
569	26	55.3	370	7	US-11-140-284-8	Sequence 8, Appl1	642	26	55.3	765	7	US-11-120-308-84	Sequence 84, Appl
570	26	55.3	370	7	US-11-140-284-36	Sequence 36, Appl	643	26	55.3	769	6	US-10-995-561-985	Sequence 985, App
571	26	55.3	376	7	US-11-055-822-152	Sequence 152, App	644	26	55.3	769	6	US-10-995-561-986	Sequence 986, App
572	26	55.3	376	7	US-11-072-512-3484	Sequence 3484, Ap	645	26	55.3	769	7	US-11-107-028-5	Sequence 5, Appl1
573	26	55.3	376	6	US-11-072-512-3532	Sequence 3532, Ap	646	26	55.3	770	7	US-11-070-627-5	Sequence 5, Appl1
574	26	55.3	377	6	US-10-467-657-680	Sequence 680, App	647	26	55.3	770	7	US-11-070-627-8	Sequence 8, Appl1
575	26	55.3	377	6	US-10-467-657-4946	Sequence 4946, Ap	648	26	55.3	770	7	US-11-070-627-10	Sequence 10, Appl
576	26	55.3	377	7	US-11-240-769-67	Sequence 67, Appl	649	26	55.3	773	6	US-10-821-234-1134	Sequence 1134, Ap
577	26	55.3	379	7	US-11-054-281-45	Sequence 45, Appl	650	26	55.3	774	7	US-11-070-627-7	Sequence 7, Appl1
578	26	55.3	381	7	US-11-054-281-2	Sequence 2, Appl1	651	26	55.3	779	7	US-11-072-512-3386	Sequence 3386, Ap
579	26	55.3	381	7	US-11-054-281-41	Sequence 41, Appl	652	26	55.3	782	6	US-10-821-234-1592	Sequence 1592, Ap
580	26	55.3	381	7	US-11-054-281-42	Sequence 42, Appl	653	26	55.3	782	7	US-11-149-513-4	Sequence 4, Appl1
581	26	55.3	381	7	US-11-054-281-43	Sequence 43, Appl	654	26	55.3	782	7	US-11-177-506-38	Sequence 38, Appl
582	26	55.3	381	7	US-11-054-281-44	Sequence 44, Appl	655	26	55.3	786	7	US-11-070-627-9	Sequence 9, Appl1
583	26	55.3	381	7	US-11-169-041-152	Sequence 152, App	656	26	55.3	807	7	US-11-124-367A-412	Sequence 412, App
584	26	55.3	401	7	US-11-055-822-336	Sequence 336, App	657	26	55.3	807	7	US-11-124-367A-413	Sequence 413, App
585	26	55.3	408	7	US-11-052-554A-383	Sequence 383, App	658	26	55.3	815	6	US-10-523-503-64	Sequence 64, Appl
586	26	55.3	413	7	US-11-071-686-4	Sequence 4, Appl1	659	26	55.3	816	7	US-11-072-512-2341	Sequence 2341, Ap
587	26	55.3	415	7	US-11-072-512-2624	Sequence 2624, Ap	660	26	55.3	818	7	US-11-120-308-94	Sequence 94, Appl
588	26	55.3	437	7	US-11-199-124-2	Sequence 2, Appl1	661	26	55.3	826	6	US-10-878-556A-68	Sequence 68, Appl
589	26	55.3	437	7	US-11-043-544-22	Sequence 22, Appl	662	26	55.3	835	7	US-11-098-686-10397	Sequence 10397, A
590	26	55.3	438	7	US-11-199-124-10	Sequence 10, Appl	663	26	55.3	842	6	US-10-645-441-2	Sequence 2, Appl1
591	26	55.3	440	7	US-11-043-544-20	Sequence 20, Appl	664	26	55.3	912	7	US-11-169-041-137	Sequence 137, App
592	26	55.3	443	6	US-10-523-503-12	Sequence 12, Appl	665	26	55.3	982	7	US-11-042-988-12	Sequence 12, Appl
593	26	55.3	444	7	US-11-052-554A-67	Sequence 67, Appl	666	26	55.3	937	7	US-11-098-686-11296	Sequence 11296, A
594	26	55.3	445	7	US-11-043-544-37	Sequence 37, Appl	667	26	55.3	931	7	US-11-121-438-14	Sequence 14, Appl
595	26	55.3	451	6	US-10-131-826A-126	Sequence 126, App	668	26	55.3	953	7	US-11-037-243-66	Sequence 66, Appl
596	26	55.3	452	7	US-11-098-686-10203	Sequence 10203, A	669	26	55.3	984	6	US-10-995-561-629	Sequence 629, App
597	26	55.3	460	7	US-11-182-016-26	Sequence 26, Appl	670	26	55.3	992	7	US-11-098-686-10761	Sequence 10761, A
598	26	55.3	466	7	US-11-127-877-41	Sequence 41, Appl	671	26	55.3	1053	6	US-10-517-939-52	Sequence 52, Appl
599	26	55.3	493	7	US-11-071-686-2	Sequence 2, Appl1	672	26	55.3	1061	7	US-11-121-438-4	Sequence 4, Appl1
600	26	55.3	502	6	US-10-131-826A-548	Sequence 548, App	673	26	55.3	1073	6	US-10-821-234-102	Sequence 1202, Ap
601	26	55.3	502	6	US-10-689-742-148	Sequence 148, App	674	26	55.3	1104	6	US-10-517-939-144	Sequence 144, App
602	26	55.3	504	6	US-10-999-782-2	Sequence 2, Appl1	675	26	55.3	1109	7	US-11-072-512-2506	Sequence 2506, Ap
603	26	55.3	515	7	US-11-093-273-38	Sequence 38, Appl	676	26	55.3	1132	7	US-11-120-544B-3	Sequence 3, Appl1
604	26	55.3	541	7	US-11-000-463-238	Sequence 238, App	677	26	55.3	1148	7	US-11-110-082-29	Sequence 29, Appl
605	26	55.3	542	6	US-11-098-686-11331	Sequence 11331, A	678	26	55.3	1149	7	US-11-110-082-30	Sequence 30, Appl
606	26	55.3	545	6	US-10-718-264-2	Sequence 2, Appl1	679	26	55.3	1234	6	US-10-517-939-306	Sequence 306, App
607	26	55.3	545	6	US-10-718-264-2	Sequence 2, Appl1	680	26	55.3	1252	6	US-10-493-909-89	Sequence 89, Appl
608	26	55.3	548	6	US-10-467-657-6000	Sequence 6000, Ap	681	26	55.3	1256	6	US-10-493-909-90	Sequence 90, Appl
609	26	55.3	550	6	US-10-878-556A-166	Sequence 166, App	682	26	55.3	1359	7	US-11-152-569-20	Sequence 20, Appl

683	26	55.3	1366	7	US-11-169-041-174	Sequence 174, App	756	25	53.2	36	6	US-10-983-120-15	Sequence 15, Appl
684	26	55.3	1373	7	US-11-098-686-11150	Sequence 1150, A	757	25	53.2	39	6	US-10-895-064-295	Sequence 295, App
685	26	55.3	1377	6	US-10-821-234-1070	Sequence 1070, Ap	758	25	53.2	39	7	US-11-129-741-295	Sequence 295, App
686	26	55.3	1379	7	US-11-114-962-4	Sequence 4, Appl1	759	25	53.2	39	7	US-11-129-741-295	Sequence 3227, Ap
687	26	55.3	1704	7	US-11-072-175-213	Sequence 213, App	760	25	53.2	41	6	US-10-511-314-2	Sequence 2, Appl1
688	26	55.3	2176	7	US-11-193-561-25	Sequence 25, Appl	761	25	53.2	41	6	US-10-511-314-2	Sequence 2, Appl1
689	26	55.3	2176	7	US-11-193-771-25	Sequence 25, Appl	762	25	53.2	41	7	US-11-226-657-206	Sequence 206, Appl
690	26	55.3	2176	7	US-11-193-789-25	Sequence 25, Appl	763	25	53.2	48	7	US-11-116-746-8	Sequence 8, Appl
691	26	55.3	2176	7	US-11-193-806-25	Sequence 25, Appl	764	25	53.2	57	6	US-10-467-657-7390	Sequence 7390, Ap
692	26	55.3	2176	7	US-11-193-857-25	Sequence 25, Appl	765	25	53.2	63	7	US-11-174-996A-51	Sequence 51, Appl
693	26	55.3	2176	7	US-11-193-857-38	Sequence 38, Appl	766	25	53.2	64	7	US-11-174-996A-89	Sequence 89, Appl
694	26	55.3	2217	7	US-11-193-771-38	Sequence 38, Appl	767	25	53.2	75	7	US-11-174-996A-91	Sequence 91, Appl
695	26	55.3	2217	7	US-11-193-789-38	Sequence 38, Appl	768	25	53.2	75	7	US-11-174-996A-97	Sequence 97, Appl
696	26	55.3	2217	7	US-11-193-806-38	Sequence 38, Appl	769	25	53.2	77	7	US-11-174-996A-53	Sequence 53, Appl
697	26	55.3	2223	7	US-11-193-857-38	Sequence 38, Appl	770	25	53.2	84	5	US-09-978-360A-69	Sequence 69, Appl
698	26	55.3	2223	7	US-11-193-561-2	Sequence 2, Appl1	771	25	53.2	86	6	US-10-511-314-1	Sequence 716, App
699	26	55.3	2223	7	US-11-193-771-2	Sequence 2, Appl1	772	25	53.2	86	6	US-10-511-722-1	Sequence 1, Appl1
700	26	55.3	2223	7	US-11-193-789-2	Sequence 2, Appl1	773	25	53.2	87	7	US-11-184-574-8	Sequence 8, Appl1
701	26	55.3	2223	7	US-11-193-806-2	Sequence 2, Appl1	774	25	53.2	91	6	US-10-511-538-56	Sequence 56, Appl1
702	26	55.3	2223	7	US-11-193-857-2	Sequence 2, Appl1	775	25	53.2	106	7	US-11-072-512-2975	Sequence 2975, Ap
703	26	55.3	2296	6	US-10-995-561-633	Sequence 633, App	776	25	53.2	112	7	US-11-129-741-4223	Sequence 4223, Ap
704	26	55.3	2296	7	US-11-193-561-23	Sequence 23, Appl	777	25	53.2	114	6	US-10-986-501-190	Sequence 190, App
705	26	55.3	2296	7	US-11-193-771-23	Sequence 23, Appl	778	25	53.2	115	7	US-11-155-288-11	Sequence 11, Appl
706	26	55.3	2296	7	US-11-193-789-23	Sequence 23, Appl	779	25	53.2	118	7	US-11-072-512-2212	Sequence 2212, Ap
707	26	55.3	2296	7	US-11-193-806-23	Sequence 23, Appl	780	25	53.2	118	7	US-10-793-626-2214	Sequence 2214, Ap
708	26	55.3	2296	7	US-11-193-857-23	Sequence 23, Appl	781	25	53.2	120	6	US-11-072-512-2462	Sequence 2462, Ap
709	26	55.3	2330	7	US-11-193-561-21	Sequence 21, Appl	782	25	53.2	132	7	US-11-098-686-10468	Sequence 10468, A
710	26	55.3	2330	7	US-11-193-771-21	Sequence 21, Appl	783	25	53.2	132	7	US-11-072-512-2099	Sequence 2099, Ap
711	26	55.3	2330	7	US-11-193-789-21	Sequence 21, Appl	784	25	53.2	132	7	US-11-072-512-3315	Sequence 3315, Ap
712	26	55.3	2330	7	US-11-193-806-21	Sequence 21, Appl	785	25	53.2	144	6	US-10-534-486-2	Sequence 2, Appl1
713	26	55.3	2330	7	US-11-193-857-21	Sequence 21, Appl	786	25	53.2	145	6	US-10-821-234-1231	Sequence 1231, Ap
714	26	55.3	2355	6	US-10-995-561-623	Sequence 623, App	787	25	53.2	146	7	US-11-226-657-63	Sequence 63, Appl
715	26	55.3	2355	6	US-10-995-561-627	Sequence 627, App	788	25	53.2	147	7	US-11-226-657-205	Sequence 205, Appl
716	26	55.3	2355	7	US-11-193-561-19	Sequence 19, Appl	789	25	53.2	156	6	US-10-821-234-1397	Sequence 1397, Ap
717	26	55.3	2355	7	US-11-193-771-19	Sequence 19, Appl	790	25	53.2	161	7	US-11-154-257-3	Sequence 3, Appl1
718	26	55.3	2355	7	US-11-193-789-19	Sequence 19, Appl	791	25	53.2	166	7	US-11-226-657-204	Sequence 204, App
719	26	55.3	2355	7	US-11-193-806-19	Sequence 19, Appl	792	25	53.2	182	5	US-09-978-360A-717	Sequence 717, App
720	26	55.3	2355	7	US-11-193-857-19	Sequence 19, Appl	793	25	53.2	182	6	US-10-131-826A-174	Sequence 174, App
721	26	55.3	2384	6	US-10-821-234-1545	Sequence 1545, Ap	794	25	53.2	183	6	US-10-467-657-6906	Sequence 6906, Ap
722	26	55.3	2386	6	US-10-995-561-626	Sequence 626, App	795	25	53.2	204	7	US-11-080-991-8	Sequence 8, Appl1
723	26	55.3	2421	7	US-11-193-561-17	Sequence 17, Appl	796	25	53.2	205	6	US-10-533-310-1	Sequence 1, Appl1
724	26	55.3	2421	7	US-11-193-771-17	Sequence 17, Appl	797	25	53.2	205	6	US-10-533-310-3	Sequence 3, Appl1
725	26	55.3	2421	7	US-11-193-806-17	Sequence 17, Appl	798	25	53.2	205	6	US-10-533-310-4	Sequence 4, Appl1
726	26	55.3	2421	7	US-11-193-857-17	Sequence 17, Appl	799	25	53.2	205	6	US-10-533-310-5	Sequence 5, Appl1
727	26	55.3	2421	7	US-11-193-857-17	Sequence 17, Appl	800	25	53.2	205	6	US-10-533-310-5	Sequence 3758, Ap
728	26	55.3	2477	7	US-11-193-561-15	Sequence 15, Appl	801	25	53.2	207	7	US-11-214-199-36	Sequence 36, Appl
729	26	55.3	2477	7	US-11-193-771-15	Sequence 15, Appl	802	25	53.2	207	7	US-11-072-512-2278	Sequence 2278, Ap
730	26	55.3	2477	7	US-11-193-789-15	Sequence 15, Appl	803	25	53.2	211	7	US-11-072-512-3219	Sequence 3219, Ap
731	26	55.3	2477	7	US-11-193-806-15	Sequence 15, Appl	804	25	53.2	221	7	US-11-080-628-2	Sequence 2, Appl1
732	26	55.3	2477	7	US-11-193-857-15	Sequence 15, Appl	805	25	53.2	221	7	US-11-080-628-342	Sequence 342, App
733	26	55.3	3623	6	US-10-995-561-593	Sequence 593, App	806	25	53.2	228	6	US-10-793-626-1862	Sequence 1862, Ap
734	26	55.3	3748	7	US-11-132-686-8	Sequence 8, Appl1	807	25	53.2	228	6	US-09-978-360A-753	Sequence 753, App
735	26	55.3	3749	7	US-11-132-686-6	Sequence 6, Appl1	808	25	53.2	229	6	US-10-131-826A-522	Sequence 522, App
736	26	55.3	3749	7	US-11-132-686-12	Sequence 12, Appl	809	25	53.2	229	6	US-10-131-826A-522	Sequence 1023, Ap
737	26	55.3	3912	7	US-11-132-686-7	Sequence 7, Appl1	810	25	53.2	232	6	US-10-821-234-1023	Sequence 2603, Ap
738	26	55.3	3913	7	US-11-132-686-5	Sequence 5, Appl1	811	25	53.2	239	7	US-11-072-512-2603	Sequence 4474, Ap
739	26	55.3	3913	7	US-11-132-686-9	Sequence 9, Appl1	812	25	53.2	241	6	US-10-467-657-4474	Sequence 4474, Ap
740	26	55.3	8655	7	US-11-205-109-15	Sequence 15, Appl	813	25	53.2	245	6	US-10-878-555A-182	Sequence 182, App
741	25.5	54.3	126	7	US-11-113-824-184	Sequence 184, Appl	814	25	53.2	246	7	US-11-072-512-2232	Sequence 2232, Ap
742	25.5	54.3	126	7	US-11-141-678-2	Sequence 2, Appl1	815	25	53.2	246	7	US-11-072-512-2283	Sequence 2283, Ap
743	25.5	54.3	1174	7	US-11-090-617-704	Sequence 704, App	816	25	53.2	247	7	US-11-072-512-1298	Sequence 1998, Ap
744	25.5	54.3	259	6	US-10-821-234-1561	Sequence 1561, Ap	817	25	53.2	247	7	US-11-072-512-2790	Sequence 2790, App
745	25.5	54.3	353	7	US-11-137-465-44	Sequence 44, Appl	818	25	53.2	250	5	US-09-978-360A-473	Sequence 473, App
746	25.5	54.3	403	6	US-10-453-372-1170	Sequence 1170, Ap	819	25	53.2	255	6	US-10-170-997-2	Sequence 2, Appl1
747	25.5	54.3	488	7	US-11-137-465-45	Sequence 45, Appl	820	25	53.2	255	7	US-11-182-946-11	Sequence 11, Appl
748	25.5	54.3	898	7	US-11-174-150-43	Sequence 43, Appl	821	25	53.2	255	7	US-11-108-257-2	Sequence 2, Appl1
749	25.5	54.3	1033	6	US-10-921-415-1	Sequence 1, Appl1	822	25	53.2	259	6	US-10-131-826A-300	Sequence 300, Appl
750	25.5	54.3	1532	6	US-10-821-234-914	Sequence 914, App	823	25	53.2	259	6	US-11-182-946-2	Sequence 2, Appl1
751	25	53.2	11	7	US-11-145-861-324	Sequence 324, App	824	25	53.2	261	6	US-11-116-746-1	Sequence 1, Appl1
752	25	53.2	12	6	US-10-511-314-3	Sequence 3, Appl1	825	25	53.2	265	7	US-10-467-657-5896	Sequence 5896, Ap
753	25	53.2	12	6	US-10-511-722-3	Sequence 3, Appl1	826	25	53.2	276	7	US-11-098-686-10630	Sequence 10630, A
754	25	53.2	28	6	US-10-895-064-984	Sequence 984, App	827	25	53.2	276	7	US-11-020-602-224	Sequence 224, App
755	25	53.2	28	7	US-11-129-741-984	Sequence 984, App	828	25	53.2	277	7	US-11-132-285-3	Sequence 3, Appl1

829	25	53.2	277	7	US-11-182-946-12	Sequence 12, Appl	902	25	53.2	537	7	US-11-144-236-6	Sequence 6, Appl1
830	25	53.2	280	5	US-09-978-360A-809	Sequence 809, App	903	25	53.2	539	6	US-10-793-626-340	Sequence 340, App
831	25	53.2	280	6	US-10-131-826A-458	Sequence 458, App	904	25	53.2	555	6	US-10-949-720-387	Sequence 387, App
832	25	53.2	280	6	US-10-689-742-160	Sequence 160, App	905	25	53.2	557	7	US-11-072-512-2707	Sequence 2707, App
833	25	53.2	280	6	US-10-821-234-1300	Sequence 1300, App	906	25	53.2	570	6	US-10-949-720-386	Sequence 386, App
834	25	53.2	289	7	US-11-037-243-70	Sequence 70, Appl	907	25	53.2	570	6	US-10-949-720-412	Sequence 412, App
835	25	53.2	292	5	US-09-978-360A-674	Sequence 674, Appl	908	25	53.2	588	6	US-10-763-712A-94	Sequence 94, Appl
836	25	53.2	292	6	US-10-967-527A-19	Sequence 19, Appl	909	25	53.2	588	6	US-10-763-712A-95	Sequence 95, Appl
837	25	53.2	299	7	US-10-538-343-4	Sequence 4, Appl1	910	25	53.2	595	7	US-11-072-512-2714	Sequence 2714, App
838	25	53.2	299	6	US-11-116-746-3	Sequence 3, Appl1	911	25	53.2	602	6	US-10-453-372-1064	Sequence 1064, App
839	25	53.2	309	6	US-10-524-647-128	Sequence 128, App	912	25	53.2	610	6	US-10-608-302-1	Sequence 1, Appl1
840	25	53.2	309	6	US-10-524-932-116	Sequence 116, App	913	25	53.2	619	7	US-11-098-666-10196	Sequence 10196, A
841	25	53.2	318	6	US-10-511-518-163	Sequence 163, App	914	25	53.2	622	6	US-10-453-372-1184	Sequence 1184, App
842	25	53.2	318	6	US-11-190-188-21	Sequence 21, App	915	25	53.2	626	7	US-11-072-512-2199	Sequence 2199, App
843	25	53.2	319	6	US-10-131-826A-134	Sequence 134, App	916	25	53.2	634	6	US-10-632-150-26	Sequence 26, Appl
844	25	53.2	336	6	US-10-467-657-5848	Sequence 5848, App	917	25	53.2	634	7	US-11-073-457-26	Sequence 26, Appl
845	25	53.2	336	6	US-10-453-372-640	Sequence 640, App	918	25	53.2	634	7	US-11-073-460-26	Sequence 26, Appl
846	25	53.2	336	6	US-11-000-463-445	Sequence 445, App	919	25	53.2	638	7	US-11-072-512-2626	Sequence 2626, App
847	25	53.2	341	6	US-10-821-234-1628	Sequence 1628, App	920	25	53.2	645	7	US-11-137-465-54	Sequence 54, Appl
848	25	53.2	342	7	US-11-098-686-10943	Sequence 10943, A	921	25	53.2	645	7	US-11-072-512-2588	Sequence 2588, App
849	25	53.2	344	6	US-10-467-657-6546	Sequence 6546, App	922	25	53.2	653	7	US-11-137-465-55	Sequence 55, Appl
850	25	53.2	344	6	US-11-000-463-917	Sequence 917, App	923	25	53.2	655	7	US-11-045-802-29	Sequence 29, Appl
851	25	53.2	348	6	US-10-520-820-5	Sequence 5, Appl1	924	25	53.2	655	7	US-11-072-512-2502	Sequence 2502, App
852	25	53.2	349	7	US-11-182-946-13	Sequence 13, Appl	925	25	53.2	656	6	US-10-821-234-1121	Sequence 1121, App
853	25	53.2	350	6	US-10-063-703-8	Sequence 8, Appl1	926	25	53.2	656	7	US-11-234-786-379	Sequence 379, App
854	25	53.2	350	7	US-11-132-285-41	Sequence 41, Appl1	927	25	53.2	671	7	US-11-234-786-380	Sequence 380, App
855	25	53.2	350	7	US-11-102-240-8	Sequence 8, Appl1	928	25	53.2	687	6	US-10-055-877-203	Sequence 203, App
856	25	53.2	353	7	US-11-072-512-2052	Sequence 2052, App	929	25	53.2	692	7	US-11-103-957-29	Sequence 29, Appl
857	25	53.2	354	7	US-11-108-528-50	Sequence 50, Appl	930	25	53.2	697	6	US-10-821-234-905	Sequence 905, App
858	25	53.2	355	6	US-10-967-527A-22	Sequence 22, Appl	931	25	53.2	698	7	US-11-177-506-46	Sequence 46, Appl
859	25	53.2	355	7	US-11-182-946-14	Sequence 14, Appl	932	25	53.2	721	7	US-11-072-512-2605	Sequence 2605, App
860	25	53.2	362	7	US-11-072-512-2384	Sequence 2384, App	933	25	53.2	728	7	US-11-072-512-3399	Sequence 3399, App
861	25	53.2	364	7	US-11-169-041-216	Sequence 216, App	934	25	53.2	729	7	US-11-130-821-4	Sequence 4, Appl1
862	25	53.2	369	7	US-11-105-268-60	Sequence 60, Appl1	935	25	53.2	750	7	US-11-132-285-2	Sequence 2, Appl1
863	25	53.2	380	7	US-11-144-236-1	Sequence 1, Appl1	936	25	53.2	771	6	US-10-949-720-369	Sequence 369, App
864	25	53.2	386	6	US-10-131-826A-340	Sequence 340, Appl	937	25	53.2	776	7	US-11-072-512-3117	Sequence 3117, App
865	25	53.2	386	7	US-11-185-878-2	Sequence 2, Appl1	938	25	53.2	783	7	US-11-037-243-67	Sequence 67, Appl
866	25	53.2	386	7	US-11-099-135-1	Sequence 1, Appl1	939	25	53.2	793	6	US-10-995-561-925	Sequence 925, App
867	25	53.2	398	7	US-11-072-512-2769	Sequence 2769, App	940	25	53.2	794	7	US-11-218-966-2	Sequence 2, Appl1
868	25	53.2	400	6	US-10-948-053-4	Sequence 4, Appl1	941	25	53.2	795	7	US-11-072-512-2810	Sequence 2810, App
869	25	53.2	400	6	US-10-948-053-5	Sequence 5, Appl1	942	25	53.2	799	7	US-11-074-176-348	Sequence 348, App
870	25	53.2	401	6	US-10-949-720-419	Sequence 419, App	943	25	53.2	804	6	US-10-453-372-650	Sequence 650, App
871	25	53.2	401	6	US-10-510-876-2	Sequence 2, Appl1	944	25	53.2	805	6	US-10-485-517-198	Sequence 198, App
872	25	53.2	401	6	US-10-510-876-4	Sequence 4, Appl1	945	25	53.2	807	7	US-11-074-176-172	Sequence 172, App
873	25	53.2	401	6	US-10-948-053-8	Sequence 8, Appl1	946	25	53.2	820	6	US-10-821-234-1176	Sequence 1176, App
874	25	53.2	401	6	US-11-072-173-224	Sequence 224, App	947	25	53.2	825	6	US-10-453-372-644	Sequence 644, App
875	25	53.2	404	6	US-10-948-053-7	Sequence 7, Appl1	948	25	53.2	833	7	US-11-076-187-5	Sequence 5, Appl1
876	25	53.2	404	7	US-11-098-686-11329	Sequence 11329, A	949	25	53.2	834	6	US-10-453-372-658	Sequence 658, App
877	25	53.2	405	6	US-10-467-657-4964	Sequence 4964, App	950	25	53.2	843	7	US-11-129-104-89	Sequence 89, Appl
878	25	53.2	406	6	US-10-948-053-6	Sequence 6, Appl1	951	25	53.2	847	6	US-10-453-372-654	Sequence 654, App
879	25	53.2	406	7	US-11-098-686-10564	Sequence 10564, A	952	25	53.2	856	7	US-11-054-281-116	Sequence 116, App
880	25	53.2	406	7	US-11-072-512-3010	Sequence 3010, App	953	25	53.2	944	7	US-11-057-058-68	Sequence 68, Appl
881	25	53.2	407	6	US-10-948-053-3	Sequence 3, Appl1	954	25	53.2	963	6	US-10-995-561-923	Sequence 923, App
882	25	53.2	409	7	US-11-137-315A-6	Sequence 6, Appl1	955	25	53.2	966	6	US-10-453-372-660	Sequence 660, App
883	25	53.2	418	6	US-10-512-325-3	Sequence 3, Appl1	956	25	53.2	967	7	US-11-057-058-67	Sequence 67, Appl
884	25	53.2	418	7	US-11-196-919-2	Sequence 2, Appl1	957	25	53.2	967	7	US-11-171-701-4	Sequence 4, Appl1
885	25	53.2	419	7	US-11-112-882-36	Sequence 36, Appl	958	25	53.2	985	7	US-11-113-424-61	Sequence 61, Appl
886	25	53.2	419	7	US-11-166-993-6	Sequence 6, Appl1	959	25	53.2	987	6	US-10-949-720-395	Sequence 395, App
887	25	53.2	422	7	US-11-166-993-7	Sequence 7, Appl1	960	25	53.2	990	6	US-10-821-234-1201	Sequence 1201, App
888	25	53.2	431	6	US-10-949-720-410	Sequence 410, App	961	25	53.2	1012	6	US-10-453-372-646	Sequence 646, App
889	25	53.2	433	6	US-10-467-657-6876	Sequence 6876, App	962	25	53.2	1143	6	US-11-072-512-2802	Sequence 2802, App
890	25	53.2	445	7	US-11-072-512-2209	Sequence 2209, App	963	25	53.2	1187	6	US-10-821-234-955	Sequence 955, App
891	25	53.2	456	5	US-09-978-360A-523	Sequence 523, App	964	25	53.2	1250	7	US-11-137-465-62	Sequence 62, Appl
892	25	53.2	477	7	US-11-055-822-338	Sequence 338, App	965	25	53.2	1544	6	US-10-453-372-1186	Sequence 1186, App
893	25	53.2	492	6	US-10-467-657-8422	Sequence 8422, App	966	25	53.2	1565	6	US-10-453-372-1180	Sequence 1180, App
894	25	53.2	502	6	US-10-763-712A-68	Sequence 68, Appl	967	25	53.2	1566	6	US-10-453-372-1190	Sequence 1190, App
895	25	53.2	505	7	US-11-124-367A-365	Sequence 365, App	968	25	53.2	1705	7	US-11-143-988A-37	Sequence 37, Appl
896	25	53.2	507	7	US-11-124-367A-351	Sequence 351, App	969	25	53.2	1719	7	US-11-234-786-378	Sequence 378, Appl
897	25	53.2	509	7	US-11-135-667-34	Sequence 34, Appl	970	25	53.2	1907	7	US-11-039-398-25	Sequence 25, Appl
898	25	53.2	513	7	US-11-135-667-51	Sequence 51, Appl	971	25	53.2	2053	6	US-10-453-372-1174	Sequence 1174, App
899	25	53.2	513	7	US-11-135-667-53	Sequence 53, Appl	972	25	53.2	2107	6	US-10-995-561-827	Sequence 827, App
900	25	53.2	522	6	US-10-949-720-425	Sequence 425, App	973	25	53.2	2143	6	US-10-453-372-1188	Sequence 1188, App
901	25	53.2	537	6	US-10-949-720-424	Sequence 424, App	974	25	53.2	2440	6	US-10-766-317-10	Sequence 10, Appl

```
975 25 53.2 2480 6 US-10-995-561-825 Sequence 825, App
976 25 53.2 2764 6 US-10-995-561-691 Sequence 691, App
977 25 53.2 2813 6 US-10-995-561-688 Sequence 688, App
978 25 53.2 2911 7 US-11-090-617-706 Sequence 706, App
979 25 53.2 2919 6 US-10-821-234-1133 Sequence 1133, App
980 25 53.2 3116 6 US-10-995-561-826 Sequence 826, App
981 25 53.2 3635 7 US-11-019-711-47 Sequence 47, App1
982 25 53.2 4374 7 US-11-128-572-2 Sequence 112, App
983 25 53.2 4913 6 US-10-453-372-1142 Sequence 1142, App
984 25 53.2 4961 6 US-10-453-372-1132 Sequence 1132, App
985 24.5 52.1 162 6 US-10-453-372-876 Sequence 876, App
986 24.5 52.1 170 6 US-10-055-877-50 Sequence 50, App1
987 24.5 52.1 170 6 US-10-453-372-858 Sequence 858, App
988 24.5 52.1 170 6 US-10-453-372-888 Sequence 888, App
989 24.5 52.1 173 6 US-10-453-372-862 Sequence 862, App
990 24.5 52.1 1418 6 US-10-453-372-864 Sequence 864, App
991 24.5 52.1 1450 6 US-10-055-877-48 Sequence 48, App1
992 24.5 52.1 1450 6 US-10-453-372-874 Sequence 874, App1
993 24 51.1 16 6 US-10-929-988-301 Sequence 301, App
994 24 51.1 19 7 US-11-157-049-31 Sequence 31, App1
995 24 51.1 26 7 US-11-119-293-24 Sequence 24, App1
996 24 51.1 35 6 US-10-957-351-117 Sequence 117, App
997 24 51.1 35 6 US-10-957-351-170 Sequence 170, App
998 24 51.1 38 6 US-10-957-351-155 Sequence 155, App
999 24 51.1 41 6 US-10-957-351-356 Sequence 356, App
1000 24 51.1 45 7 US-11-123-896-165 Sequence 165, App
```

ALIGNMENTS

```
RESULT 1
US-11-090-916-3
; Sequence 3, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide motif
US-11-090-916-3
```

```
Query Match 100.0%; Score 47; DB 7; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.3e+04;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 WCGPCK 6
Db 1 WCGPCK 6
```

RESULT 2

```
US-11-131-744-2
; Sequence 2, Application US/1131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 2
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-2
```

```
Query Match 100.0%; Score 47; DB 7; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 WCGPCK 6
Db 32 WCGPCK 37
```

```
RESULT 3
US-11-131-744-1
; Sequence 1, Application US/1131744
; Publication No. US20060023808A1
; GENERAL INFORMATION:
; APPLICANT: HAJIVANDI, MAHOD R.
; APPLICANT: POPE, ROBERT M.
; APPLICANT: SADEGHI, MEHRNOOSH
; APPLICANT: LIANG, XIQUAN
; APPLICANT: LEITE, JOHN F.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
; FILE REFERENCE: NVX-28 US
; CURRENT APPLICATION NUMBER: US/11/131,744
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/572,290
; PRIOR FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/669,373
; PRIOR FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 60/572,215
; PRIOR FILING DATE: 2004-05-17
; PRIOR APPLICATION NUMBER: 60/621,685
; PRIOR FILING DATE: 2004-10-26
; PRIOR APPLICATION NUMBER: 60/621,686
; PRIOR FILING DATE: 2004-10-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 1
; LENGTH: 91
```

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-11-131-744-1
;
Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 91;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 4
US-11-074-176-286
; Sequence 286, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klamhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
; US-11-074-176-286

Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 27 WCGPCK 32

RESULT 5
US-11-090-916-7
; Sequence 7, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
```

```

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-11-090-916-7
;
Query Match
Best Local Similarity 100.0%; Score 47; DB 7; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 29 WCGPCK 34

RESULT 6
US-10-821-234-1371
; Sequence 1371, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1371
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-821-234-1371

Query Match
Best Local Similarity 100.0%; Score 47; DB 6; Length 105;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WCGPCK 6
Db 31 WCGPCK 36

RESULT 7
US-11-090-916-8
; Sequence 8, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/650,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
```

LENGTH: 105
TYPE: PRT
ORGANISM: Gallus gallus
US-11-090-916-8

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 8
US-11-090-916-9
Sequence 9, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
LENGTH: 105
TYPE: PRT
ORGANISM: Mus musculus
US-11-090-916-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 9
US-11-090-916-10
Sequence 10, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24

PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 105
TYPE: PRT
ORGANISM: Rattus norvegicus
US-11-090-916-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 10
US-11-090-916-11
Sequence 11, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO 11
LENGTH: 105
TYPE: PRT
ORGANISM: Bos taurus
US-11-090-916-11

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 11
US-11-090-916-12
Sequence 12, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
PRIOR FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082

;; PRIOR FILING DATE: 2003-04-11
;; PRIOR APPLICATION NUMBER: 10/660,118
;; PRIOR FILING DATE: 2003-09-10
;; PRIOR APPLICATION NUMBER: 60/556,516
;; PRIOR FILING DATE: 2004-03-24
;; PRIOR APPLICATION NUMBER: 60/650,865
;; PRIOR FILING DATE: 2005-02-07
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 12
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-090-916-12

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 12
US-11-106-796-13
;; Sequence 13, Application US/11106796
;; Publication No. US20050282191A1
;; GENERAL INFORMATION:
;; APPLICANT: SUTOVSKY, PETER
;; APPLICANT: MIRANDA-VIZUELO, ANTONIO
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
;; FILE REFERENCE: UWO-033US
;; CURRENT APPLICATION NUMBER: US/11/106,796
;; CURRENT FILING DATE: 2005-04-15
;; PRIOR APPLICATION NUMBER: 60/562,526
;; PRIOR FILING DATE: 2004-04-15
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 13
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-106-796-13

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 13
US-11-144-301A-9
;; Sequence 9, Application US/11144301A
;; Publication No. US20050288227A1
;; GENERAL INFORMATION:
;; APPLICANT: Marks, Paul A.
;; APPLICANT: Johanna, Ungerestedt
;; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
;; FILE REFERENCE: 28517-501 UTIL
;; CURRENT APPLICATION NUMBER: US/11/144,301A
;; CURRENT FILING DATE: 2005-06-03
;; PRIOR APPLICATION NUMBER: US 60/577,089
;; PRIOR FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: US 10/369,094
;; PRIOR FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 60/357,383
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.3

;; SEQ ID NO: 9
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-301A-9

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 14
US-11-144-301A-10
;; Sequence 10, Application US/11144301A
;; Publication No. US20050288227A1
;; GENERAL INFORMATION:
;; APPLICANT: Marks, Paul A.
;; APPLICANT: Johanna, Ungerestedt
;; TITLE OF INVENTION: USE OF THIOREDOXIN MEASUREMENTS FOR DIAGNOSTICS AND TREATMENTS
;; FILE REFERENCE: 28517-501 UTIL
;; CURRENT APPLICATION NUMBER: US/11/144,301A
;; CURRENT FILING DATE: 2005-06-03
;; PRIOR APPLICATION NUMBER: US 60/577,089
;; PRIOR FILING DATE: 2004-06-04
;; PRIOR APPLICATION NUMBER: US 10/369,094
;; PRIOR FILING DATE: 2003-02-14
;; PRIOR APPLICATION NUMBER: US 60/357,383
;; PRIOR FILING DATE: 2002-02-15
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 10
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-11-144-301A-10

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
Db 31 WCGPCK 36

RESULT 15
US-11-032-773-943
;; Sequence 943, Application US/11032773
;; Publication No. US20060018911A1
;; GENERAL INFORMATION:
;; APPLICANT: Levy, Ronald
;; APPLICANT: Ault-Riche, Dana
;; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
;; FILE REFERENCE: 17102-013001 / 1762
;; CURRENT APPLICATION NUMBER: US/11/032,773
;; CURRENT FILING DATE: 2005-01-11
;; PRIOR APPLICATION NUMBER: 60/536,184
;; PRIOR FILING DATE: 2004-01-12
;; PRIOR APPLICATION NUMBER: 60/557,591
;; PRIOR FILING DATE: 2004-03-29
;; NUMBER OF SEQ ID NOS: 958
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 943
;; LENGTH: 105
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: Genbank BAA04881
;; DATABASE ENTRY DATE: 2002-12-25

US-11-032-773-943

Query Match 100.0%; Score 47; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 16

US-11-090-916-4
; Sequence 4, Application US/11090916
; Publication No. US20050260140A1
; GENERAL INFORMATION:
; APPLICANT: White, Carl W.
; APPLICANT: del Val, Greg
; APPLICANT: Lee, Rees
; TITLE OF INVENTION: Muscolytic and Anti-Elastase Compounds and Methods of Use Thereof
; FILE REFERENCE: 2879-98-1
; CURRENT APPLICATION NUMBER: US/11/090,916
; PRIOR FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: 60/409,960
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/462,082
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 10/660,118
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/556,516
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/550,865
; PRIOR FILING DATE: 2005-02-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-11-090-916-4

Query Match 100.0%; Score 47; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 33 WCGPCK 38

RESULT 17

US-11-106-796-11
; Sequence 11, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-106-796-11

Query Match 100.0%; Score 47; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 18

US-11-106-796-12
; Sequence 12, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZUETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UWO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; PRIOR FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 127
; TYPE: PRT
; ORGANISM: RAT
US-11-106-796-12

Query Match 100.0%; Score 47; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 31 WCGPCK 36

RESULT 19

US-10-467-657-4354
; Sequence 4354, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04
; SEQ ID NO 4354
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4354

Query Match 100.0%; Score 47; DB 6; Length 129;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||||
DB 52 WCGPCK 57

RESULT 20

US-11-131-744-3
; Sequence 3, Application US/1131744

```
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 3
LENGTH: 177
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-3

Query Match      100.0%; Score 47; DB 7; Length 177;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        31 WCGPCK 36

RESULT 21
US-11-131-744-6
Sequence 6, Application US/11/131,744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 6
LENGTH: 273
TYPE: PRT
ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-6

Query Match      100.0%; Score 47; DB 7; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        31 WCGPCK 36

RESULT 22
US-11-131-744-7
Sequence 7, Application US/11/131,744
Publication No. US20060023808A1
GENERAL INFORMATION:
APPLICANT: HAJIVANDI, MAHROD R.
APPLICANT: POPE, ROBERT M.
APPLICANT: SADEGHI, MEHRNOOSH
APPLICANT: LIANG, XIQUAN
APPLICANT: LEITE, JOHN F.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR CALIBRATION IN MASS
FILE REFERENCE: NVX-28 US
CURRENT APPLICATION NUMBER: US/11/131,744
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/572,290
PRIOR FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: 60/669,373
PRIOR FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: 60/572,215
PRIOR FILING DATE: 2004-05-17
PRIOR APPLICATION NUMBER: 60/621,685
PRIOR FILING DATE: 2004-10-26
PRIOR APPLICATION NUMBER: 60/621,686
PRIOR FILING DATE: 2004-10-26
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 7
LENGTH: 440
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-131-744-7

Query Match      100.0%; Score 47; DB 7; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
        |||||
        32 WCGPCK 37

RESULT 23
US-11-090-916-6
Sequence 6, Application US/11/090,916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
```

```
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/550,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 6
/ LENGTH: 103
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-11-090-916-6
```

```
Query Match          93.6%; Score 44; DB 7; Length 103;
Best Local Similarity 83.3%; Pred. No. 0.74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       27 WCGPCR 32
```

```
RESULT 24
US-11-090-916-5
/ Sequence 5, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Reese
/ TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ PRIOR FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 5
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Porphyromonas gingivalis
US-11-090-916-5
```

```
Query Match          93.6%; Score 44; DB 7; Length 104;
Best Local Similarity 83.3%; Pred. No. 0.74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       28 WCGPCR 33
```

```
RESULT 25
US-11-098-686-10612
/ Sequence 10612, Application US/11098686
/ Publication No. US2006024696A1
/ GENERAL INFORMATION:
/ APPLICANT: Kapur, Vijay and Gebhart, Connie J.
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
/ FROM LAMSONIA INTRACELLULARIS AND METHODS OF USING
/ FILE REFERENCE: 09531-128001
```

```
/ CURRENT APPLICATION NUMBER: US/11/098,686
/ CURRENT FILING DATE: 2005-04-04
/ PRIOR APPLICATION NUMBER: PCT/US03/31318
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: US 60/416,395
/ PRIOR FILING DATE: 2002-10-04
/ NUMBER OF SEQ ID NOS: 11433
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10612
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: Lawsonia intracellularis
US-11-098-686-10612
```

```
Query Match          93.6%; Score 44; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 0.76;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       29 WCGPCR 34
```

```
RESULT 26
US-11-195-459-12
/ Sequence 12, Application US/11195459
/ Publication No. US20050278803A1
/ GENERAL INFORMATION:
/ APPLICANT: Sewalt, Vincent
/ APPLICANT: Hastings, Craig
/ APPLICANT: Weeley, Robert
/ APPLICANT: Hantke, Sabine
/ APPLICANT: Jung, Rudolf
/ APPLICANT: Everard, John
/ APPLICANT: Allen, Stephen
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
/ FILE REFERENCE: 5718-119 (035718/241421)
/ CURRENT APPLICATION NUMBER: US/11/195,459
/ PRIOR FILING DATE: 2005-08-02
/ PRIOR APPLICATION NUMBER: US/10/005,429
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/250,703
/ PRIOR FILING DATE: 2000-12-01
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 12
/ LENGTH: 122
/ TYPE: PRT
/ ORGANISM: Zea mays
US-11-195-459-12
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db       39 WCGPCR 44
```

```
RESULT 27
US-11-195-459-16
/ Sequence 16, Application US/11195459
/ Publication No. US20050278803A1
/ GENERAL INFORMATION:
/ APPLICANT: Sewalt, Vincent
/ APPLICANT: Hastings, Craig
/ APPLICANT: Weeley, Robert
/ APPLICANT: Hantke, Sabine
/ APPLICANT: Jung, Rudolf
/ APPLICANT: Everard, John
/ APPLICANT: Allen, Stephen
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PROTEINS
```

```
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 16
LENGTH: 122
TYPE: PRT
ORGANISM: Hordeum vulgare
US-11-195-459-16
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db      45 WCGPCR 50
```

```
RESULT 28
US-11-195-459-19
Sequence 19, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
```

```
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Mealey, Robert
APPLICANT: Hanke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 19
LENGTH: 122
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: "n" at position 9, 493, 537, 548, 581, and 584 can be an a, c, g,
US-11-195-459-19
```

```
Query Match          93.6%; Score 44; DB 7; Length 122;
Best Local Similarity 83.3%; Pred. No. 0.82;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db      39 WCGPCR 44
```

```
RESULT 29
US-11-195-459-10
Sequence 10, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
```

```
APPLICANT: Sewalt, Vincent
APPLICANT: Hastings, Craig
APPLICANT: Mealey, Robert
```

```
APPLICANT: Hanke, Sabine
APPLICANT: Jung, Rudolf
APPLICANT: Everard, John
APPLICANT: Allen, Stephen
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
FILE REFERENCE: 5718-119 (035718/241421)
CURRENT APPLICATION NUMBER: US/11/195,459
CURRENT FILING DATE: 2005-08-02
PRIOR APPLICATION NUMBER: US/10/005,429
PRIOR FILING DATE: 2001-12-03
PRIOR APPLICATION NUMBER: 60/250,703
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 10
LENGTH: 123
TYPE: PRT
ORGANISM: Zea mays
US-11-195-459-10
```

```
Query Match          93.6%; Score 44; DB 7; Length 123;
Best Local Similarity 83.3%; Pred. No. 0.83;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db      40 WCGPCR 45
```

```
RESULT 30
US-11-090-916-13
Sequence 13, Application US/11090916
Publication No. US20050260140A1
GENERAL INFORMATION:
APPLICANT: White, Carl W.
APPLICANT: del Val, Greg
APPLICANT: Lee, Rees
TITLE OF INVENTION: Mucolytic and Anti-Blastase Compounds and Methods of Use Thereof
FILE REFERENCE: 2879-98-1
CURRENT APPLICATION NUMBER: US/11/090,916
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: 60/409,960
PRIOR FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/462,082
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 10/660,118
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/556,516
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/650,865
PRIOR FILING DATE: 2005-02-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 13
LENGTH: 134
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-11-090-916-13
```

```
Query Match          93.6%; Score 44; DB 7; Length 134;
Best Local Similarity 83.3%; Pred. No. 0.88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCR 6
        |||||:
Db      59 WCGPCR 64
```

```
RESULT 31
US-11-195-459-8
Sequence 8, Application US/11195459
Publication No. US20050278803A1
GENERAL INFORMATION:
```

```
/ APPLICANT: Sewalt, Vincent
/ APPLICANT: Hastings, Craig
/ APPLICANT: Meelley, Robert
/ APPLICANT: Hancke, Sabine
/ APPLICANT: Jung, Rudolf
/ APPLICANT: Everard, John
/ APPLICANT: Allen, Stephen
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
/ FILE REFERENCE: 5718-119 (035718/241421)
/ CURRENT APPLICATION NUMBER: US/11/195,459
/ CURRENT FILING DATE: 2005-08-02
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/250,703
/ PRIOR FILING DATE: 2000-12-01
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8
/ LENGTH: 134
/ TYPE: PRT
/ ORGANISM: Zea mays
US-11-195-459-8
```

```
Query Match          93.6%; Score 44; DB 7; Length 134;
Best Local Similarity 83.3%; Pred. No. 0.88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
         |||||:
Db       54 WCGPCR 59
```

```
RESULT 32
US-11-090-916-14
/ Sequence 14, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Reese
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 14
/ LENGTH: 167
/ TYPE: PRT
/ ORGANISM: Zea mays
US-11-090-916-14
```

```
Query Match          93.6%; Score 44; DB 7; Length 167;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
         |||||:
Db       88 WCGPCR 93
```

```
RESULT 33
US-11-090-916-15
```

```
/ Sequence 15, Application US/11090916
/ Publication No. US20050260140A1
/ GENERAL INFORMATION:
/ APPLICANT: White, Carl W.
/ APPLICANT: del Val, Greg
/ APPLICANT: Lee, Reese
/ TITLE OF INVENTION: Mucolytic and Anti-Elastase Compounds and Methods of Use Thereof
/ FILE REFERENCE: 2879-98-1
/ CURRENT APPLICATION NUMBER: US/11/090,916
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: 60/409,960
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: 60/462,082
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: 10/660,118
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/556,516
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/650,865
/ PRIOR FILING DATE: 2005-02-07
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 15
/ LENGTH: 172
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-11-090-916-15
```

```
Query Match          93.6%; Score 44; DB 7; Length 172;
Best Local Similarity 83.3%; Pred. No. 1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
         |||||:
Db       94 WCGPCR 99
```

```
RESULT 34
US-10-467-657-8494
/ Sequence 8494, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIANNI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: Seqwin99, version 1.04
/ SEQ ID NO 8494
/ LENGTH: 209
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8494
```

```
Query Match          93.6%; Score 44; DB 6; Length 209;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 WCGPCK 6
         |||||:
Db       101 WCGPCR 106
```

```
RESULT 35
US-10-995-561-703
/ Sequence 703, Application US/10995561
```

```
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 703
/ LENGTH: 126
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-703

Query Match          91.5%; Score 43; DB 6; Length 126;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
Db      62 WCGPCQ 67

RESULT 36
US-10-131-826A-426
/ Sequence 426, Application US/10131826A
/ Publication No. US20050245730A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Beresini, Maureen
/ APPLICANT: Deforge, Laura
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Geritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Sherwood, Steven
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumes, Daniel
/ APPLICANT: Watanabe, Colin K
/ APPLICANT: Wood, William
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P3330R1C128
/ CURRENT APPLICATION NUMBER: US/10/131,826A
/ CURRENT FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: 60/049911
/ PRIOR FILING DATE: 1997-06-18
/ PRIOR APPLICATION NUMBER: 60/056974
/ PRIOR FILING DATE: 1997-08-26
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059115
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059117
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059122
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059184
/ PRIOR FILING DATE: 1997-09-17
/ PRIOR APPLICATION NUMBER: 60/059263
/ PRIOR FILING DATE: 1997-09-18
/ PRIOR APPLICATION NUMBER: 60/059352
/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
```

```
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 426
/ LENGTH: 747
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-426

Query Match          91.5%; Score 43; DB 6; Length 747;
Best Local Similarity 83.3%; Pred. No. 3.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPCK 6
Db      653 WCGPCQ 658

RESULT 37
US-10-467-962B-6
/ Sequence 6, Application US/10467962B
/ Publication No. US20050246784A1
/ GENERAL INFORMATION:
/ APPLICANT: Plesch, Gunnar
/ APPLICANT: Blau, Astrid
/ APPLICANT: Daeschner, Klaus
/ APPLICANT: Klein, Mathieu
/ TITLE OF INVENTION: Identification of Herbicidally Active Substances
/ FILE REFERENCE: 2000 857
/ CURRENT APPLICATION NUMBER: US/10/467,962B
/ CURRENT FILING DATE: 2003-08-14
/ PRIOR APPLICATION NUMBER: PCT/EP02/01466
/ PRIOR FILING DATE: 2002-02-13
/ NUMBER OF SEQ ID NOS: 109
/ SOFTWARE: PatentIn Vers. 2.0
/ SEQ ID NO 6
/ LENGTH: 183
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-467-962B-6

Query Match          89.4%; Score 42; DB 6; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 WCGPC 5
Db      105 WCGPC 109

RESULT 38
US-10-821-234-860
/ Sequence 860, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pt_seq_genes Version 1.0
/ SEQ ID NO 860
/ LENGTH: 176
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-860

Query Match          80.9%; Score 38; DB 6; Length 176;
```

Best Local Similarity 83.3%; Pred. No. 9;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 93 WCGHCK 98

RESULT 39

US-10-000-463-344
; Sequence 344, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhilwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 344
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-344

Query Match 80.9%; Score 38; DB 7; Length 269;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 53 WCGHCK 58

RESULT 40

US-10-878-556A-114
; Sequence 114, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 114
; LENGTH: 324

; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: tr_hum/g9bvh9
; DATABASE ENTRY DATE: 2001-06-01
US-10-878-556A-114

Query Match 80.9%; Score 38; DB 6; Length 324;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 108 WCGHCK 113

RESULT 41

US-10-523-503-70
; Sequence 70, Application US/10523503
; Publication No. US20060037102A1
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
; FILE REFERENCE: 16313-0236
; CURRENT APPLICATION NUMBER: US/10/523,503
; CURRENT FILING DATE: 2005-02-02
; PRIOR APPLICATION NUMBER: US 60/400,803
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 70
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-523-503-70

Query Match 80.9%; Score 38; DB 6; Length 361;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
|||
Db 51 WCGHCK 56

RESULT 42

US-10-878-556A-1
; Sequence 1, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (307)-(307)
; OTHER INFORMATION: Xaa is an undetermined amino acid residue
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: heaupd:006101-3-0
; DATABASE ENTRY DATE: 2003-02-16
US-10-878-556A-1

Query Match 80.9%; Score 38; DB 6; Length 414;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 236 WCGHCK 241

RESULT 43
 US-10-821-234-1282

; Sequence 1282, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1282

; LENGTH: 440
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1282

Query Match 80.9%; Score 38; DB 6; Length 440;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 189 WCGHCK 194

RESULT 44
 US-10-821-234-1287

; Sequence 1287, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1287

; LENGTH: 505
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1287

Query Match 80.9%; Score 38; DB 6; Length 505;
 Best Local Similarity 83.3%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 56 WCGHCK 61

RESULT 45
 US-10-821-234-1409
 ; Sequence 1409, Application US/10821234

; Publication No. US20050255114A1

; GENERAL INFORMATION:

; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom

; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234

; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pc_seq_genes Version 1.0
 ; SEQ ID NO 1409

; LENGTH: 645
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1409

Query Match 80.9%; Score 38; DB 6; Length 645;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 90 WCGHCK 95

RESULT 46
 US-10-895-064-976

; Sequence 976, Application US/10895064
 ; Publication No. US20060018923A1
 ; GENERAL INFORMATION:

; APPLICANT: PEIRIS, JOSEPH S.M.
 ; APPLICANT: YUEN, KWOK YUNG
 ; APPLICANT: POON, LIT MAN
 ; APPLICANT: GUAN, YI

; APPLICANT: CHAN, KWOK HUNG
 ; APPLICANT: NICHOLLS, JOHN M.
 ; APPLICANT: LEUNG, FREDERICK C.

; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT INFECTION AND USES
 ; FILE REFERENCE: V0690, 0031
 ; CURRENT APPLICATION NUMBER: US/10/895,064

; CURRENT FILING DATE: 2004-07-21
 ; NUMBER OF SEQ ID NOS: 2918
 ; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 976
 ; LENGTH: 32
 ; TYPE: PRT

; ORGANISM: Corononavirius-HKU1
 US-10-895-064-976

Query Match 76.6%; Score 36; DB 6; Length 32;
 Best Local Similarity 66.7%; Pred. No. 6.1;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WCGPCK 6
 |||||
 DB 9 WCGSCR 14

RESULT 47
 US-11-129-741-976

; Sequence 976, Application US/11129741
 ; Publication No. US20060034853A1
 ; GENERAL INFORMATION:

; APPLICANT: YUEN, KWOK YUNG
 ; APPLICANT: WOO, CHIU YAT PATRICK
 ; APPLICANT: LAU, KAR PUT SUSANNA

; APPLICANT: CHAN, KWOK HUNG
 ; APPLICANT: POON, LIT MAN

```

; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 976
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Corononavirub-HKU1
US-11-129-741-976

```

```

Query Match          76.6%; Score 36; DB 7; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 9 WCGSCR 14

```

RESULT 48

```

US-11-129-741-3972
; Sequence 3972, Application US/11129741
; Publication No. US20060034853A1
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: MOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT WAR
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3972
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Corononavirub-HKU1
US-11-129-741-3972

```

```

Query Match          76.6%; Score 36; DB 7; Length 32;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 WCGPCK 6
Db 9 WCGSCR 14

```

RESULT 49

```

US-10-689-742-19
; Sequence 19, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: JACOBS, KENNETH
; APPLICANT: MCCOY, JOHN M
; APPLICANT: LAVAILLE, EDWARD R
; APPLICANT: RACIE, LISA A
; APPLICANT: EVANS, CHERYL
; APPLICANT: MERBERG, DAVID

```

```

; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-19

```

```

Query Match          76.6%; Score 36; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPCK 6
Db 32 CGPCK 36

```

RESULT 50

```

US-11-106-796-10
; Sequence 10, Application US/11106796
; Publication No. US20050282191A1
; GENERAL INFORMATION:
; APPLICANT: SUTOVSKY, PETER
; APPLICANT: MIRANDA-VIZIETE, ANTONIO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR EVALUATION OF FERTILITY
; FILE REFERENCE: UMO:033US
; CURRENT APPLICATION NUMBER: US/11/106,796
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: 60/562,526
; PRIOR FILING DATE: 2004-04-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-796-10

```

```

Query Match          76.6%; Score 36; DB 7; Length 127;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 CGPCK 6
Db 32 CGPCK 36

```

RESULT 51

```

US-11-195-459-2
; Sequence 2, Application US/11195459
; Publication No. US20050278803A1
; GENERAL INFORMATION:
; APPLICANT: Sewalt, Vincent
; APPLICANT: Hastings, Craig
; APPLICANT: Mealey, Robert
; APPLICANT: Hantke, Sabine
; APPLICANT: Jung, Rudolf
; APPLICANT: Everard, John
; APPLICANT: Allen, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PR
; FILE REFERENCE: 5718-119 (035718/241421)
; CURRENT APPLICATION NUMBER: US/11/195,459
; CURRENT FILING DATE: 2005-08-02
; PRIOR APPLICATION NUMBER: US/10/005,429
; PRIOR FILING DATE: 2001-12-03

```

;; PRIOR APPLICATION NUMBER: 60/250,703
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 2
;; LENGTH: 128
;; TYPE: PRF
;; ORGANISM: Zea mays
US-11-195-459-2

Query Match 76.6%; Score 36; DB 7; Length 128;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 52 WCGPCK 57

RESULT 52
US-11-195-459-4
;; Sequence 4, Application US/11195459
;; Publication No. US20050278803A1
;; GENERAL INFORMATION:
;; APPLICANT: Sewalt, Vincent
;; APPLICANT: Hastings, Craig
;; APPLICANT: Mealey, Robert
;; APPLICANT: Hantke, Sabine
;; APPLICANT: Jung, Rudolf
;; APPLICANT: Everard, John
;; APPLICANT: Allen, Stephen
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ALTERING THE DISULFIDE STATUS OF PRO
;; FILE REFERENCE: 5718-119 (035718/241421)
;; CURRENT FILING DATE: 2005-08-02
;; PRIOR APPLICATION NUMBER: US/10/005,429
;; PRIOR FILING DATE: 2001-12-03
;; PRIOR APPLICATION NUMBER: 60/250,703
;; PRIOR FILING DATE: 2000-12-01
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 4
;; LENGTH: 128
;; TYPE: PRF
;; ORGANISM: Zea mays
US-11-195-459-4

Query Match 76.6%; Score 36; DB 7; Length 128;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 52 WCGPCK 57

RESULT 53
US-11-072-512-2145
;; Sequence 2145, Application US/11072512
;; Publication No. US20060029945A1
;; GENERAL INFORMATION:
;; APPLICANT: ISOGAI, TAKAO
;; APPLICANT: SUGIYAMA, TOMOYASU
;; APPLICANT: OTSUKI, TETSUJI
;; APPLICANT: WAKAMATSU, AI
;; APPLICANT: SATO, HIROYUKI
;; APPLICANT: ISHII, SHIZUKO
;; APPLICANT: YAMAMOTO, JUN-ICHI
;; APPLICANT: ISONO, YUUKO
;; APPLICANT: HIO, YURI
;; APPLICANT: OTSUKA, KAORU
;; APPLICANT: NAGAI, KEIICHI
;; APPLICANT: IRIE, RYOTARO

;; APPLICANT: TAMECHIKA, ICHIRO
;; APPLICANT: SEKI, NAOHITO
;; APPLICANT: YOSHIKAWA, TSUTOMU
;; APPLICANT: OTSUKA, MOTOTYUKI
;; APPLICANT: NAGAHARI, KENJI
;; APPLICANT: MASUHO, YASUHIKO
;; TITLE OF INVENTION: Novel full length cDNA
;; FILE REFERENCE: 084335-0191
;; CURRENT APPLICATION NUMBER: US/11/072,512
;; CURRENT FILING DATE: 2005-03-07
;; PRIOR APPLICATION NUMBER: US 60/350,978
;; PRIOR FILING DATE: 2002-01-25
;; PRIOR APPLICATION NUMBER: JP 2001-379298
;; PRIOR FILING DATE: 2001-11-05
;; NUMBER OF SEQ ID NOS: 4096
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 2145
;; LENGTH: 129
;; TYPE: PRF
;; ORGANISM: Homo sapiens
US-11-072-512-2145

Query Match 76.6%; Score 36; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
DB 74 CGPCK 78

RESULT 54
US-10-510-386-126
;; Sequence 126, Application US/10510386
;; Publication No. US2005024922A1
;; GENERAL INFORMATION:
;; APPLICANT: Andersen, Jens Tonne
;; APPLICANT: Clausen, Ib Groth
;; APPLICANT: Jorgensen, Steen Troels
;; APPLICANT: Olsen, Peter Bjarke
;; APPLICANT: Rasmussen, Michael Dolberg
;; TITLE OF INVENTION: Improved Bacillus Host Cell
;; FILE REFERENCE: 10294.204-US
;; CURRENT APPLICATION NUMBER: US/10/510,386
;; CURRENT FILING DATE: 2004-10-04
;; NUMBER OF SEQ ID NOS: 248
;; SOFTWARE: PatentIn version 3.3
;; SEQ ID NO: 126
;; LENGTH: 163
;; TYPE: PRF
;; ORGANISM: Bacillus licheniformis
US-10-510-386-126

Query Match 76.6%; Score 36; DB 6; Length 163;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WCGPCK 6
DB 62 WCGPCK 67

RESULT 55
US-11-054-281-58
;; Sequence 58, Application US/11054281
;; Publication No. US20060013813A1
;; GENERAL INFORMATION:
;; APPLICANT: Mezes et al.
;; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;; FILE REFERENCE: 21402-240CIP
;; CURRENT APPLICATION NUMBER: US/11/054,281
;; CURRENT FILING DATE: 2005-02-08
;; PRIOR APPLICATION NUMBER: 60/261,014

```
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,018
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/318,410
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/261,013
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,026
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,029
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/313,170
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 10/044,564
/ PRIOR FILING DATE: 2002-01-11
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 58
/ LENGTH: 354
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-054-281-58
```

```
Query Match          76.6%; Score 36; DB 7; Length 354;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      144 CGPCK 148
```

```
RESULT 56
US-11-054-281-59
/ Sequence 59, Application US/11054281
/ Publication No. US20060013813A1
/ GENERAL INFORMATION:
/ APPLICANT: Mezes et al.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-240CIP
/ CURRENT APPLICATION NUMBER: US/11/054,281
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: 60/261,014
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,018
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/318,410
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/261,013
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,026
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/261,029
/ PRIOR FILING DATE: 2001-01-11
/ PRIOR APPLICATION NUMBER: 60/313,170
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: 10/044,564
/ PRIOR FILING DATE: 2002-01-11
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 59
/ LENGTH: 373
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-11-054-281-59
```

```
Query Match          76.6%; Score 36; DB 7; Length 373;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      163 CGPCK 167
```

```
RESULT 57
US-11-090-439-52
/ Sequence 52, Application US/11090439
/ Publication No. US2005026642A1
/ GENERAL INFORMATION:
/ APPLICANT: Squillace, Rachel
/ APPLICANT: Weiner, Michael P.
/ TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
/ FILE REFERENCE: 24318-502
/ CURRENT APPLICATION NUMBER: US/11/090,439
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: 60/556,344
/ PRIOR FILING DATE: 2004-03-25
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 380
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-439-52
```

```
Query Match          76.6%; Score 36; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      170 CGPCK 174
```

```
RESULT 58
US-11-090-439-54
/ Sequence 54, Application US/11090439
/ Publication No. US2005026642A1
/ GENERAL INFORMATION:
/ APPLICANT: Squillace, Rachel
/ APPLICANT: Weiner, Michael P.
/ TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
/ FILE REFERENCE: 24318-502
/ CURRENT APPLICATION NUMBER: US/11/090,439
/ CURRENT FILING DATE: 2005-03-25
/ PRIOR APPLICATION NUMBER: 60/556,344
/ PRIOR FILING DATE: 2004-03-25
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 54
/ LENGTH: 380
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-090-439-54
```

```
Query Match          76.6%; Score 36; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
        |||||
Db      170 CGPCK 174
```

```
RESULT 59
US-11-054-281-60
/ Sequence 60, Application US/11054281
/ Publication No. US20060013813A1
/ GENERAL INFORMATION:
/ APPLICANT: Mezes et al.
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-240CIP
/ CURRENT APPLICATION NUMBER: US/11/054,281
```

```

; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 380
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-054-281-60

Query Match
Best Local Similarity 76.6%; Score 36; DB 7; Length 380;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 CGPCK 6
   |||||
Db 170 CGPCK 174

RESULT 60
US-10-763-712A-10
; Sequence 10, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 572
; TYPE: prt
; ORGANISM: Clostridium perfringens
US-10-763-712A-10

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 CGPCK 6
   |||||
Db 98 CGPCK 102

RESULT 61
US-10-763-712A-11
; Sequence 11, Application US/10763712A
; Publication No. US20050266541A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 572
; TYPE: prt
; ORGANISM: Clostridium perfringens
US-10-763-712A-11

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 CGPCK 6
   |||||
Db 98 CGPCK 102

RESULT 62
US-10-763-712A-37
; Sequence 37, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 572
; TYPE: prt
; ORGANISM: Clostridium perfringens
US-10-763-712A-37

Query Match
Best Local Similarity 76.6%; Score 36; DB 6; Length 572;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY 2 CGPCK 6
   |||||
Db 98 CGPCK 102

RESULT 63
US-10-763-712A-109
; Sequence 109, Application US/10763712A
; Publication No. US20050266541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
```

```

; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 109
; LENGTH: 572
; TYPE: PRT
; ORGANISM: C. perfringens
US-10-763-712A-109
```

```

Query Match          76.6%; Score 36; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
      |||||
Db      98 CGPCK 102
```

```

RESULT 64
US-10-763-712A-110
; Sequence 110, Application US/10763712A
; Publication No. US2005026541A1
; GENERAL INFORMATION:
; APPLICANT: Solazyme, Inc.
; APPLICANT: Dillon, Harrison F.
; TITLE OF INVENTION: Methods and Compositions for Evolving Microbial Hydrogen
; FILE REFERENCE: H2042101-CIP
; CURRENT APPLICATION NUMBER: US/10/763,712A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: US 10/287,750
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: US 10/411,910
; PRIOR FILING DATE: 2003-04-12
; PRIOR APPLICATION NUMBER: US 60/500,032
; PRIOR FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 110
; LENGTH: 572
; TYPE: PRT
; ORGANISM: C. perfringens
US-10-763-712A-110
```

```

Query Match          76.6%; Score 36; DB 6; Length 572;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
      |||||
Db      98 CGPCK 102
```

```

RESULT 65
US-10-055-877-255
; Sequence 255, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchenev, Velizar
; APPLICANT: Zhong, Mei
```

```

; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zehrusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Paturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eissen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shinkels, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 255
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-055-877-255
```

```

Query Match          76.6%; Score 36; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 CGPCK 6
      |||||
Db      247 CGPCK 251
```

```

RESULT 66
US-10-055-877-254
; Sequence 254, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: Decristofaro, Marc
; APPLICANT: Padigar, Muralidhara
```

APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Renée
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
PRIOR FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 254
LENGTH: 660
TYPE: PRT
ORGANISM: Homo sapiens
US-10-055-877-254

Query Match 76.6%; Score 36; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
DB 249 CGPCK 253

RESULT 67
US-10-831-997-4
Sequence 4, Application US/10831997
Publication No. US2005024834A1

GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolik, Stacey
APPLICANT: Daley, George Q.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825,1027-001
CURRENT APPLICATION NUMBER: US/10/831,997
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: US/09/657,472
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 961
TYPE: PRT
ORGANISM: Homo sapiens
US-10-831-997-4

Query Match 76.6%; Score 36; DB 6; Length 961;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
DB 403 CGPCK 407

RESULT 68
US-10-055-877-252
Sequence 252, Application US/10055877
Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: Decristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
APPLICANT: Tchernev, Velizar
APPLICANT: Zhong, Mei
APPLICANT: Anderson, David
APPLICANT: Ballinger, Robert
APPLICANT: Gerlach, Valerie
APPLICANT: Spytek, Kimberly
APPLICANT: Ratelli, Luca
APPLICANT: Kekuda, Ramesh
APPLICANT: Guo, Xiaojia
APPLICANT: Zernusen, Bryan
APPLICANT: Andrew, David
APPLICANT: Mezes, Peter
APPLICANT: Paturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Eisen, Andrew
APPLICANT: Wolenc, Adam
APPLICANT: Baumgartner, Jason
APPLICANT: Shinkets, Richard
APPLICANT: Gusev, Vladimir
APPLICANT: Vernet, Corine
APPLICANT: Taupier Jr., Raymond
APPLICANT: Pena, Carol
APPLICANT: Shenoy, Suresh
APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Renée
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877

;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 252
;; LENGTH: 1857
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-252

Query Match 76.6%; Score 36; DB 6; Length 1857;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
Db 65 CGPCK 69

RESULT 69
US-10-055-877-73
;; Sequence 73, Application US/10055877
;; Publication No. US20050288241A1
;; GENERAL INFORMATION:
;; APPLICANT: Decristofaro, Marc
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Miller, Charles
;; APPLICANT: Tchervnev, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Ratelli, Luca
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Zethusen, Bryan
;; APPLICANT: Andrews, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patuturajan, Meera
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Eissen, Andrew
;; APPLICANT: Wolenc, Adam
;; APPLICANT: Baumgartner, Jason
;; APPLICANT: Shimkets, Richard
;; APPLICANT: Gusev, Vladimir
;; APPLICANT: Vermet, Corine
;; APPLICANT: Taupier Jr., Raymond
;; APPLICANT: Pena, Carol
;; APPLICANT: Shenoy, Suresh
;; APPLICANT: Li, Li
;; APPLICANT: Casman, Stacie
;; APPLICANT: Boldog, Ferenc

;; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
;; FILE REFERENCE: 21402-251
;; CURRENT APPLICATION NUMBER: US/10/055,877
;; CURRENT FILING DATE: 2002-01-22
;; PRIOR APPLICATION NUMBER: 60/262,892
;; PRIOR FILING DATE: 2001-01-19
;; PRIOR APPLICATION NUMBER: 60/263,598
;; PRIOR FILING DATE: 2001-01-23
;; PRIOR APPLICATION NUMBER: 60/263,799
;; PRIOR FILING DATE: 2001-01-24
;; PRIOR APPLICATION NUMBER: 60/264,117
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,139
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/264,478
;; PRIOR FILING DATE: 2001-01-26
;; PRIOR APPLICATION NUMBER: 60/263,351
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: 60/272,870
;; PRIOR FILING DATE: 2001-03-02
;; PRIOR APPLICATION NUMBER: 60/275,990
;; PRIOR FILING DATE: 2001-03-14
;; PRIOR APPLICATION NUMBER: 60/275,927
;; PRIOR FILING DATE: 2001-03-14
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 512
;; SOFTWARE: Patentin Ver. 2.1
;; SEQ ID NO 73
;; LENGTH: 2084
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-055-877-73

Query Match 76.6%; Score 36; DB 6; Length 2084;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
Db 317 CGPCK 321

RESULT 70
US-10-055-877-253
;; Sequence 253, Application US/10055877
;; Publication No. US20050288241A1
;; GENERAL INFORMATION:
;; APPLICANT: Decristofaro, Marc
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Miller, Charles
;; APPLICANT: Tchervnev, Velizar
;; APPLICANT: Zhong, Mei
;; APPLICANT: Anderson, David
;; APPLICANT: Ballinger, Robert
;; APPLICANT: Gerlach, Valerie
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Ratelli, Luca
;; APPLICANT: Kekuda, Ramesh
;; APPLICANT: Zethusen, Bryan
;; APPLICANT: Andrews, David
;; APPLICANT: Mezes, Peter
;; APPLICANT: Patuturajan, Meera
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Eissen, Andrew
;; APPLICANT: Wolenc, Adam
;; APPLICANT: Baumgartner, Jason
;; APPLICANT: Shimkets, Richard
;; APPLICANT: Gusev, Vladimir
;; APPLICANT: Vermet, Corine
;; APPLICANT: Taupier Jr., Raymond
;; APPLICANT: Pena, Carol
;; APPLICANT: Shenoy, Suresh

APPLICANT: Li, Li
APPLICANT: Casman, Stacie
APPLICANT: Boldog, Ferenc
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: US/10/055,877
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: 60/262,892
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263,598
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: 60/263,799
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,139
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,478
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/263,351
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,870
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/275,990
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/275,927
PRIOR FILING DATE: 2001-03-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 512
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 253
LENGTH: 2098
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-055-877-253

Query Match 76.6%; Score 36; DB 6; Length 2098;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGPCK 6
|||
Db 267 CGPCK 271

Search completed: February 23, 2006, 00:48:12
Job time : 15.5 secs

This Page Blank (usgpl)